

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:20:17 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-3  
Perfect score: 38  
Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

11 number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_16:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-unclassified:\*  
13: sp-vertebrate:\*  
14: sp-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	86.8	517	14 Q9DSP4	Q9dsp4 saint croix
2	32	84.2	174	10 Q9M2H1	Q9m2h1 arabidopsis
3	32	84.2	328	2 Q9X5G8	Q9x5g8 streptomyce
4	32	84.2	353	5 Q21051	Q21051 caenorhabdi
5	32	84.2	806	13 Q9DDL2	Q9ddl2 brachydanio
6	31	81.6	95	2 Q911X2	Q911x2 pseudomonas
7	31	81.6	98	14 Q64981	Q64981 artichoke 1
8	31	81.6	119	13 Q90253	Q90253 bombina ori
9	31	81.6	183	2 Q9RZ51	Q9rz51 deinococcus
10	31	81.6	216	11 Q9JM34	Q9jfm34 mus musculus
11	31	81.6	232	3 Q9UVE4	Q9uve4 zygosaccchar
12	31	81.6	236	2 Q85726	Q85726 streptomyce
13	31	81.6	256	3 Q9P6Y1	Q9p6y1 neurospora
14	31	81.6	266	5 Q9VZF7	Q9vzf7 drosophila
15	31	81.6	273	8 Q9TJQ5	Q9tjq5 prototheca
16	31	81.6	309	5 Q27106	Q27106 trichomonas
17	31	81.6	325	2 Q9PAR1	Q9par1 xyella fas
18	31	81.6	357	10 Q65366	Q65366 antirrhinum
19	31	81.6	359	10 Q9FUK9	Q9fuk9 pisum sativ

20 31 81.6 675 10 Q9S9V7  
21 31 81.6 696 5 Q9VCU2  
22 31 81.6 703 10 Q9LYH3  
23 31 81.6 1273 4 Q9NU68  
24 31 81.6 1275 4 Q15057  
25 30 78.9 123 13 Q9PS30  
26 30 78.9 132 2 Q9K3V3  
27 30 78.9 157 13 Q918Z9  
28 30 78.9 170 2 P74711  
29 30 78.9 224 4 Q9UI28  
30 30 78.9 252 1 Q26248  
31 30 78.9 252 10 Q9FI20  
32 30 78.9 276 2 Q9LIQ5  
33 30 78.9 283 2 Q9PCE4  
34 30 78.9 291 14 Q72694  
35 30 78.9 311 2 Q9PAE5  
36 30 78.9 318 2 Q9I066  
37 30 78.9 325 2 Q9KZG2  
38 30 78.9 375 5 Q9TVM5  
39 30 78.9 453 10 Q9M4A9  
40 30 78.9 520 10 Q65815  
41 30 78.9 691 2 Q55726  
42 30 78.9 700 2 Q07711  
43 30 78.9 719 14 P87541  
44 30 78.9 721 2 Q9K7H4  
45 30 78.9 858 5 Q17647

#### ALIGNMENTS

RESULT 1  
Q9DSP4 PRELIMINARY; PRT; 517 AA.  
AC Q9DSP4;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE NS1.  
OS Saint Croix river virus.  
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.  
OX NCBI\_TaxID=104581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Attoui H., De Micco P., de Lamballerie X.;  
RT "Complete nucleotide sequence of Saint Croix river virus".  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF145403; AAG34262.1; -.  
SQ SEQUENCE 517 AA; 58030 MW; 010A543FB2A1B1A CRG64;

Query Match 86.8%; Score 33; DB 14; Length 517;  
Best Local Similarity 71.4%; Pred. No. 51;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
Db 500 QWALAH 506  
|||: ||

RESULT 2  
Q9M2H1 PRELIMINARY; PRT; 174 AA.  
ID Q9M2H1;  
AC Q9M2H1;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE HYPOTHETICAL 19.2 KDA PROTEIN.  
GN FL4P22.40.

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eury.; II;  
OC Brassicales; Brassicaceae; Arabidopsis.

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Queier F., Salanoubat M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137082; CAB68183.1; -.
KW Hypothetical protein.
SQ SEQUENCE 174 AA; 19189 MW; 4C27267C5E3B4DB CRC64;

Query Match      84.2%; Score 32; DB 10; Length 174;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 QWAVXHL 8
:|||||
47 EWAVDHL 53

RESULT 3
ID Q9X5G8 PRELIMINARY; PRT; 328 AA.
AC Q9X5G8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE DEACYLCEPHALOSPORIN C ACETYLTRANSFERASE.
GN CVM4.
OS Streptomyces clavuligerus
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1901;
RN [1]
RP SEQUENCE FROM N.A.
RA Moshier R.H., Paraskar A.S., Anders C., Barton B., Jensen S.E.;
RX MEDLINE=99240369; PubMed=10223939;
RL "Genes specific for the biosynthesis of clavam metabolites antipodal
RT to clavulanic acid are clustered with the gene for clavaminate
RT synthase 1 in Streptomyces clavuligerus."
RL Antimicrob. Agents Chemother. 43:1215-1224(1999).
CC -!- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.
DR EMBL; AF124929; AAD30471.1; -.
KW InterPro; IPR000073; -.
KW Pfam; PF00561; abhydrolase; 1.
KW Transferase; Porin.
SQ SEQUENCE 328 AA; 34642 MW; 4CBC78DAD5215034 CRC64;

Query Match      84.2%; Score 32; DB 2; Length 328;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 QWAVXH 7
:|||||
133 QWAVSH 138

RESULT 4
ID Q21051 PRELIMINARY; PRT; 353 AA.
AC Q21051;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE COSMID F59G1.
GN F59G1.4.
OS Caenorhabditis elegans.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Latreille P.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53332; AAC71158.1; -.
SQ SEQUENCE 353 AA; 40061 MW; 7961772B498E3052 CRC64;

Query Match      84.2%; Score 32; DB 5; Length 353;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 QWAVXHL 8
:|||||
201 EWAVNHL 207

RESULT 5
ID Q9DDL2 PRELIMINARY; PRT; 806 AA.
AC Q9DDL2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARACASPASE.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11090634;
RA Uren A.G., O'Rourke K., Aravind L., Pisabarro M.T., Seshagiri S.,
RA Koonin E.V., Dixit V.M.;
RT "Identification of Paracaspases and Metacaspases. Two Ancient Families
RT of Caspase-like Proteins, One of which Plays a Key Role in MALT
RT Lymphoma."
RL Mol. Cell 6:961-967(2000).
DR EMBL; AF316598; AAC38590.1; -.
SQ SEQUENCE 806 AA; 90754 MW; 589A8BC2013B0A51 CRC64;

Query Match      84.2%; Score 32; DB 13; Length 806;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 2 QWAVXHL 8  
|||||  
DB 559 OWAIAHV 565

RESULT 6  
Q911X2 PRELIMINARY; PRT; 95 AA.  
ID Q911X2  
AC Q911X2  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE HYPOTHETICAL PROTEIN PA2143.  
GN PA2143.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
STRAIN=PA01;  
MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
RT opportunistic pathogen."  
RL Nature 406:959-964(2000).  
DR EMBL; AE004641; AAG0531.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 95 AA; 10821 MW; 5723E5D0CD08841F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 95;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
|||||  
DB 63 QWVHHL 69

RESULT 7  
Q64981 PRELIMINARY; PRT; 98 AA.  
ID Q64981  
AC Q64981  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE MRNA UNKNOWN FUNCTION (523BP) (FRAGMENT).  
OS Artichoke latent potyvirus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
OX NCBI\_TaxID=46076;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Grieco F.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X87255; CAA60708.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 98 AA; 11570 MW; C4A6316685E31078 CRC64;

Query Match 81.6%; Score 31; DB 14; Length 98;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
DB 89 QWAVEH 94

RESULT 8  
Q90253 PRELIMINARY; PRT; 119 AA.  
ID Q90253  
AC Q90253  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PHE-13 BOMBESIN PREPROHORMONE.  
OS Bombina orientalis (Oriental fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8346;  
RN [1]  
RP SEQUENCE FROM N.A.  
MEDLINE=96205965; PubMed=8631814;  
RA Nagalla S.R., Barry B.J., Falick A.M., Gibson B.W., Taylor J.,  
RA Dong J.Z., Spindel E.R.;  
RT "There are three distinct forms of bombesin. Identification of  
RT [leu13]bombesin, [phe13]bombesin, and [ser3,Arg10,Phe13]bombesin in  
RT the frog Bombina orientalis."  
RL J. Biol. Chem. 271:7731-7737(1996).  
DR EMBL; U49450; AAC59784.1; -.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
FT CHAIN 45 59 PHE-13 BOMBESIN.  
SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 81.6%; Score 31; DB 13; Length 119;  
Best Local Similarity 83.3%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
DB 51 QWAVGH 56

RESULT 9  
Q9RZ51 PRELIMINARY; PRT; 183 AA.  
ID Q9RZ51  
AC Q9RZ51  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 20.5 KDA PROTEIN.  
GN DRA0103.  
OS Deinococcus radiodurans.  
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.  
OX NCBI\_TaxID=1299;  
RN [1]  
RP SEQUENCE FROM N.A.  
STRAIN=R1;  
MEDLINE=20036896; PubMed=10567266;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus  
RT radiodurans R1."  
RL Science 286:1571-1577(1999).  
DR EMBL; AE001862; AAF12366.1; -.  
DR TIGR; DRA0103; -.  
KW Hypothetical protein.  
SQ SEQUENCE 183 AA; 20468 MW; 6EEAB3B483DC1BB7 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;

```
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
Db 49 RWAFFHL 55

RESULT 10
Q9JM34 PRELIMINARY; PRT; 216 AA.
AC Q9JM34;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
OS Mus musculus domesticus (western European house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10092;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20183981; PubMed-10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates.";
Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
RL EMBL: AF073957; AAD43416.1; -.
DR InterPro: IPR000276; -.
DR Pfam: PF00001; 7tmL1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 24097 MW; B2732A1870584D47 CRC64;

Query Match 81.6%; Score 31; DB 11; Length 216;
Best Local Similarity 83.3%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHL 8
Db 82 WAVSHL 87

RESULT 11
Q9JVE4 PRELIMINARY; PRT; 232 AA.
AC Q9JVE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 26.4 KDA PROTEIN.
OS Zygosaccharomyces rouxii (Candida mogii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
OX NCBI_TaxID=4956;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 732;
RA Sychrova H., Braun V., Potier S., Souciet J.L.;
RT "Genomic organization of Pichia sorbitophila and Zygosaccharomyces
RT rouxii genomes: comparison with Saccharomyces cerevisiae.";
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: Y18560; CAB62288.1; -.
DR InterPro: IPR001601; -.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 232;
Best Local Similarity 71.4%; Pred. No. 58;

QY 2 QWAVXHL 8
Db 170 KWAVDHL 176

Query Match 81.6%; Score 31; DB 2; Length 236;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
Db 140 QWCYVHL 146

RESULT 12
O85726 PRELIMINARY; PRT; 236 AA.
ID O85726;
AC O85726;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CEPHALOSPORIN HYDROXYLASE CMCI.
GN CMCI.
OS Streptomyces clavuligerus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1901;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=NRRL 3585;
RA Alexander D.C., Jensen S.E.;
RT "Investigation of the streptomyces clavuligerus cephamycin C gene
RT cluster and its regulation by the Ccar protein.";
J. Bacteriol. 180:4068-4079(1998).
RL EMBL: AF073896; AAC32491.1; -.
DR EMBL: AF073896; AAC32491.1; -.
SQ SEQUENCE 236 AA; 27584 MW; FDL1F1B650AF8070 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 256;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
Db 170 KWAVDHL 176

RESULT 13
Q9P6Y1 PRELIMINARY; PRT; 256 AA.
ID Q9P6Y1;
AC Q9P6Y1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN 13E11.350.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL353820; CAB88603.1; -.
DR InterPro: IPR001601; -.
SQ SEQUENCE 256 AA; 27789 MW; 5251FBC58B6BDD99 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 256;
Best Local Similarity 71.4%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
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Db 162 QMCVGH 168  
||| |||

## RESULT 14

Q9VZF7 PRELIMINARY; PRT; 266 AA.  
AC Q9VZF7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE IMPL2 PROTEIN.  
GN IMPL2 OR CG15009.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Fostler C., Gabrielista A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL; AE003480; AAF47866.2; -.  
DR HSSP; P56276; ITLK.  
DR FlyBase; FBgn0001257; ImpL2.  
DR InterPro; IPR003006; -.  
DR Pfam; PF00047; 19; 4.  
SQ SEQUENCE 266 AA; 29823 MW; FC97694BDF8F33 CRC64;

Query Match 81.6%; Score 31; DB 5; Length 266;  
Best Local Similarity 71.4%; Pred. No. 66;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| |||  
Db 90 QWVGH 96  
RESULT 15  
Q9TJQ5 PRELIMINARY; PRT; 273 AA.  
AC Q9TJQ5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAR-2001 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE 50S RIBOSOMAL PROTEIN L2.  
GN RPL2.  
OS Prototheca wickerhamii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorales,  
OC Chlorrellaceae; Prototheca.  
OX NCBI\_TaxID=3111;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=263-11;  
RA Knauf U., Hachtel W.;  
RT "A 22 kb fragment of the 53 kb plastid genome of the colourless alga  
Prototheca wickerhamii containing atp-, rpl-, rps-, rrn-, and trp-  
genes.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ245645; CAB53116.1; -.  
DR HSSP; P04257; IRL2.  
DR InterPro; IPR001412; -.  
DR InterPro; IPR002171; -.  
DR InterPro; IPR002222; -.  
DR Pfam; PF00181; Ribosomal\_L2; 1.  
DR ProDom; PD001012; 1.  
DR PROSITE; PS00178; AA-TRNA-LIGASE\_I; UNKNOWN\_1.  
DR PROSITE; PS00467; RIBOSOMAL\_L2; 1.  
KW Ribosomal protein; Chloroplast.  
SQ SEQUENCE 273 AA; 29952 MW; EE05656E77830BD4 CRC64;

Query Match 81.6%; Score 31; DB 8; Length 273;  
Best Local Similarity 71.4%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QWAVXHL 8  
||| |||  
Db 170 QWATLHL 176

Search completed: October 25, 2001, 11:27:41  
Job time: 444 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:19:47 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-3

Perfect score: 38

Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Minimum number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	14	1 BSTDY	bombesin - fire-be
2	35	92.1	107	1 BSTDY	bombesin precursor
3	35	92.1	119	2 A39261	bombesin precursor
4	32	84.2	174	2 T45665	hypothetical prote
5	32	84.2	353	2 T34312	hypothetical prote
6	31	81.6	9	2 S07204	litorin I - Austr
7	31	81.6	13	2 A60409	bombesin-like pept
8	31	81.6	82	2 B28945	ranatensin precurs
9	31	81.6	95	2 H83378	hypothetical prote
10	31	81.6	183	2 A75605	hypothetical prote
11	31	81.6	232	2 S32963	hypothetical prote
12	31	81.6	256	2 T48787	hypothetical prote
13	31	81.6	309	2 S41427	cysteine proteinase
14	31	81.6	325	2 F82558	lipopolysaccharide
15	31	81.6	357	2 T17027	MYB-related transc
16	31	81.6	360	1 A25732	inhibin alpha chai
17	31	81.6	364	1 WFPGA	inhibin alpha chai
18	31	81.6	366	1 JC1106	inhibin alpha chai
19	31	81.6	366	1 A40056	inhibin alpha chai
20	31	81.6	703	2 T48559	probable receptor-
21	31	81.6	769	2 S36657	SWI6 protein - yea
22	30	78.9	10	2 PQ0177	neuromedin C - lau
23	30	78.9	10	2 A60647	neuromedin C - bov
24	30	78.9	25	2 S06263	gastrin-releasing
25	30	78.9	27	1 RHPGA	gastrin-releasing
26	30	78.9	27	1 RHGPGA	gastrin-releasing
27	30	78.9	27	1 RHCHA	gastrin-releasing
28	30	78.9	120	2 I47201	bombesinlike pepti
29	30	78.9	134	2 I47010	gastrin-releasing

30	30	78.9	138	2 A26182	gastrin-releasing
31	30	78.9	147	2 A40922	gastrin-releasing
32	30	78.9	148	1 B26182	gastrin-releasing
33	30	78.9	155	2 A42437	gastrin-releasing
34	30	78.9	170	2 S76918	hypothetical prote
35	30	78.9	250	2 T07902	MADS box protein
36	30	78.9	252	2 A69060	conserved hypothet
37	30	78.9	283	2 B82631	hypothetical prote
38	30	78.9	311	2 H82541	conserved hypothet
39	30	78.9	318	2 H83298	conserved hypothet
40	30	78.9	366	1 A24248	inhibin alpha chai
41	30	78.9	375	2 T43049	hypothetical prote
42	30	78.9	453	2 T50645	glucan endo-1,3-be
43	30	78.9	458	2 S58816	GTPase-activating
44	30	78.9	505	2 T10896	cytochrome P450 (E
45	30	78.9	691	1 S76521	hypothetical prote

ALIGNMENTS

RESULT 1

BSTD

bombesin - fire-bellied toad

C:Species: Bombina bombina (fire-bellied toad)

C>Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998

C:Accession: A01564

R:Anastasi, A.; Erspamer, V.; Bucci, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A:Title: Isolation and amino acid sequences of alytesin and bombesin, two anal.

A:Reference number: A01564; MUID:72163516

A:Accession: A01564

A:Molecule type: protein

A:Residues: 1-14 <ANA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyr.

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 92.1%; Score 35; DB 1; Length 14;

Best Local Similarity 85.7%; Pred. No. 0.33;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 2 QWAVXHL 8

|||||

Db 7 QWAVGHL 13

RESULT 2

BSTDY

bombesin precursor - yellow-bellied toad

C:Species: Bombina variegata (yellow-bellied toad)

C>Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 08-Dec-2000

C:Accession: S09095; B01564; A01564

R:Richter, K.; Egger, R.; Kreil, G.

FEBS Lett. 262, 353-355, 1990

A:Title: Molecular cloning of a cDNA encoding the bombesin precursor in skin o.

A:Reference number: S09095; MUID:90242964

A:Accession: S09095

A:Molecule type: mRNA

A:Residues: 1-107 <RIC>

R:Anastasi, A.; Erspamer, V.; Bucci, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A:Title: Isolation and amino acid sequences of alytesin and bombesin, two anal.

A:Reference number: A01564; MUID:72163516

A:Accession: B01564

A:Molecule type: protein

A:Residues: 42-55 <ANA>

C:Superfamily: ranatensin

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyr.

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-41/Domain: amino-terminal propeptide #status predicted <PRO>

F:42-55/Product: bombesin #status experimental <MAT>  
 F:56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
 F:42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F:55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 92.1%; Score 35; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 2.5;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||||  
 Db 48 QWAVGHL 54

RESULT 3  
 A39261  
 bombesin precursor - Bombina orientalis  
 C:Species: Bombina orientalis  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999  
 C:Accession: A39261

R:Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990  
 A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet  
 A:Reference number: A39261; MUID:91088602

A:Accession: A39261  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <SPI>  
 A:Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017  
 C:Superfamily: ranatensin  
 C:Keywords: neuropeptide

Query Match 92.1%; Score 35; DB 2; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 2.8;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||||  
 Db 51 QWAVGHL 57

RESULT 4  
 T45665  
 hypothetical protein F14P22.40 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C:Accession: T45665  
 submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23011  
 A:Accession: T45665  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-174 <DAN>  
 A:Cross-references: EMBL:AL137082  
 A:Experimental source: cultivar Columbia; BAC clone F14P22

C:Genetics:  
 A:Map position: 3  
 A:Introns: 90/1; 126/3; 166/2  
 A:Note: F14P22.40

Query Match 84.2%; Score 32; DB 2; Length 174;  
 Best Local Similarity 71.4%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||||  
 Db 47 EWAVDHL 53

RESULT 5

T34312  
 hypothetical protein F59G1.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T34312

R:Latreille, P.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid F59G1.  
 A:Reference number: Z21504

A:Accession: T34312  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA

A:Residues: 1-353 <LAT>  
 A:Cross-references: EMBL:U53332; PIDN:AAC71158.1; GSPDB:GN00020; CESP:F59G1.4  
 A:Experimental source: strain Bristol N2; clone F59G1

C:Genetics:  
 A:Gene: CESP:F59G1.4

A:Map position: 2

A:Introns: 23/1; 47/2; 83/3; 114/3; 151/1; 187/2; 229/3; 257/3; 316/1  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F59G1.4

Query Match 84.2%; Score 32; DB 2; Length 353;  
 Best Local Similarity 71.4%; Pred. No. 33;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||||  
 Db 201 EWAVNHL 207

RESULT 6

S07204  
 litorin I - Australian tree frog (Litoria aurea)

C:Species: Litoria aurea

C:Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000

C:Accession: S07204

R:Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 510-511, 1975

A:Title: Amino acid composition and sequence of litorin, a bombesin-like nonapep

A:Reference number: S07204; MUID:75187011

A:Accession: S07204

A:Molecule type: protein

A:Residues: 1-9 <ANA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 7  
 |||||  
 Db 2 QWAVGH 7

RESULT 7

A60409  
 bombesin-like peptide L - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C:Accession: A60409

R:Stimmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of

A:Reference number: A60409; MUID:90287814

A:Accession: A60409

A:Molecule type: protein

A:Residues: 1-13 <SIM>

C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F:13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
DB 6 QWAVGH 11

## RESULT 8

B28945  
ranatensin precursor - northern leopard frog  
C:Species: Rana pipiens (northern leopard frog)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
C:Accession: B28945  
R:Kane, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.  
J. Biol. Chem. 263, 13317-13323, 1988  
A:Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromedin  
A:Reference number: A92667; MUID:88330837  
A:Accession: B28945  
A:Molecule type: mRNA  
A:Residues: 1-82 <KRA>  
A:Cross-references: GB:M21552; GB:J03948; NID:g213693; PIDN:AAA49533.1; PID:g213694  
C:Superfamily: ranatensin  
C:Keywords: neuropeptide

Query Match 81.6%; Score 31; DB 2; Length 82;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 QWAVXH 7  
|||||  
DB 51 QWAVGH 56

## RESULT 9

H83378  
hypothetical protein PA2143 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83378  
R:Cover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brogan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: H83378  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-95 <STO>  
A:Cross-references: GB:AE004641; GB:AE004091; NID:g9948150; PIDN:AG05531.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2143

Query Match 81.6%; Score 31; DB 2; Length 95;  
Best Local Similarity 71.4%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXH 8  
||| |  
DB 63 QWVHHL 69

## RESULT 10

A75605  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 24-Jul-2000  
C:Accession: A75605  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Doolittle, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, P.; Zollewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans  
A:Reference number: A75250; MUID:20036896  
A:Accession: A75605  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-183 <WHI>  
A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN: -2366.1  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRA0103  
A:Map position: 2  
C:Superfamily: Deinococcus radiodurans hypothetical protein DRA01

Query Match 81.6%; Score 31; DB 2; Length 183;  
Best Local Similarity 71.4%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
: ||| |  
DB 49 RWAVFHL 55

## RESULT 11

S32963  
hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YBR1729  
C:Species: Saccharomyces cerevisiae  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
C:Accession: S32963; S46142  
R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
Yeast 9, 189-199, 1993  
A:Title: The complete sequence of a 19,482 bp segment located on the right arm of  
A:Reference number: S29348; MUID:93220397  
A:Accession: S32963  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-232 <DOI>

A:Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; P1: g296560  
R:Aigle, M.; Bacle, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45940  
A:Accession: S46142  
A:Molecule type: DNA  
A:Residues: 1-232 <AIG>  
A:Cross-references: EMBL:X36130; NID:g536688; PIDN:CAA5224.1; PID:g3668  
C:Genetics:  
A:Map position: 2R  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 232;  
Best Local Similarity 71.4%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| |  
DB 139 QWCVGHL 145

## RESULT 12

T48787  
hypothetical protein 13E11.350 [imported] - Neurospora crassa

C:Species: Neurospora crassa  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 28-Jul-2000  
C:Accession: T48787  
R:Schulte, U.; Align, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000  
A:Reference number: 224541  
A:Accession: T48787  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-256 <SCH>  
A:Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.350  
A:Experimental source: cosmid contig 13E11; strain 74  
C:Genetics:  
A:Gene: NCSP:13E11.350  
A:Map position: 2  
A:Introns: 213/2  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 256;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| ||  
Db 162 QWCVGHL 168

RESULT 13  
S41427  
cysteine proteinase (EC 3.4.22.-) CPl precursor - Trichomonas vaginalis  
C:Species: Trichomonas vaginalis  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 04-Feb-2000  
C:Accession: S41427  
R:Mallinson, D.J.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41425  
A:Accession: S41427  
A:Molecule type: mRNA  
A:Residues: 1-309 <MAL>  
A:Cross-references: EMBL:X77218; NID:g452291; PIDN:CAA54435.1; PID:g452292  
A:Experimental source: G3  
C:Genetics:  
A:Gene: CPl  
C:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase  
F:1-89/Domain: signal sequence #status predicted <SIG>  
F:309/Product: cysteine proteinase CPl #status predicted <MAT>  
P:4,254,274/Active site: Cys, His, Asn #status predicted

Query Match 81.6%; Score 31; DB 2; Length 309;  
Best Local Similarity 83.3%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
||| |  
Db 126 QWAVKH 131

RESULT 14  
F82558  
lipopolysaccharide core biosynthesis protein XF2434 [imported] - Xylella fastidiosa (str  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: F82558  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: F82558  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-325 <STM>  
A:Cross-references: GB:AE004052; GB:AE003849; NID:g9107617; PIDN:AAF85233.1; GS:  
A:Experimental source: strain 9a5C  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarado  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.;  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.;  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.; La  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Ma  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, F.C.; Miyak  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF2434

Query Match 81.6%; Score 31; DB 2; Length 325;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| ||  
Db 6 QWVVLHL 12

RESULT 15  
T17027  
MYB-related transcription factor - garden snapdragon  
C:Species: Antirrhinum majus (garden snapdragon)  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T17027  
R:Waites, R.; Selvadurai, H.R.; Oliver, I.R.; Hudson, A.  
Cell 93, 779-789, 1998  
A:Title: The PHANTASTICA gene encodes a MYB transcription factor involved in grow  
A:Reference number: Z18662; MUID:98292176  
A:Accession: T17027  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-357 <WAI>  
A:Cross-references: EMBL:AJ005586; NID:g3183616; PIDN:CAA06612.1; PID:g3183617  
A:Experimental source: cultivar JI.98; inflorescence  
C:Genetics:  
A:Gene: phan  
C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repe  
C:Keywords: transcription factor

Query Match 81.6%; Score 31; DB 2; Length 357;  
Best Local Similarity 71.4%; Pred. No. 54;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| ||  
Db 330 QWAAKHL 336

Search completed: October 25, 2001, 11:25:19  
Job time: 332 sec

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:20:32 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-3  
Perfect score: 38  
Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
1 number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	35	92.1	14	1 ALYT_ALYOB	P08944 alytes obst
2	35	92.1	107	1 BOMB_BOMVA	P01296 bombina var
3	35	92.1	119	1 BOMB_BOMOR	P21591 bombina ori
4	31	81.6	9	1 LITO_LITAU	P08945 littoria aur
5	31	81.6	13	1 BOML_PSEGU	P42991 pseudophryn
6	31	81.6	82	1 RANA_RANPI	P08950 rana pipien
7	31	81.6	232	1 YB9H_YEAST	P38340 saccharomyc
8	31	81.6	263	1 TML2_DROME	Q09024 drosophila
9	31	81.6	265	1 IHA_SHEEP	P38440 ovis aries
10	31	81.6	360	1 IHA_BOVIN	P07994 bos taurus
11	31	81.6	364	1 IHA_PIG	P04087 sus scrofa
12	31	81.6	366	1 IHA_MOUSE	Q04997 mus musculu
13	31	81.6	366	1 IHA_RAT	P17490 rattus norv
14	31	81.6	769	1 SW16_KLJLA	P40418 kluyveromyc
15	30	78.9	10	1 GRP_RANRI	P23260 rana ridibu
16	30	78.9	25	1 GRP_SCYCA	P09472 scyllorhinu
17	30	78.9	27	1 GRP_CANFA	P08989 canis fami
18	30	78.9	27	1 GRP_CHICK	P01295 gallus gall
19	30	78.9	27	1 GRP_PIG	P01294 sus scrofa
20	30	78.9	28	1 GRP_ALLMI	P31886 alligator m
21	30	78.9	120	1 NEUB_XENLA	P43443 xenopus lae
22	30	78.9	134	1 GRP_SHEEP	P47851 ovis aries
23	30	78.9	147	1 GRP_RAT	P24393 rattus norv
24	30	78.9	148	1 GRP_HUMAN	P07492 homo saplen
25	30	78.9	155	1 GRP_BOMOR	P29007 bombina ori
26	30	78.9	250	1 AGL8_SOLCO	O22328 solanum com
27	30	78.9	361	1 IHA_TRIVU	O77755 trichosurus
28	30	78.9	366	1 IHA_HUMAN	P05111 homo saplen
29	30	78.9	367	1 IHA_HORSE	P55101 equus cabal
30	30	78.9	458	1 GTP6_YEAST	P32806 saccharomyc
31	29	76.3	219	1 YDRE_SCHPO	O13748 schizosacch
32	29	76.3	227	1 PGSA_MYCPN	P75520 mycoplasma
33	29	76.3	301	1 GCVA_HAEIN	P45099 haemophilus

34 29 76.3 384 1 AAPM\_RHILV Q52814 rhizobium j  
35 29 76.3 510 1 ACHG\_XENLA P05376 xenopus la  
36 28 73.7 197 1 YCB7\_PSEDE P29940 yersinia i  
37 28 73.7 239 1 CYSH\_THIRO P52672 thiocapsa t  
38 28 73.7 244 1 CYSH\_BUCAL P57501 buchnera ap  
39 28 73.7 308 1 ACPL\_ENTHI P36184 entamoeba h  
40 28 73.7 353 1 COA2\_POVBO P24849 bovine poly  
41 28 73.7 362 1 LDOX\_VITVI P51093 vitis vinif  
42 28 73.7 406 1 UL43\_VZVD P09273 varicella-z  
43 28 73.7 430 1 LDOX\_PETHY P51092 petunia hyb  
44 28 73.7 496 1 C7B1\_THLAR P49264 thlaspi arv  
45 28 73.7 543 1 CP1B\_HUMAN Q16678 hmo sapien

## ALIGNMENTS

RESULT 1  
ALYT\_ALYOB  
ID ALYT\_ALYOB STANDARD; PRT; 14 AA.  
AC P08944;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE ALYTESIN.  
OS Alytes obstetricans (Midwife toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; A  
OX NCBI\_TaxID=8443;  
RN [1]  
RP MEDLINE=84131098; PubMed=6141890;  
RX ERSPAMER V., ERSPAMER G.F., MAZZANTI G., ENDEAN R.;  
RA "Active peptides in the skins of one hundred amphibian species from  
RT Australia and Papua New Guinea."  
ET Australia and Papua New Guinea."  
RL Comp. Biochem. Physiol. 77C:99-108(1984).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/RANUPEPTIN B/RANATENS  
CC FAMILY.  
DR InterPro; IPR000874; .  
DR PFAM; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT MOD\_RES 1 1  
FT MOD\_RES 14 14  
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;  
PYRROLIDONE CARBOXYLIC ACID.  
AMIDATION.

Query Match 92.1%; Score 35; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 0.17;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; gaps

QY 2 QWAVXHL 8  
DB 7 QWAVGHL 13

RESULT 2  
BOMB\_BOMVA  
ID BOMB\_BOMVA STANDARD; PRT; 107 AA.  
AC P01296;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE BOMBESIN PRECURSOR.  
OS Bombina variegata (yellow-bellied toad), and  
OS Bombina bombina (Fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; B  
OX NCBI\_TaxID=8348, 8345;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.variegata; TISSUE=Skin;  
RX MEDLINE=90242964; PubMed=2335218;

RA Richter K., Egger R., Kreil G.;  
RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
of Bombina variegata";  
RL FEBS Lett. 262:353-355(1990).  
RN [2]  
RP SEQUENCE OF 42-55.  
RC SPECIES=B.variegata, and B.bombina;  
RX MEDLINE=72163516; PubMed=4537042;  
RA Anastasi A., Erspamer V., Bucci M.;  
RT "Isolation and amino acid sequences of alytesin and bombesin, two  
analogous active tetradecapeptides from the skin of European  
archeglossid frogs";  
RT Arch. Biochem. Biophys. 148:443-446(1972).  
RL Arch. Biochem. Biophys. 148:443-446(1972).  
CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
GASTROINTESTINAL HORMONES.  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
FAMILY.  
CC  
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CC  
CC EMBL; X52447; CAA36686.1; -.  
DR PIR; A01564; BSTD.  
DR PIR; B01564; BSTDY.  
DR PIR; S09095; S09095.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT PEPTIDE 42 55 BOMBESIN.  
FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;  
  
Query Match 92.1%; Score 35; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 1.2;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
2 QWAVXHL 8  
|||||  
48 QWAVGHL 54  
  
RESULT 3  
BOMB\_BOMOR STANDARD; PRT; 119 AA.  
AC P21591;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE BOMBESIN PRECURSOR.  
OS Bombina orientalis (Oriental fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8346;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91088602; PubMed=2263631;  
RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;  
RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
relationship between bombesin and gastrin-releasing peptide";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
CC -!- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN  
THE SKIN AND THE BRAIN.  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
FAMILY.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M55255; AAA48551.1; -.  
DR PIR; A39261; A39261.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 7 BOMBESIN.  
FT PEPTIDE 45 58  
FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2445A44A CRC64;  
  
Query Match 92.1%; Score 35; DB 1; Length 119;  
Best Local Similarity 85.7%; Pred. No. 1.3;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
2 QWAVXHL 8  
|||||  
51 QWAVGHL 57  
  
RESULT 4  
LITO\_LITAU STANDARD; PRT; 9 AA.  
ID LITO\_LITAU  
AC P08945;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE LITORIN.  
OS Litoria aurea (Australian frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=8371;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75187011; PubMed=1140241;  
RA Anastasi A., Erspamer V., Endean R.;  
RT "Amino acid composition and sequence of litorin, a bombesin-like  
nonapeptide from the skin of the Australian leptodactylid fr  
Litoria aurea";  
RT Litoria aurea;.  
RL Experientia 31:510-511(1975).  
RN [2]  
RP SEQUENCE (METHYLATED VARIANT).  
RX MEDLINE=78003546; PubMed=908397;  
RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;  
RT "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in  
methanol extracts of the skin of the Australian frog Litoria aurea";  
RL Experientia 33:1289-1289(1977).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
FAMILY.  
CC  
CC PIR; S07204; S07204.  
CC PIR; S07205; S07205.  
CC InterPro; IPR000874; -.  
CC Pfam; PF02044; Bombesin; 1.  
CC PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Methylation.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

```
FT MOD_RES 2 2 METHYLATION (IN A VARIANT').
RT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1103 MW; D7CCCIE862CDC366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 9.3e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7
   |||||
Db 2 QWAVGH 7

RESULT 5
BOML_PSEGU STANDARD; PRT; 13 AA.
ID BOML_PSEGU STANDARD; PRT; 13 AA.
AC P42991.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
OS BOMBESIN-LIKE PEPTIDE L (PG-L).
OS Pseudophryne guentheri (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; A60409; A60409.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1
FT MOD_RES 13 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7
   |||||
Db 6 QWAVGH 11

RESULT 6
RANA_RANPI
ID RANA_RANPI STANDARD; PRT; 82 AA.
AC P08950;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RANATENSIN PRECURSOR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330837; PubMed=2458345;
RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;
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RT "Molecular cloning of cDNAs encoding the human bombesin-like peptide
RT neuromedin B. Chromosomal localization and comparison to cDNAs
RT encoding its amphibian homolog ranatensin.";
RL J. Biol. Chem. 263:13317-13323(1988).
RN [2]
RP SEQUENCE OF 48-58.
RA Nakajima T., Tanimura T., Pisano J.J.;
RT "Isolation and structure of a new vasoactive polypeptide."
RL Fed. Proc. 29:282-282(1970).
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; M21552; AAA49533.1; -.
DR PIR; B28945; B28945.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation; Cleavage on pair of basic residues.
KW Signal.
FT SIGNAL 1 27
FT PROPEP 28 47
FT PEPTIDE 48 58
FT MOD_RES 58 58
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 81.6%; Score 31; DB 1; Length 82;
Best Local Similarity 83.3%; Pred. No. 6.1;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7
   |||||
Db 51 QWAVGH 56

RESULT 7
YB9H_YEAST
ID YB9H_YEAST STANDARD; PRT; 232 AA.
AC P38340;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 26.1 KDA PROTEIN IN POP4-SHM1 INTERGENIC REGION.
GN YBR261C OR YBR1729.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycet
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93220397; PubMed=8465606;
RA Daignon F., Biteau N., Crouzet M., Aigle M.;
RT "The complete sequence of a 19,482 bp segment located on the cent
RT arm of chromosome II from Saccharomyces cerevisiae.";
RL Yeast 9:189-199(1993).
CC -!- SIMILARITY: TO S.POMBE SPAC16B8.14C.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC -----
DR EMBL; X70529; CAA49926.1; -.
DR EMBL; Z36130; CAA85224.1; -.
DR PIR; S32963; S32963.
DR SGD; S0000465; YBR261C.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 232;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8
Db 139 QMCVGH 145

RESULT 8
DROME IML2 DROME STANDARD; PRT; 263 AA.
AC Q09024;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2 PRECURSOR.
GN IMPL2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S; TISSUE=Embryo;
RX MIMLINE=941139565; PubMed=8306886;
RA Garbe J.C., Yang E., Fristrom J.W.;
RT "IMP-L2: an essential and secreted immunoglobulin family member
RT implicated in neural and ectodermal development in Drosophila.";
RL Development 119;1237-1250(1993).
CC -1- FUNCTION: ESSENTIAL DEVELOPMENTAL ROLE DURING EMBRYOGENESIS, IN
CC PARTICULAR THE NORMAL DEVELOPMENT OF THE NERVOUS SYSTEM. MAY BE
CC INVOLVED IN SOME ASPECT OF CELL ADHESION.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: DETECTED IN SEVERAL SITES INCLUDING THE
CC VENTRAL NEUROECTODERM, THE TRACHEAL PITS, THE PHARYNX AND
CC OESOPHAGUS, AND SPECIFIC NEURONAL CELL BODIES, WHERE IT IS
CC PRIMARILY EXPRESSED.
CC -1- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT THE CELLULAR BLASTODERM
CC STAGE AND CONTINUES TO BE EXPRESSED THROUGH SUBSEQUENT
CC DEVELOPMENT.
CC -1- INDUCTION: BY 20-HYDROXYECDSONE.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC EMBL; L23066; AAB59251.1; -.
CC HSP; P56276; ITLK.
CC FlyBase; FBgn0001257; Impl2.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 2.
CC Immunoglobulin domain; Cell adhesion; Signal.
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 263 NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-
CC L2.
CC DOMAIN 69 142 IG-LIKE C2-TYPE DOMAIN.
CC DOMAIN 184 247 IG-LIKE C2-TYPE DOMAIN.

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FT DISULFID 76 135 BY SIMILARITY.
FT DISULFID 191 240 BY SIMILARITY.
FT VARIANT 173 173 V -> I.
SQ SEQUENCE 263 AA; 29421 MW; 44AADB1B22DD1804 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 263;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8
Db 87 QWVGH 93

RESULT 9
IHA_SHEEP IHA_SHEEP STANDARD; PRT; 265 AA.
AC P38440;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INHIBIN ALPHA CHAIN (FRAGMENT).
GN INHA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Sadanandan S.L., Jeyaseelan K.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L28815; AAA31553.1; -.
CC InterPro; IPR001839; -.
CC Pfam; PF00019; TGF-beta; 1.
CC PROSITE; PS00250; TGF-BETA_1; 1.
CC Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein.
KW NON_TER 1 227 BY SIMILARITY.
FT DISULFID 161 227 BY SIMILARITY.
FT DISULFID 190 262 BY SIMILARITY.
FT DISULFID 194 264 BY SIMILARITY.
FT DISULFID 226 226 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 265 AA; 28754 MW; D880E9AB156B6656 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 265;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8
Db 74 RWAVLHL 80

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RESULT 10
ID IHA_BOVIN STANDARD; PRT; 360 AA.
AC P07994;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
INHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicular fluid;
RX MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., King J.M., Brown R.W., McInerney B.V., Cobon G.S.,
Gregon R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
"Cloning and sequence analysis of cDNA species coding for the two
subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
RN [2]
RP SEQUENCE OF 1-87 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
"Genomic cloning and sequence analyses of the bovine alpha-, beta A-
and beta B-inhibin/activin genes. Identification of transcription
factor AP-2-binding sites in the 5'-flanking regions by DNase I
footprinting.";
RL Eur. J. Biochem. 226:751-764(1994).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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-----
EMBL; M13273; AAA97414.1; -.
DR EMBL; A14416; CAA01156.1; -.
DR EMBL; U16237; AAB60262.1; -.
DR PIR; A25732; A25732.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 226
FT CHAIN 227 360 INHIBIN ALPHA CHAIN.
FT DISULFID 256 322 BY SIMILARITY.
FT DISULFID 285 357 BY SIMILARITY.
FT DISULFID 289 359 BY SIMILARITY.
FT DISULFID 321 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 360 AA; 38809 MW; FBF385DDIEFE46 CRC64;
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Query Match 81.6%; Score 31; DB 1; Length 360;  
Best Local Similarity 71.4%; Pred. No. 25;

```
Matches 5; Conservative 1; Mismatches 1; Indels 6
QY 2 QWAVXHL 8
Db 169 RWAVLHL 175
:|||||
RESULT 11
ID IHA_PIG STANDARD; PRT; 364 AA.
AC P04087;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
INHA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86287350; PubMed=3016724;
RA Mayo K.E., Cerelli G.M., Spiess J., Rivier J., Rosenfeld M.G.,
Evans R.M., Vale W.;
"INHIBIN A-subunit cDNAs from porcine ovary and human placenta.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 231-256.
RC TISSUE=ovarian follicular fluid;
RX MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying . . .
Guillemin R., Niall H., Seeburg P.H.;
"Complementary DNA sequences of ovarian follicular fluid inhibin show
precursor structure and homology with transforming growth
factor-beta.";
RL Nature 318:659-663(1985).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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-----
EMBL; M13980; AAA31057.1; -.
DR EMBL; X03285; CAA27019.1; -.
DR PIR; A01392; WFPGA.
DR PIR; A25947; A25947.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 230 INHIBIN ALPHA CHAIN.
FT CHAIN 231 364 BY SIMILARITY.
FT DISULFID 260 326 BY SIMILARITY.
FT DISULFID 289 361 BY SIMILARITY.
FT DISULFID 293 363 BY SIMILARITY.
FT DISULFID 325 325 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 120 120 R -> H (IN REF. 2).
FT CONFLICT 125 125 A -> T (IN REF. 2).
```

SQ SEQUENCE 364 AA; 39160 MW; BB595B9B7958A168 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 364;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 QWAVXHL 8  
 :||| ||  
 Db 173 RWAHL 179

RESULT 12  
 ID IHA\_MOUSE STANDARD; PRT; 366 AA.  
 AC Q04997;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 INHIBIN ALPHA CHAIN PRECURSOR.  
 INHA.  
 Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93321614; PubMed=8330535;  
 RA Albano P.M., Groome N., Smith J.C.;  
 RT "Activins are expressed in preimplantation mouse embryos and in ES  
 and EC cells and are regulated on their differentiation.";  
 RL Development 117:711-723(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92337610; PubMed=1632772;  
 RA Su J.G.W., Hsueh A.J.W.;  
 RT "Characterization of mouse inhibin alpha gene and its promoter.";  
 RL Biochem. Biophys. Res. Commun. 186:293-300(1992).  
 RN [3]  
 RP SEQUENCE OF 49-366 FROM N.A.  
 RC STRAIN-SWISS WEBSTER;  
 RX MEDLINE=91071531; PubMed=2253839;  
 RA Tone S., Katoh Y., Fujimoto H., Togashi S., Yanazawa M., Kato Y.,  
 RA Higashinakagawa T.;  
 RT "Expression of inhibin alpha-subunit gene during mouse  
 gametogenesis.";  
 RL Differentiation 44:62-68(1990).  
 CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE  
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND  
 IT ACTIVATES THE SECRETION OF FOLLITROPIN.  
 CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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 CC  
 CC EMBL; X69618; CAA49324.1; -;  
 CC EMBL; M95525; AAA39314.1; -;  
 CC EMBL; M95526; AAA39314.1; JOINED.  
 CC EMBL; X55957; CAA39424.1; -;  
 CC PIR; S31439;  
 CC PIR; JCI106; JCI106.  
 CC MGD; MGI:96569; Inha.  
 CC InterPro; IPR001839; -;  
 CC InterPro; IPR002405; -;  
 CC Pfam; PF00019; TGF-beta; 1.

DR PRINTS; PR00669; INHIBINA.  
 KW PROSITE; PS00250; TGF\_BETA\_1; 1.  
 DR Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1 20  
 FT PROPEP 21 233  
 FT CHAIN 234 366  
 FT DISULFID 263 328  
 FT DISULFID 292 363  
 FT DISULFID 296 365  
 FT DISULFID 327 327  
 FT CARBOHYD 147 147  
 FT CARBOHYD 269 269  
 FT CARBOHYD 165 165  
 FT CONFLICT 171 171  
 FT CONFLICT 336 336  
 SQ SEQUENCE 366 AA; 39536 MW; 8F3851B722FE0011 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 QWAVXHL 8  
 :||| ||  
 Db 176 RWAHL 182

RESULT 13  
 ID IHA\_RAT STANDARD; PRT; 366 AA.  
 AC P17490;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE INHIBIN ALPHA CHAIN PRECURSOR.  
 GN INHA.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90190649; PubMed=2628729;  
 RA Feng Z.-M., Li Y.-P., Chen C.-L.C.;  
 RT "Analysis of the 5'-flanking regions of rat inhibin alpha and  
 beta-B-subunit genes suggests two different regulatory mechanisms.";  
 RL Mol. Endocrinol. 3:1914-1925(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91042598; PubMed=3153478;  
 RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;  
 RT "Rat inhibin: molecular cloning of alpha- and beta-subunit  
 complementary deoxyribonucleic acids and expression in the ovary.";  
 RL Mol. Endocrinol. 1:561-568(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90331931; PubMed=2484214;  
 RA Esch F.S., Shimasaki S., Cooksey K., Mercado M., Mason A.J.,  
 RA Ying S.Y., Ueno N., Ling N.;  
 RT "Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence  
 analysis of rat ovarian inhibins.";  
 RL Mol. Endocrinol. 1:388-396(1987).  
 CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE  
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND  
 IT ACTIVATES THE SECRETION OF FOLLITROPIN.  
 CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC -!- TISSUE SPECIFICITY: ALPHA- AND BETA-B-SUBUNITS ARE THE  
 PREDOMINANT FORMS FOUND IN RAT TESTIS.  
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC

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 CC -----

DR EMBL; M32755; AAA41437.1; JOINED.  
 DR EMBL; M32754; AAA41437.1; JOINED.  
 DR EMBL; M36453; AAA41435.1; JOINED.  
 DR PIR; A40905; A40905.  
 DR PIR; A41398; A41398.  
 DR PIR; A40056; A40056.  
 DR InterPro; IPR001839; .  
 DR InterPro; IPR002405; .  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR PRINTS; PR00669; INHIBIN.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.  
 CC SIGNAL 1 20  
 CC PROPEP 21 233  
 CC CHAIN 234 366  
 CC INHIBIN ALPHA CHAIN.  
 FT DISULFID 263 328  
 CC BY SIMILARITY.  
 FT DISULFID 292 363  
 CC BY SIMILARITY.  
 FT DISULFID 296 365  
 CC BY SIMILARITY.  
 FT DISULFID 327 327  
 CC INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 147 147  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 269 269  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 366 AA; 39496 MW; 327A233B9FEFDCDC CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 :||| ||  
 Db 176 RWAHL 182

RESULT 14  
 SWI6\_KLULA  
 ID SWI6\_KLULA STANDARD; PRT; 769 AA.  
 AC P40418;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE REGULATORY PROTEIN SWI6 (CELL-CYCLE BOX FACTOR, CHAIN SWI6) (TRANS-  
 ACTING ACTIVATOR OF HO ENDONUCLEASE GENE) (MBF SUBUNIT P90).  
 GN SWI6.  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93383264; PubMed=8372350;  
 RA Koch C., Moll T., Neuberg M., Ahorn H., Nasmith K.;  
 RT "A role for the transcription factors Mbpl and Swi4 in progression  
 RT from G1 to S phase."  
 RL Science 261:1551-1557(1993).  
 CC -!- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT  
 CC TRANSCRIPTION. SWI4 AND SWI6 ARE REQUIRED FOR FORMATION OF THE  
 CC CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE  
 CC UPSTREAM REGION OF HO (5'-CACGAAAA-3') IS CALLED THE CELL CYCLE  
 CC BOX (CCB).  
 CC -!- SUBUNIT: MBF CONTAINS SWI6 AND MBP1; SBF CONTAINS SWI6 AND SWI4.  
 CC -!- SIMILARITY: STRONG, TO S.POMBE CDC10.  
 CC -!- SIMILARITY: CONTAINS 2 ANK REPEATS.  
 CC -----

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 CC -----

DR EMBL; X74292; CAA52345.1; .  
 DR PIR; S36657; S36657.  
 DR InterPro; IPR002110; .  
 DR Pfam; PF00023; ank; 2.  
 DR PROSITE; PS50088; ANK\_REPEAT; 2.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 2.  
 KW Transcription regulation; DNA-binding; ANK repeat; Repeat.  
 FT REPEAT 286 315  
 CC ANK 1.  
 FT REPEAT 422 451  
 CC ANK 2.  
 SQ SEQUENCE 769 AA; 86669 MW; E3A5328B4DA084FB CRC64;

Query Match 81.6%; Score 31; DB 1; Length 769;  
 Best Local Similarity 57.1%; Pred. No. 51;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 :||: ||  
 Db 409 QWVTHL 415

RESULT 15  
 GRP\_RANRI  
 ID GRP\_RANRI STANDARD; PRT; 10 AA.  
 AC P23260;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE NEUROMEDIN C.  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Brain;  
 RX MEDLINE=91315477; PubMed=1859413;  
 RA Conlon J.M., O'Harte F., Vaudry H.;  
 RT "Primary structures of the bombesin-like neuropeptides in frog brain  
 RT show that bombesin is not the amphibian gastrin-releasing peptide."  
 RL Biochem Biophys Res Commun. 178:526-530(1991).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 CC PIR; PQ0177; PQ0177.  
 DR InterPro; IPR000874; .  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 10 10  
 CC AMIDATION.  
 SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHL 8  
 :||| ||  
 Db 4 WAVGHL 9

Search completed: October 25, 2001, 11:28:28  
 Job time: 476 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:19:07 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-3  
Perfect score: 38  
Sequence: 1 XQWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
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16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
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19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	94.7	7	10 AAP91147	Sequence of new ne
2	36	94.7	7	13 AAR20585	Antagonist of bomb
3	36	94.7	7	13 AAR32998	[D-Ala11]-bombesin
4	36	94.7	7	20 AAW94610	Bombesin/gastrin r
5	36	94.7	8	3 AAP20294	Bombesin analog pe
6	36	94.7	8	12 AAR11241	Linear litorin ana
7	36	94.7	8	12 AAR11242	Linear litorin ana
8	36	94.7	8	12 AAR29155	Bombesin analogue
9	36	94.7	8	13 AAR29157	Bombesin analogue
10	36	94.7	8	16 AAW64911	Bombesin receptor
11	36	94.7	9	11 AAR09335	Sequence of Bombes

12	36	94.7	9	12 AAR11522	Example of peptide
13	36	94.7	9	12 AAR14865	Peptide analogue #
14	36	94.7	9	12 AAR14866	Peptide analogue #
15	36	94.7	9	12 AAR14867	Peptide analogue #
16	36	94.7	9	12 AAR14873	Peptide analogue #
17	36	94.7	9	14 AAR40903	Bombesin analogue
18	36	94.7	9	19 AAW51195	Peptide derivative fr
19	36	94.7	9	19 AAW51201	Sequence of new ne
20	36	94.7	10	10 AAP96113	Bombesin/gastrin-r
21	35	92.1	7	22 AAB48341	Non-cyclic analogue
22	35	92.1	8	11 AAR04531	Linear litorin ana
23	35	92.1	8	12 AAR11224	Linear litorin ana
24	35	92.1	8	12 AAR11240	Peptide analogue #
25	35	92.1	8	12 AAR14877	Bombesin antagonist
26	35	92.1	8	13 AAR28456	Bombesin antagonist
27	35	92.1	8	13 AAR28459	Bombesin receptor
28	35	92.1	8	16 AAW64910	Bombesin antagonist
29	35	92.1	8	19 AAW50941	Bombesin peptide a
30	35	92.1	8	20 AAW92740	Amino acid sequenc
31	35	92.1	8	21 AAB08302	Amino acid sequenc
32	35	92.1	8	21 AAB08308	Bombesin analogue
33	35	92.1	8	22 AAB72406	Non-cyclic analogue
34	35	92.1	9	11 AAR04526	Non-cyclic analogue
35	35	92.1	9	11 AAR04527	Non-cyclic analogue
36	35	92.1	9	11 AAR04529	Non-cyclic analogue
37	35	92.1	9	11 AAR04528	Non-cyclic analogue
38	35	92.1	9	11 AAR04530	Peptide bombesin a
39	35	92.1	9	11 AAR08345	Example of peptide
40	35	92.1	9	12 AAR11520	Example of peptide
41	35	92.1	9	12 AAR11521	Example of peptide
42	35	92.1	9	12 AAR11525	Example of peptide
43	35	92.1	9	12 AAR11529	Bombesin antagonist
44	35	92.1	9	12 AAR12033	Peptide analogue #
45	35	92.1	9	12 AAR14860	

## ALIGNMENTS

RESULT 1  
AAP91147  
ID AAP91147 standard; protein; 7 AA.  
XX  
AC AAP91147;  
XX  
DT 13-MAY-1990 (first entry)  
DT 22-DEC-1990 (corrected)  
XX  
DE Sequence of new neuromedin C deriv.  
XX  
KW Bombesin antagonist; malignant disease; therapy; gastric acid secret  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /label=OTHER  
FT /note="Ac-D-Gln"  
FT Misc-difference 5 /label=OTHER  
FT /note="D-Ala"  
FT Misc-difference 7 /label=OTHER  
FT /note="Leu-Ome"

XX  
XX EP315367-A.  
XX  
XX 10-MAY-1989.  
XX  
XX 27-OCT-1988; 88EP-0310094.  
XX  
XX 06-JUN-1988; 88GB-0013355.  
XX  
XX (ICIL ) IMPERIAL CHEM INDS PLC.  
XX

PI Camble R, Cotton R, Dutta AS, Hayward CF;  
 XX WPI; 1989-139341/19.  
 XX New Neuromedin C polypeptide derivs. -  
 PT are potent bombesin antagonist used for treating malignant  
 PT disease and conditions associated with gastrin or gastric acid  
 PT secretion  
 XX  
 XX Disclosure; Page 929; 49pp; English.  
 XX  
 XX It is a potent bombesin antagonist. It may be used for the treatment of  
 CC e.g. malignant disease, conditions associated with the over-prodn. of  
 CC bombesin and conditions associated with failure of normal physiological  
 CC control of the regulation of gastric acid secretion.  
 XX  
 XX Sequence 7 AA;

Query Match 94.7%; Score 36; DB 10; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 111111  
 Db 1 qwavahl 7

RESULT 2  
 AAR20585  
 ID AAR20585 standard; Peptide; 7 AA.

XX  
 AC AAR20585;  
 XX  
 DT 07-MAY-1992 (first entry)  
 XX  
 DE Antagonist of bombesin/GRP.  
 XX  
 KW Antitumour agent; leukaemia.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 5  
 FT /note= "D-Ala"

XX EP468497-A.  
 XX 29-JAN-1992.  
 XX  
 PF 25-JUL-1991; 91EP-0112504.  
 XX  
 PR 26-JUL-1990; 90US-0558031.  
 XX  
 PA (RICH ) MERRELL DOW PHARM INC.  
 XX  
 PI Krstenansky JL;  
 XX  
 DR WPI; 1992-034251/05.

XX New peptide bombesin-GRP antagonists - used as antitumour agents  
 PT to treat e.g. leukaemia, small cell lung and prostatic carcinoma  
 PT and to inhibit gastric acid secretion.  
 XX  
 XX Claim 7; Page 12; 14pp; English.

XX The peptide is modified at the N-terminal with a lauryl, palmitoyl  
 CC or esp. an octanoyl gp. The leu at position 7 may be absent. The  
 CC C-terminal (leu or His) is amidated. The peptides and derived  
 CC salts can be used to treat small cell lung carcinoma, prostatic  
 CC carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-  
 CC ciated conditions, and to effect antagonism of bombesin/gastrin  
 CC releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at

CC 5-200 mg/dose.  
 XX  
 SQ Sequence 7 AA;

Query Match 94.7%; Score 36; DB 13; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWAVXHL 8  
 111111  
 Db 1 qwavahl 7

RESULT 3  
 AAR32998  
 ID AAR32998 standard; peptide; 7 AA.

XX  
 AC AAR32998;  
 XX  
 DT 13-APR-1993 (first entry)  
 XX  
 DE [D-Ala11]-bombesin(7-13)amide derivs.

XX Intracellular signal; inhibition; gastrointestinal tract;  
 KW litorin; Gastrin Releasing Peptide; GRP.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= OTHER  
 FT /note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,  
 FT N-alpha-lauryl-Gln or N-alpha-palmityl Gln"  
 FT Misc-difference 5  
 FT /note= "D-Ala"  
 FT Modified-site 7  
 FT /note= "amidated"

XX WO9220707-A.  
 XX  
 PN 26-NOV-1992.  
 XX  
 PF 21-APR-1992; 92WO-US03287.  
 XX  
 PR 23-MAY-1991; 91US-0704863.  
 XX  
 PA (RICH ) MERRELL DOW PHARM INC.  
 XX  
 PI Edwards JV, Fanger BO;  
 XX  
 DR WPI; 1992-415707/50.

XX New bombesin peptide agonists and antagonists - stimulate or  
 PT inhibit digestion, increase susceptibility of tumours to  
 PT chemotherapeutic agents, treat gastric ulcers and tumours etc.  
 XX  
 PS Example; Page 40; 64pp; English.

XX The peptides in this example are bombesin analogues. The peptides  
 CC were tested in a competitive binding assay and a Phosphatidyl Inositol  
 CC (PI)-turnover assay in mouse pancreas. None of the peptides  
 CC demonstrated agonist activity but all inhibited PI-turnover (c.f.  
 CC stimulation produced by 100nM GRP). Analogues of bombesin are  
 CC potentially useful for growth therapy and the treatment of digestive  
 CC disorders, e.g. for stimulating digestion, stimulating growth of  
 CC tissue in the lung, pancreas and intestine, stimulating NK cell  
 CC activity against tumour cells and stimulating growth of tumours to  
 CC increase susceptibility to chemotherapeutic agents.

XX Sequence 7 AA;

Query Match 94.7%; Score 36; DB 13; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 Db 1 qwavahl 7

RESULT 4  
 AAW94610  
 ID AAW94610 standard; peptide; 7 AA.  
 XX  
 AC AAW94610;  
 XX  
 DT 27-APR-1999 (first entry)  
 XX  
 DE Bombesin/gastrin releasing peptide type inhibitor peptide #2.  
 XX  
 Bombesin; gastrin releasing peptide; GRP; inhibitor; antagonist;  
 small cell lung carcinoma; tumour; frog; antimitotic; antiseecretory;  
 peptic ulcer.  
 XX  
 OS Synthetic.  
 OS Bombina Bombina.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "optionally modified by octanoyl, lauroyl or  
 FT palmitoyl"  
 FT Modified-site 7  
 FT /note= "amidated"  
 XX  
 US5834433-A.  
 PN  
 PD 10-NOV-1998.  
 XX  
 PF 23-FEB-1996; 96US-0960130.  
 XX  
 PR 24-JUL-1991; 91US-0735402.  
 PR 26-JUL-1990; 90US-0558031.  
 PR 21-JUL-1994; 94US-0278692.  
 PR 23-MAY-1995; 95US-0447528.  
 PR 23-FEB-1996; 96US-0960130.  
 XX  
 PA (RICH ) MERRELL PHARM INC.  
 PI Krstenansky JL;  
 WPI; 1999-141255/12.  
 PT New peptide antagonists of bombesin or gastrin releasing peptide -  
 PT are useful as antimitotic and antiseecretory agents in treating,  
 PT e.g., small cell lung carcinoma or peptic ulcers  
 PS Claim 5; Column 14; 9pp; English.  
 XX  
 The present sequence represents a bombesin/gastrin releasing peptide  
 type inhibitor peptide. The peptide may be used as an antimitotic and  
 antiseecretory peptide. It can control growth of small cell lung and  
 prostatic carcinomas, and it can also inhibit gastric secretions which  
 are causative and symptomatic of peptic ulcers. Administration may be  
 oral but is preferably subcutaneous, intravenous, intramuscular or  
 intraperitoneal, by depot injection, by implant preparation or by  
 application to the mucous membranes (e.g. of the nose or bronchial  
 tubes) by aerosol.  
 XX  
 Sequence 7 AA;

Query Match 94.7%; Score 36; DB 20; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 Db 1 qwavahl 7

RESULT 5  
 AAP20294  
 ID AAP20294 standard; peptide; 8 AA.  
 XX  
 AC AAP20294;  
 XX  
 DT 09-DEC-1992 (first entry)  
 XX  
 DE Bombesin analog peptide.  
 XX  
 KW Bombesin; hypothermic; analgesic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /label= D-Glu  
 FT Misc-difference 5  
 FT /label= D-Ala  
 XX  
 US4331661-A.  
 PN  
 PD 25-MAY-1982.  
 XX  
 PF 03-OCT-1980; 80US-0193621.  
 XX  
 PR 03-OCT-1980; 80US-0193621.  
 XX  
 PA (SALK-) SALK INST BIOLOGICA.  
 PI Marki WE, Brown MR, Rivier JEF;  
 WPI; 1982-48049E/23 (48049E).  
 DR  
 PT Octa:peptide bombesin analogues - having hypothermic and  
 PT analgesic props.  
 XX  
 PS Claim 8; Column 8; 5pp; English.  
 XX  
 The peptide may be preceded by a formyl, acetyl, propionyl, acetyl  
 or benzoyl group at its C-terminal. The peptide may be used for  
 reducing the body temp. of a mammal, as well as for inducing  
 analgesia. It produces hypothermia when injected i.c., but not  
 when given i.v. or s.c. See also AAP20291-3.  
 XX  
 Sequence 8 AA;

Query Match 94.7%; Score 36; DB 3; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 Db 1 qwavahl 7

RESULT 6  
 AAR11241  
 ID AAR11241 standard; Protein; 8 AA.  
 XX  
 AC AAR11241;  
 XX  
 DT 17-MAY-1991 (first entry)  
 XX  
 DE Linear litorin analogue (III).  
 XX

KW Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 XX diabetes.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 Modified-site 1..1  
 /label= D-p-chloro-phenylalanine

WO9102746-A.

07-MAR-1991.

17-AUG-1990; 90WO-US04646.

21-AUG-1989; 89US-0397169.

30-MAR-1990; 90US-0502438.

(TULA ) ADMIN TULANE EDUCATIONAL.  
 (BIOM-) BIOMEASURE INC.

Coy DH, Moreau JP, Kim SH;

WPI; 1991-087241/12.

New linear peptide analogues of bombesin - modified to eliminate biological activity while retaining receptor affinity, for treating cancer, diabetes, etc.

Claim 18; Page 54; 58pp; English.

This peptide is a specifically claimed example of a generic formula. The C-terminal amino acid (Met) of the naturally occurring peptide has been converted to an amide and Phe 8 has been replaced by beta-Leu. Gly 6 has also been replaced by D-Ala.

The peptide is useful for treating benign or malignant tissue proliferation, arteriosclerosis, gastrointestinal disorders and diabetes. They act as competitive inhibitors of natural peptides, since they bind to the cell receptors but have no biological activity.

The analogue may also be of a naturally occurring peptide terminating at the C-terminus with a Met residue, such as the 10 amino acid C-terminal region of mammalian GRP or amphibian bombesin.

See also AAR11239-242.

Sequence 8 AA;

Query Match 94.7%; Score 36; DB 12; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

Db 2 qwavahl 8

RESULT 7

AAR11242  
 ID AAR11242 standard; Protein; 8 AA.

XX

AC AAR11242;

17-MAY-1991 (first entry)

Linear litorin analogue (IV).

Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 XX diabetes.

OS Synthetic.

XX

Key Location/Qualifiers  
 Modified-site 1..1  
 /label=D-Phe, pentafluoro-Phe  
 Modified-site 6..6  
 /label= N-methyl-D-Ala

WO9102746-A.

07-MAR-1991.

17-AUG-1990; 90WO-US04646.

21-AUG-1989; 89US-0397169.

30-MAR-1990; 90US-0502438.

(TULA ) ADMIN TULANE EDUCATIONAL.  
 (BIOM-) BIOMEASURE INC.

Coy DH, Moreau JP, Kim SH;

WPI; 1991-087241/12.

New linear peptide analogues of bombesin - modified to eliminate biological activity while retaining receptor affinity, for treating cancer, diabetes, etc.

Claim 20+21; Page 54; 58pp; English.

These peptides are specifically claimed examples of a generic formula. The C-terminal amino acid (Met) of the naturally occurring peptide has been converted to a methyl ester.

The peptide is useful for treating benign or malignant tissue proliferation, arteriosclerosis, gastrointestinal disorders and diabetes. They act as competitive inhibitors of natural peptides, since they bind to the cell receptors but have no biological activity.

The analogue may also be of a naturally occurring peptide terminating at the C-terminus with a Met residue, such as the 10 amino acid C-terminal region of mammalian GRP or amphibian bombesin.

See also AAR11239-242.

Sequence 8 AA;

Query Match 94.7%; Score 36; DB 12; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

Db 2 qwavahl 8

RESULT 8

AAR29155  
 ID AAR29155 standard; peptide; 8 AA.

XX

AC AAR29155;

16-APR-1993 (first entry)

Bombesin analogue (5).

Hepatoma; liver cancer; antagonist.

Synthetic.

Key Location/Qualifiers  
 Misc-difference 1  
 /note= "D-form residue"

Modified-site 6

/note= "NMe-D-Ala"

FT

FT Modified-site 8  
FT /note= "Leu-OMe"

XX PN W09220363-A.

XX PD 26-NOV-1992.

XX PF 11-MAY-1992; 92WO-US03916.

XX PR 10-MAY-1991; 91US-0698681.

XX PA (BIOM-) BIOMEASURE INC.

XX PA (TULA ) TULANE EDUCATIONAL FUND.

XX PI Bodgen AE, Coy DH, Kim SH, Moreau J;

XX WPI; 1992-415466/50.

XX Treatment of hepatoma - by admin. of admixed bombesin analogue  
XX with carrier

XX Claim 14; Page 48; 54pp; English.

XX The peptide is an example of a highly generic formula. It is used  
XX in a medicament for treating hepatoma. The cpd. acts as antagonist  
XX to bombesin, which has been detected in a number of human cancer  
XX lines.

XX SQ Sequence 8 AA;

Query Match 94.7%; Score 36; DB 13; Length 8;

Best Local Similarity 85.7%; Pred. NO. 3.4e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8

Db 111111

2 qwavahl 8

RESULT 9

AAR29157

ID AAR29157 standard; peptide; 8 AA.

XX AC AAR29157;

XX DT 16-APR-1993 (first entry)

XX Bombesin analogue (6).

XX Hepatoma; liver cancer; antagonist.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "D-F5-Phe"

FT Misc-difference 6

FT /note= "D-form residue"

FT Modified-site 8

FT /note= "Leu-OMe"

XX PN W09220363-A.

XX PD 26-NOV-1992.

XX PF 11-MAY-1992; 92WO-US03916.

XX PR 10-MAY-1991; 91US-0698681.

XX PA (BIOM-) BIOMEASURE INC.

XX PA (TULA ) TULANE EDUCATIONAL FUND.

XX

PI Bodgen AE, Coy DH, Kim SH, Moreau J;

XX WPI; 1992-415466/50.

XX Treatment of hepatoma - by admin. of admixed bombesin analogue

XX with carrier

XX Claim 15; Page 48; 54pp; English.

XX The peptide is an example of a highly generic formula. It is used  
XX in a medicament for treating hepatoma. The cpd. acts as antagonist  
XX to bombesin, which has been detected in a number of human cancer  
XX lines.

XX SQ Sequence 8 AA;

Query Match 94.7%; Score 36; DB 13; Length 8;

Best Local Similarity 85.7%; Pred. NO. 3.4e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8

Db 111111

2 qwavahl 8

RESULT 10

AAW64911

ID AAW64911 standard; peptide; 8 AA.

XX AC AAW64911;

XX DT 06-JUL-1999 (first entry)

XX Bombesin receptor antagonist.

XX Bombesin; antagonist; chlorambucil; peptic ulcer; pancreatitis;

XX eating disorder; diabetes; acromegaly; enterocutaneous fistula;

XX psoriasis; growth retardation; gastrointestinal motility disorder;

XX antitumour.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "The amino terminal is acylated with acetyl,  
FT bromoacetyl, chloroacetyl, [bis(2-chloroethyl) amino]  
FT L-phenylalanine or a chlorambucil group"

FT Modified-site 8

FT /note= "The carboxy terminal is in the form of an  
FT ethyl ester"

XX PN W09500542-A1.

XX PD 05-JAN-1995.

XX PF 15-JUN-1994; 94WO-US06757.

XX PR 17-DEC-1993; 93US-0168390.

XX PR 18-JUN-1993; 93US-0078062.

XX (PEPT-) PEPTIDE TECHNOLOGIES CORP.

XX Chandrasekhar B, Knight M, Takahashi K;

XX WPI; 1995-052004/07.

XX New bombesin, gastrin releasing peptide or Neuromedin B or C derivs.  
XX - antagonists for treating conditions such as gastrointestinal  
XX disorders, psoriasis and cancers  
XX Claim 6; Page 34; 45pp; English.

CC The patent discloses (1) the peptide sequence of bombesin (BBN),  
 CC gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C,  
 CC the peptide sequence having a chlorambucil group attached to the  
 CC amino terminal; (2) a BBN receptor antagonist of formula  
 CC R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
 CC antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
 CC In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
 CC Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
 CC amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His.  
 CC The compounds act as potent BBN/GRP-like peptide antagonists. They  
 CC can be used to inhibit the growth of cells that are sensitive to the  
 CC growth-promoting effects of BBN, GRP or a related peptide such as  
 CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
 CC cancerous cells or tumours. They can also be used to inhibit the  
 CC binding of BBN, GRP or a related peptide to cells capable of such  
 CC binding. They can be used for treating e.g. peptic ulcer, pancreatitis,  
 CC eating disorders, diabetes, acromegaly, enterocutaneous fistula,  
 CC psoriasis, growth retardation, gastrointestinal motility disorders or  
 CC tumours. The terminal structures of the compounds protect them from  
 CC in vivo proteolysis and provide highly potent antagonist effects that  
 CC persist for extended periods of time upon administration.

XX Sequence 8 AA;

Query Match 94.7%; Score 36; DB 16; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 | | | | |  
 Db 2 qwavahl 8

RESULT 11  
 AAR09335  
 ID AAR09335 standard; peptide; 9 AA.

XX AAR09335;

XX 30-MAR-1992 (first entry)

XX Sequence of Bombesin receptor peptide ligand with irreversible effects.

XX Bombesin receptor; agonist; antagonist.

XX Key Location/Qualifiers  
 FT Modified-site 1 /label= H-pMel  
 FT /note= "pMel= p-bis (2-chloroethyl)  
 FT amino-L-phenylalanine"

FT Modified-site 9 /label= Met-NH2

XX WO9001037-A.

XX 08-FEB-1990.

XX 19-JUL-1989; 89WO-EP00842.

XX 28-MAR-1989; 89GB-0006900.

XX 21-JUL-1988; 88GB-0017379.

XX (FARM ) FARMITALIA C ERBA SPA.

XX de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciomei M;  
 PI Molinari I;  
 PI WPI; 1990-067161/09.

XX Bombesin receptor peptide ligands with irreversible effects - as  
 PT agonists and antagonists both weak and strong

XX Claim 2; Page 26; 32pp; English.  
 XX The inventors claim 36 peptides. Also claimed are:  
 CC (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.  
 CC of the peptides.  
 XX Sequence 9 AA;

Query Match 94.7%; Score 36; DB 11; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 | | | | |  
 Db 2 qwavahl 8

RESULT 12  
 AAR11522  
 ID AAR11522 standard; Protein; 9 AA.

XX AAR11522;

XX 13-JUN-1991 (first entry)

XX Example of peptide agonist of GRP, neuromedin, bombesin and litorin.

XX Non-malignant proliferative disease; cancer.

XX Key Location/Qualifiers  
 FT Modified-site 1.1 /label= OTHER  
 FT /note= "D-p-chlorophenylalanine"

XX WO9104040-A.

XX 04-APR-1991.

XX 17-SEP-1990; 90WO-US05271.

XX 05-MAY-1990; 90US-0520225.

XX 15-SEP-1989; 89US-0408125.

XX 21-NOV-1989; 89US-0440039.

XX (BIOM-) BIOMEASURE INC.

XX Bogden AE, Moreau J-P;

XX WPI; 1991-117320/16.

XX Treatment of non malignant proliferative disease and cancer - by  
 PT administration of natural peptide or fragment selected from  
 PT gastrin-releasing peptide, neuromedin, amphibian bombesin or  
 PT litorin

XX Claim 22; page 54; 73pp; English.

XX This is a peptide analogue of mammalian gastrin releasing peptide  
 CC (GRP), neuromedin-B or -C, amphibian bombesin and litorin.  
 CC It is an agonist of these cpds. and is used to treat smooth muscle  
 CC proliferation and cancer of the prostate, breast or lung.  
 CC Residue 6 (Ala) is D-alanine.  
 CC See also AAR11519-21 and AAR11523-30.

XX Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 |||| ||  
 Db 2 qwavahl 8

## RESULT 13

AAR14865  
 ID AAR14865 standard; Protein; 9 AA.

XX AC AAR14865;  
 XX DT 14-FEB-1992 (first entry)  
 XX DE Peptide analogue #6 of litorin, GRP, neuromedin or bombesin.

XX KW tissue proliferation; gastrin related peptide; peptide hormone.  
 XX OS Synthetic.  
 XX Key Location/Qualifiers  
 Modified-site 1  
 /label= D-Phe  
 FT Modified-site 6  
 /label= D-Ala

XX PN WO9117181-A.

XX PD 14-NOV-1991.  
 XX PF 09-MAY-1991; 91WO-0003265.  
 XX PR 09-MAY-1990; 90US-0520226.  
 XX PA (TULA ) TULANE E FUND ADMINISTRA.  
 XX PA (BIOM-) BIOMEASURE INC.

XX PI Coy DH, Kim SH, Moreau JP;  
 XX WPI; 1991-353721/48.

XX PT Peptide agonists of litorin, gastrin releasing peptide -

XX PT neuromedin B or C or bombesin, for treating cancer, preventing  
 PT smooth muscle proliferation and suppressing appetite and alcohol  
 PT craving  
 XX PS Claim 8; Page 18; 25pp; English.

XX CC The C-terminal residue is amidated. This peptide is one of 27

specific examples of a highly generic formula. The peptides are all  
 analogues of either litorin; the 10 amino acid C-terminal region of  
 mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 C-terminal region of amphibian bombesin. They act as at least partial  
 agonists of the natural peptides. The peptide analogues are made by  
 standard methods of synthesis and can be cyclised.  
 CC See AAR14860-R14880 and AAR15035-R15040.

XX SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 |||| ||  
 Db 2 qwavahl 8

## RESULT 14

AAR14866  
 ID AAR14866 standard; Protein; 9 AA.

XX AC AAR14866;

XX DT 14-FEB-1992 (first entry)  
 XX DE Peptide analogue #7 of litorin, GRP, neuromedin or bombesin  
 XX KW tissue proliferation; gastrin related peptide; peptide hormone.  
 XX OS Synthetic.

XX Key Location/Qualifiers  
 Modified-site 1  
 /label= D-Phe  
 FT Modified-site 6  
 /label= D-Ala

XX PN WO9117181-A.

XX PD 14-NOV-1991.

XX PF 09-MAY-1991; 91WO-0003265.

XX PR 09-MAY-1990; 90US-0520226.

XX PA (TULA ) TULANE E FUND ADMINISTRA.  
 XX PA (BIOM-) BIOMEASURE INC.

XX PI Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

XX PT Peptide agonists of litorin, gastrin releasing peptide -  
 XX PT neuromedin B or C or bombesin, for treating cancer, preventing  
 PT smooth muscle proliferation and suppressing appetite and alcohol  
 PT craving

XX PS Claim 9; Page 18; 25pp; English.

XX CC The C-terminal residue is amidated. This peptide is one of 27  
 specific examples of a highly generic formula. The peptides are all  
 analogues of either litorin; the 10 amino acid C-terminal region of  
 mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 C-terminal region of amphibian bombesin. They act as at least partial  
 agonists of the natural peptides. The peptide analogues are made by  
 standard methods of synthesis and can be cyclised.  
 CC See AAR14860-R14880 and AAR15035-R15040.

XX SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 |||| ||  
 Db 2 qwavahl 8

## RESULT 15

AAR14867  
 ID AAR14867 standard; Protein; 9 AA.

XX AC AAR14867;

XX DT 14-FEB-1992 (first entry)

XX DE Peptide analogue #8 of litorin, GRP, neuromedin or bombesin.

XX KW tissue proliferation; gastrin related peptide; peptide hormone.

XX OS Synthetic.

XX FH Key

Location/Qualifiers

FT Modified-site 1 /label= OTHER  
 FT /note= "D-para-chloro-Phe"  
 FT Modified-site 6  
 FT /label= D-Ala

XX WO9117181-A.

XX 14-NOV-1991.

XX 09-MAY-1991; 91WO-0003265.

XX 09-MAY-1990; 90US-0520226.

XX (TULA ) TULANE E FUND ADMINISTRA.

XX (BIOM-) BIOMEASURE INC.

XX Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

PT Peptide agonists of litorin, gastrin releasing peptide -  
 PT neuromedin B or C or bombesin, for treating cancer, preventing  
 PT smooth muscle proliferation and suppressing appetite and alcohol  
 PT craving

XX Claim 10; Page 18; 25pp; English.

XX The C-terminal residue is amidated. This peptide is one of 27  
 CC specific examples of a highly generic formula. The peptides are all  
 CC analogues of either litorin; the 10 amino acid C-terminal region of  
 CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 CC C-terminal region of amphibian bombesin. They act as at least partial  
 CC agonists of the natural peptides. The peptide analogues are made by  
 CC standard methods of synthesis and can be cyclised.  
 CC See AAR14860-R14880 and AAR15035-R15040.

XX SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 Db 2 qwavahl 8

Search completed: October 25, 2001, 11:22:45  
 Job time: 218 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:19:27 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-3  
Perfect score: 38  
Sequence: 1 XQWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	8	1	US-08-168-390-12
2	36	94.7	8	6	Sequence 12, Appl Patent No. 5217955
3	36	94.7	8	6	Patent No. 5217955-36
4	36	94.7	9	6	Sequence 2, Appl Patent No. 5217955
5	36	94.7	9	6	Patent No. 5217955-13
6	36	94.7	9	6	Sequence 4, Appl Patent No. 5217955
7	36	94.7	9	6	Patent No. 5217955-15
8	35	92.1	8	1	US-08-168-390-11
9	35	92.1	8	2	Sequence 11, Appl Patent No. 5217955
10	35	92.1	8	6	US-08-337-127-9
11	35	92.1	8	6	Sequence 9, Appl Patent No. 5217955-34
12	35	92.1	9	1	US-07-619-747B-1
13	35	92.1	9	1	Sequence 2, Appl Patent No. 5217955
14	35	92.1	9	1	US-07-619-747B-2
15	35	92.1	9	1	Sequence 4, Appl Patent No. 5217955
16	35	92.1	9	1	US-07-619-747B-5
17	35	92.1	9	1	Sequence 5, Appl Patent No. 5217955
18	35	92.1	9	1	US-07-619-747B-9
19	35	92.1	9	1	Sequence 10, Appl Patent No. 5217955
20	35	92.1	9	1	US-07-619-747B-12
21	35	92.1	9	1	Sequence 14, Appl Patent No. 5217955
22	35	92.1	9	1	US-07-619-747B-15
23	35	92.1	9	1	Sequence 15, Appl Patent No. 5217955
24	35	92.1	9	1	US-07-619-747B-17
25	35	92.1	9	1	Sequence 17, Appl Patent No. 5217955
26	35	92.1	9	1	US-07-619-747B-18
27	35	92.1	9	1	Sequence 18, Appl Patent No. 5217955
28	35	92.1	9	1	Sequence 22, Appl Patent No. 5217955
29	35	92.1	9	1	US-07-619-747B-23
30	35	92.1	9	1	Sequence 23, Appl Patent No. 5217955
31	35	92.1	9	1	US-07-619-747B-24
32	35	92.1	9	1	Sequence 24, Appl Patent No. 5217955
33	35	92.1	9	1	US-07-619-747B-25
34	35	92.1	9	1	Sequence 25, Appl Patent No. 5217955
35	35	92.1	9	1	US-07-619-747B-26

28 35 92.1 9 1 US-07-619-747B-27 Sequence 27, Appl  
29 35 92.1 9 1 US-07-619-747B-28 Sequence 28, Appl  
30 35 92.1 9 1 US-07-619-747B-29 Sequence 29, Appl  
31 35 92.1 9 1 US-07-619-747B-30 Sequence 30, Appl  
32 35 92.1 9 1 US-07-619-747B-31 Sequence 31, Appl  
33 35 92.1 9 1 US-07-619-747B-32 Sequence 32, Appl  
34 35 92.1 9 1 US-07-619-747B-33 Sequence 33, Appl  
35 35 92.1 9 1 US-07-619-747B-34 Sequence 34, Appl  
36 35 92.1 9 1 US-07-619-747B-35 Sequence 35, Appl  
37 35 92.1 9 1 US-07-619-747B-36 Sequence 36, Appl  
38 35 92.1 9 1 US-07-619-747B-37 Sequence 37, Appl  
39 35 92.1 9 1 US-07-619-747B-38 Sequence 38, Appl  
40 35 92.1 9 1 US-07-619-747B-39 Sequence 39, Appl  
41 35 92.1 9 1 US-07-619-747B-40 Sequence 40, Appl  
42 35 92.1 9 1 US-08-031-325A-37 Sequence 37, Appl  
43 35 92.1 9 1 US-08-263-905-4 Sequence 4, Appl  
44 35 92.1 9 1 US-08-263-905-5 Sequence 5, Appl  
45 35 92.1 9 1 US-08-263-905-6 Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end groups."

;  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-12

Query Match 94.7%; Score 36; DB 1; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAV AHL 8

RESULT 2  
5217955-35  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:35:  
; LENGTH: 8  
5217955-35

Query Match 94.7%; Score 36; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAV AHL 8

RESULT 3  
5217955-36  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:36:  
; LENGTH: 8  
5217955-36

Query Match 94.7%; Score 36; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAV AHL 8

RESULT 4  
5217955-13  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:13:  
; LENGTH: 9  
5217955-13

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAV AHL 8

RESULT 5  
5217955-14  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:14:  
; LENGTH: 9  
5217955-14

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAV AHL 8

RESULT 6  
5217955-15  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989  
; SEQ ID NO:15:  
; LENGTH: 9  
5217955-15

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAVAHL 8

## RESULT 7

5217955-22  
; Patent No. 5217955  
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:22:  
; LENGTH: 9  
5217955-22

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
DB 2 QWAVAHL 8

## RESULT 8

US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /note= "The amino-terminal residue

; OTHER INFORMATION: comprises one of several chemical end caps."

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 8

; OTHER INFORMATION: /note= "The carboxy-terminal

; OTHER INFORMATION: residue comprises an ethyl ester."

US-08-168-390-11

Query Match 92.1%; Score 35; DB 1; Length 8;

Best Local Similarity 85.7%; Pred. No. 1.5e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

| | | | |

DB 2 QWAVGHL 8

## RESULT 9

US-08-337-127-9  
; Sequence 9, Application US/08337127  
; Patent No. 5877277  
; GENERAL INFORMATION:  
; APPLICANT: Coy, David H.  
; APPLICANT: Moreau, Jacques-Pierre  
; APPLICANT: Kim, Sun H.  
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
; TITLE OF INVENTION: ANALOGS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,127  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/779,039  
; FILING DATE: 10/18/91  
; APPLICATION NUMBER: 07/502,438  
; FILING DATE: 03/30/90  
; APPLICATION NUMBER: 07/397,169  
; FILING DATE: 08/21/89  
; APPLICATION NUMBER: 07/376,555  
; FILING DATE: 07/07/89  
; APPLICATION NUMBER: 07/317,941  
; FILING DATE: 03/02/89  
; APPLICATION NUMBER: 07/282,328  
; FILING DATE: 12/09/88  
; APPLICATION NUMBER: 07/257,998

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;
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/00900D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
;
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an methylester C-terminus (i.e., COOCH3),
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).
US-08-337-127-9
```

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Query Match 92.1%; Score 35; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 QWAVXHL 8
Db 2 QWAVGHL 8
```

```
RESULT 10
5217955-32
; Patent No. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:32:
; LENGTH: 8
5217955-32
```

```
Query Match 92.1%; Score 35; DB 6; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 QWAVXHL 8
Db 2 QWAVGHL 8
```

```
RESULT 11
5217955-34
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```
; Patent No. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:34:
; LENGTH: 8
5217955-34
```

```
Query Match 92.1%; Score 35; DB 6; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 QWAVXHL 8
Db 2 QWAVGHL 8
```

```
RESULT 12
US-07-619-747B-1
; Sequence 1, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren Zhi
; APPLICANT: Schally, Andrew V.,
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
```

;  
;  
;  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-1

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||||||  
DB 2 QWAVGHL 8

RESULT 13  
US-07-619-747B-2  
; Sequence 2, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619.747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-2

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

DB 2 QWAVGHL 8  
||||||

RESULT 14  
US-07-619-747B-4  
; Sequence 4, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619.747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is 5F-D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-4

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||||||  
DB 2 QWAVGHL 8

RESULT 15  
US-07-619-747B-5  
; Sequence 5, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,

; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
 ; TITLE OF INVENTION: Antagonists  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dr. Andrew V. Schally  
 ; STREET: 5025 Kawanue Avenue  
 ; CITY: Metairie  
 ; STATE: Louisiana  
 ; COUNTRY: USA  
 ; ZIP: 70002  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 360K Diskette  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: DOS 5.0  
 ; SOFTWARE: WP 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/619,747B  
 ; FILING DATE: 19901129  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: No. 5244883e  
 ; FILING DATE: N/A  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Behr, Omri M.  
 ; REGISTRATION NUMBER: 22,940  
 ; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908)494-5240  
 ; TELEFAX: 1-908-494-0428  
 ; TELEX: 511642 BEPATEDIN  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9  
 ; TYPE: AMINO  
 ; STRANDEDNESS: Unknown  
 ; TOPOLOGY: Unknown  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; OTHER INFORMATION: Position 1 is D-Tpi  
 ; OTHER INFORMATION: Position 8 is a reduced  
 ; OTHER INFORMATION: isostere of named aminoacid  
 ; US-07-619-747B-5

Query Match 92.1%; Score 35; DB 1; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Caps 0;  
 QY 2 QWAVXHL 8  
 Db 2 QWAVGHL 8

Search completed: October 25, 2001, 11:23:56  
 Job time: 269 sec

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	37	92.5	266	5	Q9VZF7		Q9vzf7 drosophila
2	36	90.0	224	4	Q9UI28		Q9ui28 homo sapien
3	36	90.0	232	3	Q9UVE4		Q9uve4 zygosaaccha
4	36	90.0	256	3	Q9P6Y1		Q9p6y1 neurospora
5	35	87.5	252	10	Q9F120		Q9fi20 arabidopsis
6	34	85.0	119	13	Q9O253		Q9o253 bombina ori
7	34	85.0	276	5	Q9V5C9		Q9v5c9 drosophila
8	33	82.5	23	13	Q9PS30		Q9ps30 oncorhynchu
9	33	82.5	157	13	Q9I829		Q9i829 carassius a
10	33	82.5	211	2	Q9WWT3		Q9wwt3 pseudomonas
11	33	82.5	372	2	Q9HVL9		Q9hvl9 pseudomonas
12	33	82.5	387	2	Q9JN79		Q9jnn79 streptomyce
13	33	82.5	396	4	Q99986		Q99986 homo sapien
14	33	82.5	399	5	Q9U0V1		Q9u0v1 leishmania
15	33	82.5	700	2	Q07711		Q07711 staphylococ
16	33	82.5	721	2	Q9K7H4		Q9k7h4 bacillus ha
17	33	82.5	822	2	Q33831		Q33831 thermotoga
18	33	82.5	1121	2	Q9RNX9		Q9rnrx9 escherichia
19	32	80.0	109	14	Q9WD80		Q9wd80 influenza b

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AE003480; AAF47866.2; -.  
 DR HSP: P56276; 1TLK.  
 DR FlyBase: FBgn0001257; Impl2.  
 DR Pfam: PF00047; Ig: 4.  
 SQ SEQUENCE 266 AA; 29823 MW; FC97694BDF80F33 CRC64;

Query Match 92.5%; Score 37; DB 5; Length 266;  
 Best Local Similarity 85.7%; Pred. No. 5.1;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVVGHL 8  
 || |||||  
 Db 90 QWVVGHL 96

RESULT 2  
 ID Q9UI28 PRELIMINARY; PRT; 224 AA.  
 AC Q9UI28;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE ADRENAL GLAND PROTEIN AD-003.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RS TISSUE=ADRENAL GLAND;  
 RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,  
 Han Z., Wang Y., Chen Z., Fu G.;  
 RT "A novel gene expressed in human adrenal gland."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF110776; AAF14859.1; -.  
 DR InterPro: IPR000051; -.  
 DR InterPro: IPR001601; -.  
 SQ SEQUENCE 224 AA; 25474 MW; 8BB11B3FA7804CD3 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 224;  
 Best Local Similarity 71.4%; Pred. No. 6.8;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVVGHL 8  
 || |||||  
 Db 136 QWVVGHL 142

RESULT 3  
 ID Q9UIE4 PRELIMINARY; PRT; 232 AA.  
 AC Q9UIE4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE HYPOTHETICAL 26.4 KDA PROTEIN  
 OS Zygosaccharomyces rouxii (Candida mogii).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.  
 OX NCBI\_TaxID=4956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RS STRAIN=CBS 732;  
 RA Sychrova H., Braun V., Potier S., Souciet J.L.;  
 RT "Genomic organization of *Pichia sorbitophila* and *Zygosaccharomyces*  
 RT rouxii genomes: comparison with *Saccharomyces cerevisiae*."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y18560; CAB62288.1; -.  
 DR InterPro: IPR001601; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match 90.0%; Score 36; DB 3; Length 232;  
 Best Local Similarity 85.7%; Pred. No. 7.1;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVVGHL 8  
 || |||||  
 Db 140 QWVVGHL 146

RESULT 4  
 ID Q9P6Y1 PRELIMINARY; PRT; 256 AA.  
 AC Q9P6Y1;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE CONSERVED HYPOTHETICAL PROTEIN.  
 GN 13E11.350.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RS Schulte U., Aign V., Hoheisel J., Brandt P., Farlmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RS German Neurospora genome project;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL353820; CAB88603.1; -.  
 DR InterPro: IPR001601; -.  
 SQ SEQUENCE 256 AA; 27789 MW; 5251FBC58B6BDD9 CRC64;

Query Match 90.0%; Score 36; DB 3; Length 256;  
 Best Local Similarity 85.7%; Pred. No. 7.8;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVVGHL 8  
 || |||||  
 Db 162 QWVVGHL 168

RESULT 5  
 ID Q9FI20 PRELIMINARY; PRT; 252 AA.  
 AC Q9FI20;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MFC16.  
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=99397451; PubMed=10470850;  
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,  
 RA Miyajima N., Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.  
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen  
 RT p1 and TAC clones.";  
 RL DNA Res. 6:183-195(1999).  
 DR EMBL; AB017065; BAB09152.1; -.  
 SQ SEQUENCE 252 AA; 28622 MW; F93F8E657D284B2 CRC64;

Query Match 87.5%; Score 35; DB 10; Length 252;  
 Best Local Similarity 71.4%; Pred. No. 12;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVGHL 8  
 DB 147 QWCIGHL 153  
 II :|||

RESULT 6  
 Q90253 PRELIMINARY; PRT; 119 AA.  
 ID Q90253  
 AC Q90253  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE PHE-13 BOMBESIN PREPROHORMONE.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=96205965; PubMed=8631814;  
 RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,  
 RA Dong J.Z., Spindel E.R.;  
 RT "There are three distinct forms of bombesin. Identification of  
 RT [Leu13]bombesin, [Phe13]bombesin, and [Ser3,Arg10,Phe13]bombesin in  
 RT the frog Bombina orientalis.";  
 RT J. Biol. Chem. 271:7731-7737(1996).  
 DR EMBL; U49450; AAC59784.1; -.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 FT CHAIN 45 59 PHE-13 BOMBESIN.  
 SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 85.0%; Score 34; DB 13; Length 119;  
 Best Local Similarity 83.3%; Pred. No. 9.3;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVGHL 7  
 DB 51 QWAVGH 56  
 II :|||

RESULT 7  
 Q9V5C9 PRELIMINARY; PRT; 276 AA.  
 ID Q9V5C9  
 AC Q9V5C9  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE, GRP.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GN CG1675.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscumorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=107311132;  
 RA Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.A.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davis P.  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purf V., Rees M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003831; AAF58883.1; -.  
 DR FlyBase; FBgn0033457; CG1675.  
 DR InterPro; IPR001601; -.  
 SQ SEQUENCE 276 AA; 30601 MW; 917222EFC544A385 CRC64;

Query Match 85.0%; Score 34; DB 5; Length 276;  
 Best Local Similarity 71.4%; Pred. No. 22;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8  
 DB 182 QWVLGHL 188  
 II :|||

RESULT 8  
 Q9PS30 PRELIMINARY; PRT; 23 AA.  
 ID Q9PS30  
 AC Q9PS30;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE, GRP.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=93126164; PubMed=1480521;  
 RA Jensen J., Conlon J.M.;  
 RT "Isolation and primary structure of gastrin-releasing peptide from a  
 RT teleost fish, the trout (*Oncorhynchus mykiss*).";  
 RL Peptides 13:995-999(1992).  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 SQ SEQUENCE 23 AA: 2479 MW: 94CD79F70E3DB637 CRC64;

Query Match 82.5%; Score 33; DB 13; Length 23;  
 Best Local Similarity 83.3%; Pred. No. 2.8;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 3 WXVGH 8  
 | ||||  
 Db 17 WAVGHL 22

RESULT 9  
 Q9I829 PRELIMINARY; PRT; 157 AA.  
 AC Q9I829  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE PRECURSOR.  
 GN GRP.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20336817; PubMed=10876046;  
 RA Volkoff H., Peyon P., Lin X., Peter R.E.;  
 RT "Molecular cloning and expression of cDNA encoding a brain  
 RT bombesin/gastrin-releasing peptide-like peptide in goldfish.";  
 RL Peptides 21:639-648(2000).  
 DR EMBL; AF111028; AAF82387.1; -.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW SIGNAL.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 157 GASTRIN-RELEASING PEPTIDE.  
 SQ SEQUENCE 157 AA: 18201 MW: DD927EE19FD43117 CRC64;

Query Match 82.5%; Score 33; DB 13; Length 157;  
 Best Local Similarity 83.3%; Pred. No. 20;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 3 WXVGH 8  
 | ||||  
 Db 43 WAVGHL 48

RESULT 10  
 Q9WWT3 PRELIMINARY; PRT; 211 AA.  
 AC Q9WWT3  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE HYPOTHETICAL 23.6 KDA PROTEIN (FRAGMENT).

OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=PRS2000;  
 RA Nichols N.N., Harwood C.S.;  
 RT "Aerotaxis receptor of Pseudomonas putida PRS2000.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF079997; AAD22404.1; -.  
 DR InterPro; IPR000114; -.  
 DR InterPro; IPR000160; -.  
 DR InterPro; IPR000700; -.  
 DR InterPro; IPR001610; -.  
 DR Pfam; PF00785; PAC; 1.  
 DR Pfam; PF00989; PAS; 1.  
 DR Pfam; PF00990; DUF9; 1.  
 DR SMART; SM00267; DUF1; 1.  
 KW Hypothetical protein.  
 FT NON\_TER 211 211  
 SQ SEQUENCE 211 AA: 23566 MW: F113AF955610BBE5 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 211;  
 Best Local Similarity 83.3%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 7  
 || |||  
 Db 125 QWRVGH 130

RESULT 11  
 Q9HVL9 PRELIMINARY; PRT; 372 AA.  
 AC Q9HVL9  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE GLUTAMATE 5-KINASE.  
 GN PROB OR PA4565.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=PA01;  
 RC MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.K., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL; AE004870; AAG07953.1; -.  
 DR InterPro; IPR001048; -.  
 DR InterPro; IPR001057; -.  
 DR InterPro; IPR002478; -.  
 DR Pfam; PF00696; aakinas; 1.  
 DR Pfam; PF01472; PUA; 1.  
 DR PRINTS; PR00474; GLUTSKINASE.  
 DR PROSITE; PS00902; GLUTAMATE\_5\_KINASE; UNKNOWN\_1.  
 KW Kinase.  
 SQ SEQUENCE 372 AA: 39845 MW: FAF2E81F6A8DEC36 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 372;  
 Best Local Similarity 71.4%; Pred. No. 47;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWXXVGH 8

II III

Db 271 QWLGLH 277

RESULT 12

Q9JN79

ID Q9JN79 PRELIMINARY; PRT; 387 AA.

AC Q9JN79;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE PUTATIVE ENOYL REDUCTASE.

GN MYE.

OS Streptomyces coelicolor.

OG Plasmid pSCP1.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI\_TaxID=1902;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Bruton C.J.; Wietzorrek A., Hartley N., Woodburn L., Chater K.F.;

RT "Genes involved in methylenomycin biosynthesis from plasmid SCP1 of

Streptomyces coelicolor A3(2).";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RX MEDLINE=88112873; PubMed=2828187;

RA Neal R.J., Chater K.F.;

RT "Nucleotide sequence analysis reveals similarities between proteins

determining methylenomycin A resistance in Streptomyces and

tetracycline resistance in eubacteria.";

RL Gene 58:229-241(1987).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RX MEDLINE=85284984; PubMed=2992952;

RA Chater K.F., Bruton C.J.;

RT "Resistance, regulatory and production genes for the antibiotic

methylenomycin are clustered.";

RL EMBO J. 4:1893-1897(1985).

DR EMBL; AJ276673; CAB82878.1; -.

DR InterPro: IPR001155; -.

DR Pfam: PF00724; oxidored\_FMN; 1.

Plasmid.

SEQUENCE 387 AA; 40974 MW; 0149B42D0F6B90A3 CRC64;

Query Match

Best Local Similarity 82.5%; Score 33; DB 2; Length 387;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 7

II III

Db 246 QWKVGH 251

RESULT 13

Q99986

ID Q99986 PRELIMINARY; PRT; 396 AA.

AC Q99986;

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE VRK1, COMPLETE CDS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

QY

2 QWXXVGH 8

II III

RN

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=98008921; PubMed=9344656;

RA Nezu J., Oku A., Jones M.H., Shimane M.;

RT "Identification of two novel human putative serine/threonine kinases,

VRK1 and VRK2, with structural similarity to vaccinia virus H1R

kinase.";

RT Kinase.";

RL Genomics 45:327-331(1997).

CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AB000449; BAA19108.1; -.

DR HSP; Q06486; ICKI.

DR InterPro: IPR000719; -.

DR InterPro: IPR002290; -.

DR Pfam; PF00069; pkinase; 2.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

DR SMART; SM00220; S\_TKc; 1.

KW ATP-binding; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 396 AA; 45476 MW; 5640C624BF059949 CRC64;

Query Match

Best Local Similarity 82.5%; Score 33; DB 4; Length 396;

Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QWXXVGH 8

II III

Db 253 QWLTGHL 259

RESULT 14

Q9U0V1

ID Q9U0V1 PRELIMINARY; PRT; 399 AA.

AC Q9U0V1;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE MITOCHONDRIAL CARRIER PROTEIN.

GN L8342.02.

OS Leishmania major.

OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI\_TaxID=5664;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;

RA Masuy D., Purnelle B., Goffeau A., Ivens A.C., Lawson D., Quail M.,

Rajandream M.A., Barrell B.G.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;

RX MEDLINE=98146435; PubMed=9477341;

RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,

Smith D.F.;

RT "A physical map of the Leishmania major Friedlin genome.";

RL Genome Res. 8:135-145(1998).

DR EMBL; AL122012; CAB58416.1; -.

DR InterPro: IPR000847; -.

DR InterPro: IPR001993; -.

DR Pfam; PF00153; mito\_carr; 3.

DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; UNKNOWN\_1.

DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_2.

SQ SEQUENCE 399 AA; 43755 MW; A3D4E510517865C8 CRC64;

Query Match

Best Local Similarity 82.5%; Score 33; DB 5; Length 399;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8

II III

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Db 131 QWTLGHI 137

RESULT 15
Q07711
ID Q07711 PRELIMINARY; PRT; 700 AA.
AC Q07711
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
DE (UNTWISTING ENZYME) (SWIVELASE).
GN TRAI OR TRSI.
OS Staphylococcus aureus.
OG Plasmid pg01, and Plasmid pSV41.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RN [1] SEQUENCE FROM N.A.
PLASMID=PG01;
MEDLINE=93322322; PubMed=7687249;
RA Morton T.M., Eaton D.M., Johnston J.L., Archer G.L.;
RT "DNA sequence and units of transcription of the conjugative transfer
RT gene complex (trs) of Staphylococcus aureus plasmid pg01.";
RL J. Bacteriol. 175:4436-4447(1993).
RN [2]
RN [2] SEQUENCE FROM N.A.
PLASMID=PSV41;
MEDLINE=94123990; PubMed=8293996;
RA Firth N., Ridgway K.P., Byrne M.E., Fink P.D., Johnson L.,
RA Paulsen I.T., Skurray R.A.;
RT "Analysis of a transfer region from the staphylococcal conjugative
RT plasmid pSK41.";
RL Gene 136:13-25(1993).
RN [3]
RN [3] SEQUENCE FROM N.A.
PLASMID=PSV41;
MEDLINE=9839645; PubMed=9721269;
RA Berg T., Firth N., Apisiridej S., Hettiaratchi A., Leelaporn A.,
RA Skurray R.A.;
RT "Complete nucleotide sequence of pSK41: evolution of staphylococcal
RT conjugative multiresistance plasmids.";
RL J. Bacteriol. 180:4350-4359(1998).
DR EMBL; L11998; AAA71960.1; -
DR EMBL; AF051917; AAC61961.1; -
DR InterPro; IPR000380; -
DR InterPro; IPR002936; -
DR Pfam; PF01131; Topoisom_bac; 1.
DR Pfam; PF01396; zf-C4_Topoisom; 1.
DR Pfam; PF01751; Toprim; 1.
DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; UNKNOWN_1.
DR SMART; SMO0493; TOPRIM; 1.
KW Isomerase; Topoisomerase; DNA-binding; Plasmid.
SQ SEQUENCE 700 AA; 80742 MW; 1BB6BF2F2DB6142D CRC64;

Query Match 82.5%; Score 33; DB 2; Length 700;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WVGHL 8
Db 45 WVGHL 50

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Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	38	95.0	14	1	ALVT_ALYOB	P08944 alytes obst
2	38	95.0	107	1	BOMB_BOMVA	P01296 bombina var
3	37	95.0	119	1	BOMB_BOMOR	P21591 bombina ori
4	37	92.5	263	1	IML2_DROME	Q09024 drosophila
5	36	90.0	232	1	YB9H_YEAST	P38340 saccharomyc
6	34	85.0	9	1	LITO_LITAU	P08945 litoria aur
7	34	85.0	13	1	BOML_PSEUG	P42991 pseudophryn
8	34	85.0	82	1	RANA_RANPI	P08950 rana pipien
9	33	85.0	10	1	GRP_RANRI	P23260 rana ridibu
10	33	82.5	25	1	GRP_SCYCA	P08472 scyllorhinu
11	33	82.5	27	1	GRP_CANFA	P08989 canis famill
12	33	82.5	27	1	GRP_CHICK	P01295 gallus gall
13	33	82.5	27	1	GRP_PIG	P01294 sus scrofa
14	33	82.5	28	1	GRP_ALIMI	P31886 alligator m
15	33	82.5	120	1	NEUB_XENLA	P43443 xenopus lae
16	33	82.5	134	1	GRP_SHEEP	P47851 ovis aries
17	33	82.5	147	1	GRP_RAT	P24393 rattus norv
18	33	82.5	148	1	GRP_HUMAN	P07492 homo sapien
19	33	82.5	155	1	GRP_BOMOR	P29007 bombina ori
20	33	82.5	308	1	LIVH_ECOLI	P08340 escherichia
21	33	82.5	391	1	HERP_HUMAN	Q15011 homo sapien
22	33	82.5	1122	1	EXSC_ECOLI	P07648 escherichia
23	32	80.0	195	1	VMT2_INBAC	P13881 influenza b
24	32	80.0	195	1	VMT2_INBAD	P13882 influenza b
25	32	80.0	195	1	VMT2_INBLE	P03493 influenza b
26	32	80.0	195	1	VMT2_INBSI	P08383 influenza b
27	31	77.5	366	1	YBAB_BACIN	P44843 bacillus ci
28	31	77.5	651	1	TOP3_HAEIN	P43704 haemophilus
29	31	77.5	2151	1	RRPL_HANTV	P23456 hantaan vir
30	31	77.5	2151	1	RRPL_SBOU8	P27314 seoul virus
31	30	75.0	11	1	RANC_RANPI	P08951 rana pipien
32	30	75.0	17	1	RANR_RANRU	P08952 rana rugosa
33	30	75.0	133	1	ECHA_ECHCA	P81017 echis carin

RA Richter K., Egger R., Kreil G.;  
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
 RL of Bombina variegata.";  
 RN FEBS Lett. 262:353-355(1990).  
 RN [2]  
 RP SEQUENCE OF 42-55.  
 RC SPECIES=B variegata, and B.bombina;  
 RX MEDLINE=72163516; PubMed=4537042;  
 RA Anastasi A., Erspaner V., Buccì M.;  
 RT "Isolation and amino acid sequences of alytesin and bombesin, two  
 RT analogous active tetradecapeptides from the skin of European  
 RT discoglossid frogs.";  
 RL Arch. Biochem. Biophys. 148:443-446(1972).  
 CC -1- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 CC OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
 CC GASTROINTESTINAL HORMONES.  
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
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 CC -----  
 CC EMBL; X52447; CAA36686.1; -;  
 DR PIR; A01564; BSTD.  
 DR PIR; B01564; BSTDY.  
 DR PIR; S09095; S09095.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT PEPTIDE 1 24 POTENTIAL.  
 FT MOD\_RES 42 55 BOMBESIN.  
 FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;  
 Query Match 95.0%; Score 38; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 0.52;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVVGHL 8  
 DB 48 QWAVGHL 54  
 RESULT 3  
 BOMB\_BOMOR  
 ID BOMB\_BOMOR STANDARD; PRT; 119 AA.  
 AC P21591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE BOMBESIN PRECURSOR.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088602; PubMed=2263631;  
 RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;  
 RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
 RT relationship between bombesin and gastrin-releasing peptide.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
 CC -1- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 CC OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
 CC TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN  
 CC THE SKIN AND THE BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M55255; AAA48551.1; -;  
 DR PIR; A39261; A39261.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT PEPTIDE 1 58 BOMBESIN.  
 FT MOD\_RES 45 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 119 AA; 13863 MW; 3A3DB4EA2A45A44A CRC64;  
 Query Match 95.0%; Score 38; DB 1; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 0.57;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVVGHL 8  
 DB 51 QWAVGHL 57  
 RESULT 4  
 IML2\_DROME  
 ID IML2\_DROME STANDARD; PRT; 263 AA.  
 AC Q09024;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2 PRECURSOR.  
 GN IMPL2.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=CANTON-S; TISSUE=Embryo;  
 RX MEDLINE=94139565; PubMed=8306886;  
 RA Garbe J.C., Yang E., Fristrom J.W.;  
 RT "IMP-L2: an essential secreted immunoglobulin family member  
 RT implicated in neural and ectodermal development in Drosophila.";  
 RL Development 119:1237-1250(1993).  
 CC -1- FUNCTION: ESSENTIAL DEVELOPMENTAL ROLE DURING EMBRYOGENESIS, IN  
 CC PARTICULAR THE NORMAL DEVELOPMENT OF THE NERVOUS SYSTEM. MAY BE  
 CC INVOLVED IN SOME ASPECT OF CELL ADHESION.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: DETECTED IN SEVERAL SITES INCLUDING THE  
 CC VENTRAL NEUROECTODERM, THE TRACHEAL PITS, THE PHARYNX AND  
 CC OESOPHAGUS, AND SPECIFIC NEURONAL CELL BODIES, WHERE IT IS  
 CC PRIMARILY EXPRESSED.  
 CC -1- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT THE CELLULAR BLASTODERM  
 CC STAGE AND CONTINUES TO BE EXPRESSED THROUGH SUBSEQUENT  
 CC DEVELOPMENT.  
 CC -1- INDUCTION: BY 20-HYDROXYECDYSONE.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS  
 CC -----  
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CC -----

DR EMBL; L23066; AAB59251.1; -;  
DR HSSP; P56276; 1TLK.  
DR FLYBase; FBgn0001257; Impl2.  
DR InterPro; IPR003006; -;  
DR Pfam; PF00047; Ig; 2.  
KW Immunoglobulin domain; Cell adhesion; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 263  
FT -----  
FT DOMAIN 69 142 IG-LIKE C2-TYPE DOMAIN.  
FT DOMAIN 184 247 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFID 76 135 BY SIMILARITY.  
FT DISULFID 191 240 BY SIMILARITY.  
FT VARIANT 173 173 V -> I.  
SEQUENCE 263 AA; 29421 MW; 44AADB1B22DD1804 CRC64;

Query Match 92.5%; Score 37; DB 1; Length 263;  
Best Local Similarity 85.7%; Pred. No. 1.9;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8  
DB 87 QWVGH 93  
||| |||

RESULT 5  
ID YB9H\_YEAST  
AC YB9H\_YEAST STANDARD; PRT; 232 AA.  
DR P36340;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE HYPOTHETICAL 26.1 KDA PROTEIN IN POPA-SH1 INTERGENIC REGION.  
GN YBR261C OR YBR1729.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
PP SEQUENCE FROM N.A.  
STRAIN=S288C;  
MEDLINE=93220397; PubMed=8465606;  
RA Dognon F., Biteau N., Crouzet M., Aigle M.;  
RT "The complete sequence of a 19,482 bp segment located on the right  
RT arm of chromosome II from Saccharomyces cerevisiae.";  
RL Yeast 9:189-199(1993).  
CC -!- SIMILARITY: TO S.POMBE SPAC16B8.14C.  
CC -----

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CC -----

DR EMBL; X70529; CAA49926.1; -;  
DR EMBL; Z36130; CAA85224.1; -;  
DR PIR; S32963; S32963.  
DR SGD; S0000465; YBR261C.  
KW Hypothetical protein.  
SQ SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 232;

Best Local Similarity 85.7%; Pred. No. 2.7;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8  
DB 139 QWCVGH 145  
||| |||

RESULT 6  
LITO\_LITAU  
ID LITO\_LITAU STANDARD; PRT; 9 AA.  
AC P08945;

DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE LITORIN.  
OS Litoria aurea (Australian frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyllidae,  
OC Litoria.  
OX NCBI\_TaxID=8371;  
RN [1]  
PP SEQUENCE.

RX MEDLINE=75187011; PubMed=1140241;

RA Anastasi A., Erspamer V., Endeian R.;

RT "Aminoacid composition and sequence of litorin, a bombesin-like

RT nonapeptide from the skin of the Australian leptodactylid frog

RT Litoria aurea.";

RL Experientia 31:510-511(1975).

RN [2]

RP SEQUENCE (METHYLATED VARIANT).

RX MEDLINE=78003546; PubMed=908397;

RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endeian R.;

RT "Glu(Ome)3-litorin, the second bombesin-like peptide occurring in

RT methanol extracts of the skin of the Australian frog Litoria aurea.";

RL Experientia 33:1289-1289(1977).

CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN

CC FAMILY.

DR PIR; S07204; S07204.

DR PIR; S07205; S07205.

DR InterPro; IPR000874; -;

DR Pfam; PF02044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.

KW Bombesin family; Amidation; Methylation.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 2 2 METHYLATION (IN A VARIANT).

FT MOD\_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1103 MW; D7CCC1E86ZCDC366 CRC64;

QY 2 QWXXVGH 7  
DB 2 QWAVGH 7  
||| |||

RESULT 7

BOML\_PSEGU

ID BOML\_PSEGU STANDARD; PRT; 13 AA.

AC P42991;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE BOMBESIN-LIKE PEPTIDE L (PG-L).

OS Pseudophryne guentheri (Frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;

OC Pseudophryne.

OX NCBI\_TaxID=30349;

RN [1]

```

RP SEQUENCE.
RC TISSUE-Skin;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR: A60409; A60409.
DR InterPro: IPR000874; -.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.45;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWYVGH 7
DB 6 QWAVGH 11

RESULT 8
RANA_RANPI
ID RANA_RANPI STANDARD; PRT; 82 AA.
AC P08950;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RANATENSIN PRECURSOR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330837; PubMed=2458345;
RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;
RT "Molecular cloning of cDNAs encoding the human bombesin-like peptide
RT neuromedin B. Chromosomal localization and comparison to cDNAs
RT encoding its amphibian homolog ranatensin.";
J. Biol. Chem. 263:13317-13323(1988).
[2]
RP SEQUENCE OF 48-58.
RA Nakajima T., Tanimura T., Pisano J.J.;
RT "Isolation and structure of a new vasoactive polypeptide.";
Fed. Proc. 29:282-282(1970).
RL -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
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CC -----
DR EMBL: M21552; AAA49533.1; -.
DR PIR: B28945; B28945.
DR InterPro: IPR000874; -.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL 1 27 POTENTIAL.

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FT PROPEP 28 47
FT PEPTIDE 48 58
FT MOD_RES 58 58
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 85.0%; Score 34; DB 1; Length 82;
Best Local Similarity 83.3%; Pred. No. 2.5;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWYVGH 7
DB 51 QWAVGH 56

RESULT 9
GRP_RANRI
ID GRP_RANRI STANDARD; PRT; 10 AA.
AC P23260;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE NEUROMEDIN C.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE-Brain;
RX MEDLINE=91315477; PubMed=1859413;
RA Conlon J.M., O'Harte F., Vaudry H.;
RT "Primary structures of the bombesin-like neuropeptides in frog brain
RT show that bombesin is not the amphibian gastrin-releasing peptide.";
Biochem. Biophys. Res. Commun. 178:526-530(1991).
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR: PQ0177; PQ0177.
DR InterPro: IPR000874; -.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.56;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVGH 8
DB 4 WYVGH 9

RESULT 10
GRP_SCYCA
ID GRP_SCYCA STANDARD; PRT; 25 AA.
AC P09472;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE GASTRIN-RELEASING PEPTIDE (GRP).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RA Conlon J.M., Henderson I.W., Thim L.;
RT "Gastrin-releasing peptide from the intestine of the elasmobranch

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RT fish, Scyliorhinus canicula (common dogfish).";  
 RL Gen. Comp. Endocrinol. 68:415-420(1987).  
 CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 CC PIR; S06263; S06263.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 25 25  
 SQ SEQUENCE 25 AA; 2781 MW; B735F911B89007F8 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3 WXVGH 8  
 I I I I I  
 19 WVGHL 24

RESULT 11  
 GRP\_CANFA STANDARD; PRT; 27 AA.  
 ID GRP\_CANFA  
 AC P08989;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP-10)].  
 GN GRP.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83213518; PubMed=6853532;  
 RA Reeve J.R. Jr., Walsh J.H., Chew P., Clark B., Hawke D.,  
 RA Shively J.E.;  
 RT "Amino acid sequences of three bombesin-like peptides from canine  
 RT intestine extracts.";  
 RL J. Biol. Chem. 258:5582-5588(1983).  
 CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT PEPTIDE 18 27  
 FT MOD\_RES 27 27  
 SQ SEQUENCE 27 AA; 2889 MW; 9D9317261B7C7D65 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.4;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3 WXVGH 8  
 I I I I I  
 21 WVGHL 26

RESULT 12  
 GRP\_CHICK STANDARD; PRT; 27 AA.  
 ID GRP\_CHICK  
 AC P01295;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE (GRP) (PROVENTRICULAR PEPTIDE) [CONTAINS:  
 DE NEUROMEDIN C (GRP-10)].  
 GN GRP.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81164953; PubMed=7215543;  
 RA McDonald T.J., Joernvall H., Ghatel M., Bloom S.R., Mutt V.;  
 RT "Characterization of an avian gastric (proventricular) peptide having  
 RT sequence homology with the porcine gastrin-releasing peptide and the  
 RT amphibian peptides bombesin and aldynesin.";  
 RL FEBS Lett. 122:45-48(1980).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=90112926; PubMed=2297533;  
 RA Campbell B.J., Young J., Dimalline R., Dockray G.J.;  
 RT "Isolation, sequence and biosynthetic significance of a novel  
 RT fragment of gastrin-releasing peptide from chicken proventriculus.";  
 RL Biochim. Biophys. Acta 1048:66-71(1990).  
 CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR; A01563; RHCHA.  
 DR PIR; S08150; S08150.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT PEPTIDE 18 27  
 FT MOD\_RES 27 27  
 SQ SEQUENCE 27 AA; 2842 MW; 3C121D0118D551C7 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.4;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3 WXVGH 8  
 I I I I I  
 21 WVGHL 26

RESULT 13  
 GRP\_PIG STANDARD; PRT; 27 AA.  
 ID GRP\_PIG  
 AC P01294;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP-10)].  
 GN GRP.  
 OS Sus scrofa (Pig), and Cavia porcellus (Guinea pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=9823, 10141;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Pig;  
 RX MEDLINE=80042433; PubMed=496973;  
 RA McDonald T.J., Joernvall H., Nilsson G., Vagne M., Ghatel M.,  
 RA Bloom S.R., Mutt V.;  
 RT "Characterization of a gastrin releasing peptide from porcine  
 RT non-antral gastric tissue.";  
 RL Biochem. Biophys. Res. Commun. 90:227-233(1979).  
 RN [2]  
 RP SEQUENCE OF 18-27.  
 RC SPECIES=Pig;

XX MEDLINE=84153890; PubMed=6546686;  
RA Minamino N., Kangawa K., Matsuo H.;  
RT "Neuromedin C: a bombesin-like peptide identified in porcine spinal  
cord.";  
RL Biochem. Biophys. Res. Commun. 119:14-20(1984).  
RN [3]  
RN SEQUENCE.  
RC SPECIES=C.porcullus;  
RX MEDLINE=88034997; PubMed=3668528;  
RA Shaw C., Thim L., Conlon J.M.;  
RT "Primary structure and tissue distribution of guinea pig gastrin-  
releasing peptide.";  
RL J. Neurochem. 49:1348-1354(1987).  
CC -|- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
CC GASTROINTESTINAL HORMONES.  
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR PIR; A01562; RHPGA.  
DR PIR; A60206; RHGPGA.  
DR InterPro; IPR000874; -.  
PFam; PF02044; Bombesin; 1.  
PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT PEPTIDE 18 27 NEUROMEDIN C.  
FT MOD\_RES 27 27 AMIDATION.  
SQ SEQUENCE 27 AA; 2806 MW; FA1017260210410F CRC64;  
  
Query Match 82.5%; Score 33; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 1.4; Indels 1; Gaps 0;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
  
QY 3 WXXVGH 8  
| ||||  
Db 21 WAVGHL 26  
  
RESULT 14  
GRP\_ALLMI STANDARD; PRT; 28 AA.  
AC P31886; 1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP-10)].  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylia; Alligatoridae; Alligator.  
NCBI\_TaxID=8496;  
[1]  
RP SEQUENCE.  
RC TISSUE=Stomach;  
RX MEDLINE=93324451; PubMed=8101369;  
RA Wang Y., Conlon J.M.;  
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain  
and stomach of the alligator.";  
RL Peptides 14:573-579(1993).  
CC -|- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
CC GASTROINTESTINAL HORMONES.  
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT PEPTIDE 19 28 NEUROMEDIN C.  
FT MOD\_RES 28 28 AMIDATION.  
SQ SEQUENCE 28 AA; 2786 MW; A74DB0487D844963 CRC64;  
  
Query Match 82.5%; Score 33; DB 1; Length 28;  
Best Local Similarity 83.3%; Pred. No. 1.5; Indels 1; Gaps 0;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 WXXVGH 8  
| ||||  
Db 22 WAVGHL 27  
  
RESULT 15  
NEUB\_XENLA STANDARD; PRT; 120 AA.  
ID P43443;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE NEUROMEDIN B PRECURSOR.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OC NCBI\_TaxID=8355;  
[1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93028554; PubMed=1409705;  
RA Wechselberger C., Kreil G., Richter K.;  
RT "Isolation and sequence of a cDNA encoding the precursor of a  
bombesin-like peptide from brain and early embryos of Xenopus  
laevis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:9819-9822(1992).  
CC -|- FUNCTION: MAY BE A GROWTH FACTOR REQUIRED FOR THE HIGH RATE OF  
CELL DIVISION ENSUING AFTER FERTILIZATION, OR MAY HAVE A ROLE AS A  
SECRETAGOGUE THAT TRIGGERS THE RELEASE OF STORED COMPONENTS.  
CC -|- TISSUE SPECIFICITY: BRAIN, INTESTINE, AND OVARIES AND EARLY  
CC EMBRYOS (STAGES 2 AND 10).  
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L01530; AAA49912.1; -.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 29 POTENTIAL.  
FT PROPEP 30 44  
FT PEPTIDE 45 54 NEUROMEDIN B.  
FT MOD\_RES 54 54 AMIDATION (G-55 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 120 AA; 14384 MW; 2CB146BA082A2442 CRC64;  
  
Query Match 82.5%; Score 33; DB 1; Length 120;  
Best Local Similarity 66.7%; Pred. No. 5.6;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 QWVXGH 7  
| | :|  
Db 47 QWAIGH 52  
  
Search completed: October 25, 2001, 11:28:28  
Job time: 476 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:19 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-4  
Perfect score: 40  
Sequence: 1 QWXXVGH 8  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
1 number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	14	1 BSTD	bombesin - fire-be
2	38	95.0	107	1 BSTDY	bombesin precursor
3	38	95.0	119	2 A39261	bombesin precursor
4	36	90.0	232	2 S32963	hypothetical prote
5	36	90.0	256	2 T48787	hypothetical prote
6	34	85.0	9	2 S07204	litorin I - Austr
7	34	85.0	13	2 A60409	bombesin-like pept
8	34	85.0	82	2 B28945	ranatensin precurs
9	33	82.5	10	2 P00177	neuromedin C - lau
10	33	82.5	10	2 A60647	neuromedin C - bov
11	33	82.5	25	2 S06263	gastrin-releasing
12	33	82.5	27	1 RHGPGA	gastrin-releasing
13	33	82.5	27	1 RHGPGA	gastrin-releasing
14	33	82.5	27	1 RUCGA	gastrin-releasing
15	33	82.5	120	2 A47201	bombesinlike pepti
16	33	82.5	134	2 I47010	gastrin-releasing
17	33	82.5	138	2 A26182	gastrin-releasing
18	33	82.5	147	2 A40922	gastrin-releasing
19	33	82.5	148	1 B26182	gastrin-releasing
20	33	82.5	155	2 A42437	gastrin-releasing
21	33	82.5	308	1 QRECLH	leucine transport
22	33	82.5	308	2 H86012	hypothetical prote
23	33	82.5	372	2 G83074	glutamate 5-kinase
24	33	82.5	700	2 A56976	transfer complex p
25	33	82.5	721	2 C84073	DNA topoisomerase
26	33	82.5	1122	1 NCECXV	exodeoxyribonuclea
27	33	82.5	1122	2 A85934	hypothetical prote
28	32	80.0	195	1 MFIV2	matrix protein M2
29	32	80.0	195	1 MFIVB2	matrix protein M2

matrix protein M2  
matrix protein M2  
alpha-L-arabino-fur  
hypothetical prote  
hypothetical prote  
litorin 2 Glu - Au  
probable nitrite  
DNA topoisomerase  
RNA virus polymera  
genome polyprotein  
hypothetical prote  
hypothetical prote  
probable bacitraci  
hypothetical prote  
probable methylla  
hypothetical prote  
palmitoyl-protein

## ALIGNMENTS

RESULT 1  
BSTD  
bombesin - fire-bellied toad  
C:Species: Bombina bombina (fire-bellied toad)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998  
C:Accession: A01564  
R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin, two analogous a  
A:Reference number: A01564; MUID:72163516  
A:Accession: A01564  
A:Molecule type: protein  
A:Residues: 1-14 <ANA>  
C:Superfamily: gastrin-releasing peptide  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyroglutam  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 95.0%; Score 38; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 0.076;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWXXVGH 8  
Db 7 QWXXVGH 13  
RESULT 2  
BSTDY  
bombesin precursor - yellow-bellied toad  
C:Species: Bombina variegata (yellow-bellied toad)  
C:Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 18-Dec-2000  
C:Accession: S09095; B01564; A01564  
R:Richter, K.; Egger, R.; Kreil, G.  
FEBS Lett. 262, 353-355, 1990  
A:Title: Molecular cloning of a cDNA encoding the bombesin precursor in skin of Bombi  
A:Reference number: S09095; MUID:90242964  
A:Accession: S09095  
A:Molecule type: mRNA  
A:Residues: 1-107 <RIC>  
R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin, two analogous a  
A:Reference number: A01564; MUID:72163516  
A:Accession: B01564  
A:Molecule type: protein  
A:Residues: 42-55 <ANA>  
C:Superfamily: ranatensin  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide, pyroglutam  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-41/Domain: amino-terminal propeptide #status predicted <PRO>

F;42-55/Product: bombesin #status experimental <MAT>  
 F;56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
 F;42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F;55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 95.0%; Score 38; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 0.65;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8  
 || ||||  
 Db 48 QWAVGHL 54

RESULT 3  
 A39261  
 bombesin precursor - Bombina orientalis  
 C:Species: Bombina orientalis  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999  
 C:Accession: A39261  
 R:Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990  
 A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet  
 A:Reference number: A39261; MUID:91088602  
 A:Accession: A39261  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <SPI>  
 A:Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017  
 C:Superfamily: ranatensin  
 C:Keywords: neuropeptide

Query Match 95.0%; Score 38; DB 2; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 0.72;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8  
 || ||||  
 Db 51 QWAVGHL 57

RESULT 4  
 S32963  
 hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein YBR1729  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
 C:Accession: S32963; S46142  
 R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
 Yeast 9, 189-199, 1993  
 A:Title: The complete sequence of a 19,482 bp segment located on the right arm of chromo  
 A:Reference number: S29348; MUID:93220397  
 A:Accession: S32963  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-232 <DOI>  
 A:Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; PID:g296560  
 R:Aigle, M.; Bailet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45940  
 A:Accession: S46142  
 A:Molecule type: DNA  
 A:Residues: 1-232 <AIG>  
 A:Cross-references: EMBL:Z36130; NID:g5366688; PIDN:CAA85224.1; PID:g5366689; MIPS:YBR261c  
 C:Genetics:  
 A:Map position: 2R  
 C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 90.0%; Score 36; DB 2; Length 232;  
 Best Local Similarity 85.7%; Pred. No. 3.7;

QY 2 QWXXVGH 8  
 || ||||  
 Db 51 QWAVGHL 57

RESULT 4  
 S32963  
 hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein YBR1729  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
 C:Accession: S32963; S46142  
 R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
 Yeast 9, 189-199, 1993  
 A:Title: The complete sequence of a 19,482 bp segment located on the right arm of chromo  
 A:Reference number: S29348; MUID:93220397  
 A:Accession: S32963  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-232 <DOI>  
 A:Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; PID:g296560  
 R:Aigle, M.; Bailet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45940  
 A:Accession: S46142  
 A:Molecule type: DNA  
 A:Residues: 1-232 <AIG>  
 A:Cross-references: EMBL:Z36130; NID:g5366688; PIDN:CAA85224.1; PID:g5366689; MIPS:YBR261c  
 C:Genetics:  
 A:Map position: 2R  
 C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 90.0%; Score 36; DB 2; Length 232;  
 Best Local Similarity 85.7%; Pred. No. 3.7;

QY 2 QWXXVGH 8  
 || ||||  
 Db 51 QWAVGHL 57

RESULT 4  
 S32963  
 hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein YBR1729  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
 C:Accession: S32963; S46142  
 R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
 Yeast 9, 189-199, 1993  
 A:Title: The complete sequence of a 19,482 bp segment located on the right arm of chromo  
 A:Reference number: S29348; MUID:93220397  
 A:Accession: S32963  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-232 <DOI>  
 A:Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; PID:g296560  
 R:Aigle, M.; Bailet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45940  
 A:Accession: S46142  
 A:Molecule type: DNA  
 A:Residues: 1-232 <AIG>  
 A:Cross-references: EMBL:Z36130; NID:g5366688; PIDN:CAA85224.1; PID:g5366689; MIPS:YBR261c  
 C:Genetics:  
 A:Map position: 2R  
 C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8  
 || ||||  
 Db 139 QWCVGHL 145

RESULT 5  
 T48787  
 hypothetical protein 13E11.350 [imported] - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 28-Jul-2000  
 C:Accession: T48787  
 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu  
 submitted to the Protein Sequence Database, April 2000  
 A:Reference number: Z24541  
 A:Accession: T48787  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-256 <SCH>  
 A:Cross-references: EMBL:AL353820; GSPDB:GMO0112; NCSP:13E11.350  
 A:Experimental source: cosmid contig 13E11; strain 74  
 C:Genetics:  
 A:Gene: NCSP:13E11.350  
 A:Map position: 2  
 A:Introns: 213/2  
 C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 90.0%; Score 36; DB 2; Length 256;  
 Best Local Similarity 85.7%; Pred. No. 4.1;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 8  
 || ||||  
 Db 162 QWCVGHL 168

RESULT 6  
 S07204  
 Litorin I - Australian tree frog (Litoria aurea)  
 C:Species: Litoria aurea  
 C:Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
 C:Accession: S07204  
 R:Anastasi, A.; Erspamer, V.; Endean, R.  
 Experientia 31, 510-511, 1975  
 A:Title: Amino acid composition and sequence of litorin, a bombesin-like nonapeptide f  
 A:Reference number: S07204; MUID:75187011  
 A:Accession: S07204  
 A:Molecule type: protein  
 A:Residues: 1-9 <ANA>  
 C:Superfamily: gastrin-releasing peptide  
 C:Keywords: amidated carboxyl end; neuroptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 85.0%; Score 34; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 7  
 || ||||  
 Db 2 QWAVGH 7

RESULT 7  
 A60409  
 bombesin-like peptide L - frog (Pseudophryne guentheri)  
 C:Species: Pseudophryne guentheri  
 C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
 C:Accession: A60409  
 R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; M...

Peptides 11, 299-304, 1990  
 A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian rainforest frog  
 A:Reference number: A60409; MUID:90287814  
 A:Accession: A60409  
 A:Molecule type: protein  
 A:Residues: 1-13 <SIM>

C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 F:13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 85.0%; Score 34; DB 2; Length 13;  
 Best Local Similarity 83.3%; Pred. No. 0.48;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGVH 7

Db 6 QWVGVH 11

RESULT 8

B28945  
 ranatensin precursor - northern leopard frog  
 C:Species: Rana pipiens (northern leopard frog)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
 C:Accession: B28945  
 R:Krahn, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.  
 J. Biol. Chem. 263, 13317-13323, 1988

A:Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromedin  
 A:Reference number: A92667; MUID:88330837  
 A:Accession: B28945

A:Molecule type: mRNA

A:Residues: 1-82 <KRA>

A:Cross-references: GB:M21552; GB:M21552; PIDN:AAA49533.1; PID:g213694

C:Superfamily: ranatensin

C:Keywords: neuropeptide

Query Match 85.0%; Score 34; DB 2; Length 82;  
 Best Local Similarity 83.3%; Pred. No. 3.3;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGVH 7

Db 51 QWVGVH 56

RESULT 9

neuromedin C - laughing frog  
 C:Species: Rana ridibunda (laughing frog)  
 C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 11-Jan-2000  
 C:Accession: PQ0177  
 R:Conlon, J.M.; O'Harte, F.; Vaudry, H.

Biochem. Biophys. Res. Commun. 178, 526-530, 1991

A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show that  
 A:Reference number: PQ0177; MUID:91315477  
 A:Accession: PQ0177

A:Molecule type: protein

A:Residues: 1-10 <CON>

C:Experimental source: brain

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end

F:10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 82.5%; Score 33; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 0.59;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVGH 8

Db 11 WYVGH 11

Db 4 WAVGHL 9

RESULT 10

neuromedin C - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999  
 C:Accession: A60647  
 R:Lemaire, S.; Trifaro, J.M.; Chouinard, L.; Cecyre, D.; Dessureault, J.; Mercier, P.

Peptides 10, 355-360, 1989

A:Title: Structural identification, subcellular localization and secretion of

A:Reference number: A60647; MUID:89331342

A:Accession: A60647

A:Molecule type: protein

A:Residues: 1-10 <LEM>

A:Note: this neuropeptide was purified from secretory granules of cells in the

C:Superfamily: gastrin-releasing peptide

C:Keywords: adrenal gland; neuropeptide

Query Match 82.5%; Score 33; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 0.59;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVGH 8

Db 4 WAVGHL 9

RESULT 11

S06263  
 gastrin-releasing peptide - smaller spotted catshark (tentative sequence) (fragment)  
 C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)  
 C:Date: 31-Mar-1990 #sequence\_revision 30-Jan-1998 #text\_change 31-Mar-2000  
 C:Accession: S06263

R:Conlon, J.M.; Henderson, I.W.; Thim, L.

Gen. Comp. Endocrinol. 68, 415-420, 1987

A:Title: Gastrin-releasing peptide from the intestine of the elasmobranch fish, Scyli

A:Reference number: S06263; MUID:88137922

A:Accession: S06263

A:Molecule type: protein

A:Residues: 1-25 <CON>

A:Note: the sequence from the summary is inconsistent with that from table 1 and tabl

C:Superfamily: gastrin-releasing peptide

C:Keywords: neuropeptide

Query Match 82.5%; Score 33; DB 2; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.5;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVGH 8

Db 19 WAVGHL 24

RESULT 12

RHPGA

gastrin-releasing peptide - pig

N:Contains: neuromedin C

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1981 #sequence\_revision 31-Mar-1981 #text\_change 20-Nov-1998

C:Accession: A01562; A32738; C60301

R:McDonald, T.J.; Jornvall, H.; Nilsson, G.; Vagne, M.; Ghatel, M.; Bloom, S.R.; Mutt

Biochem. Biophys. Res. Commun. 90, 227-233, 1979

A:Title: Characterization of a gastrin releasing peptide from porcine non-antral gast

A:Reference number: A01562; MUID:80042433

A:Accession: A01562

A:Molecule type: protein

A:Residues: 1-27 <MCD>

R:Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 119, 14-20, 1984

A;Title: Neuromedin C: a bombesin-like peptide identified in porcine spinal cord.  
 A;Reference number: A32738; MUID:84153890  
 A;Accession: A32738  
 A:Molecule type: protein  
 A;Residues: 18-27 <MIN>  
 C;Superfamily: gastrin-releasing peptide  
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; spinal cord; stomach  
 F:1-27/Product: gastrin-releasing peptide #status experimental <MAT>  
 F:18-27/Product: neuromedin C #status experimental <NEU>  
 F:27/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.7;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXVGH 8  
 Db 21 WVGHL 26

# RESULT 13

RHGPGA  
 N;Contains: gastrin-releasing peptide - guinea pig  
 C;Species: Cavia porcellus (guinea pig)  
 C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 20-Mar-1998  
 C;Accession: A60206  
 R;Shaw, C.; Thim, L.; Conlon, J.M.  
 J. Neurochem. 49, 1348-1354, 1987.  
 A;Title: Primary structure and tissue distribution of guinea pig gastrin-releasing peptide  
 A;Reference number: A60206; MUID:88034997  
 A;Accession: A60206  
 A:Molecule type: protein  
 A;Residues: 1-27 <SHA>  
 A;Note: the carboxyl-terminal residue was not determined directly, but an alpha-amidated ion times  
 C;Superfamily: gastrin-releasing peptide  
 C;Keywords: amidated carboxyl end; brain; hormone; intestine; neuropeptide; stomach  
 F:18-27/Product: neuromedin C #status predicted <NEU>  
 F:27/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.7;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXVGH 8  
 Db 21 WVGHL 26

# RESULT 14

RHCHA  
 N;Contains: gastrin-releasing peptide - chicken (fragment)  
 C;Species: Gallus gallus (chicken)  
 C;Date: 28-Feb-1981 #sequence\_revision 19-Apr-1996 #text\_change 19-Apr-1996  
 C;Accession: A01563; S08150  
 R;McDonald, T.J.; Jorvall, H.; Ghatel, M.; Bloom, S.R.; Mutt, V.  
 FEBS Lett. 122, 45-48, 1980  
 A;Title: Characterization of an avian gastric (proventricular) peptide having sequence  
 A;Reference number: A01563; MUID:81164953  
 A;Accession: A01563  
 A:Molecule type: protein  
 A;Residues: 1-27 <MCD>  
 R;Campbell, B.J.; Young, J.; Dimaline, R.; Dockray, G.J.  
 Biochim. Biophys. Acta 1048, 66-71, 1990  
 A;Title: Isolation, sequence and biosynthetic significance of a novel fragment of gastrin  
 A;Reference number: S08150; MUID:90122926  
 A;Accession: S08150  
 A:Molecule type: protein  
 A;Residues: 1-27 <CAM>

C;Superfamily: gastrin-releasing peptide  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F:1-27/Product: proventricular peptide #status experimental <PVPT>  
 F:27/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.7;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXVGH 8  
 Db 21 WVGHL 26

# RESULT 15

A47201  
 bombesinlike peptide - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998  
 C;Accession: A47201  
 R;Wechselberger, C.; Kreil, G.; Richter, K.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 9819-9822, 1992  
 A;Title: Isolation and sequence of a cDNA encoding the precursor of a bombesinlike peptide  
 A;Reference number: A47201; MUID:93028554  
 A;Accession: A47201  
 A;Status: preliminary  
 A:Molecule type: nucleic acid  
 A;Residues: 1-120 <WEC>  
 A;Note: sequence inconsistent with the nucleotide translation  
 A;Note: sequence extracted from NCBI backbone (NCBIN:115857, NCBIP:115858)  
 C;Superfamily: ranatensin

Query Match 82.5%; Score 33; DB 2; Length 120;  
 Best Local Similarity 66.7%; Pred. No. 7.8;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 7  
 Db 47 QWVGH 52

Search completed: October 25, 2001, 11:25:20  
 Job time: 333 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-4  
Perfect score: 40  
Sequence: 1 XOMXVGH 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

1 number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pap:\*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pap:\*  
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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	95.0	8	1	US-08-168-390-11
2	38	95.0	8	2	US-08-337-127-9
3	38	95.0	8	6	Patent No. 5217955
4	38	95.0	8	6	Patent No. 5217955-32
5	38	95.0	9	1	US-07-619-747B-1
6	38	95.0	9	1	US-07-619-747B-2
7	38	95.0	9	1	US-07-619-747B-4
8	38	95.0	9	1	US-07-619-747B-5
9	38	95.0	9	1	US-07-619-747B-9
10	38	95.0	9	1	US-07-619-747B-10
11	38	95.0	9	1	US-07-619-747B-12
12	38	95.0	9	1	US-07-619-747B-14
13	38	95.0	9	1	US-07-619-747B-15
14	38	95.0	9	1	US-07-619-747B-17
15	38	95.0	9	1	US-07-619-747B-18
16	38	95.0	9	1	US-07-619-747B-22
17	38	95.0	9	1	US-07-619-747B-23
18	38	95.0	9	1	US-07-619-747B-24
19	38	95.0	9	1	US-07-619-747B-25
20	38	95.0	9	1	US-07-619-747B-26
21	38	95.0	9	1	US-07-619-747B-27
22	38	95.0	9	1	US-07-619-747B-28
23	38	95.0	9	1	US-07-619-747B-29
24	38	95.0	9	1	US-07-619-747B-30
25	38	95.0	9	1	US-07-619-747B-31
26	38	95.0	9	1	US-07-619-747B-32
27	38	95.0	9	1	US-07-619-747B-33

28	38	95.0	9	1	US-07-619-747B-34	Sequence 1, Appl
29	38	95.0	9	1	US-07-619-747B-35	Sequence 3, Appl
30	38	95.0	9	1	US-07-619-747B-36	Sequence 5, Appl
31	38	95.0	9	1	US-07-619-747B-37	Sequence 6, Appl
32	38	95.0	9	1	US-07-619-747B-38	Sequence 7, Appl
33	38	95.0	9	1	US-07-619-747B-39	Sequence 8, Appl
34	38	95.0	9	1	US-07-619-747B-40	Sequence 9, Appl
35	38	95.0	9	1	US-08-031-325A-37	Sequence 10, Appl
36	38	95.0	9	1	US-08-263-905-4	Sequence 11, Appl
37	38	95.0	9	1	US-08-263-905-5	Sequence 3, Appl
38	38	95.0	9	1	US-08-263-905-6	Sequence 116, Appl
39	38	95.0	9	1	US-08-263-905-7	Sequence 6, Appl
40	38	95.0	9	1	US-08-263-905-10	Sequence 7, Appl
41	38	95.0	9	1	US-08-263-905-11	Sequence 10, Appl
42	38	95.0	9	1	US-07-919-731-3	Sequence 11, Appl
43	38	95.0	9	1	US-08-287-957-116	Sequence 3, Appl
44	38	95.0	9	1	US-08-240-711-6	Sequence 116, Appl
45	38	95.0	9	1	US-08-240-711-7	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2500  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-11

Query Match 95.0%; Score 38; DB 1; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
DB 2 QWVGH 8

RESULT 2

US-08-337-127-9  
Sequence 9, Application US/08337127  
Patent No. 5877277  
GENERAL INFORMATION:  
APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun H.  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
TITLE OF INVENTION: ANALOGS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,127  
FILING DATE: 07/07/89

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/779,039  
FILING DATE: 10/18/91  
APPLICATION NUMBER: 07/502,438  
FILING DATE: 03/30/90  
APPLICATION NUMBER: 07/397,169  
FILING DATE: 08/21/89  
APPLICATION NUMBER: 07/376,555  
FILING DATE: 07/07/89  
APPLICATION NUMBER: 07/317,941  
FILING DATE: 03/02/89  
APPLICATION NUMBER: 07/282,328  
FILING DATE: 12/09/88  
APPLICATION NUMBER: 07/257,998  
FILING DATE: 10/14/88  
APPLICATION NUMBER: 07/248,771  
FILING DATE: 09/23/88  
APPLICATION NUMBER: 07/207,759  
FILING DATE: 06/16/88  
APPLICATION NUMBER: 07/204,171  
FILING DATE: 06/08/88  
APPLICATION NUMBER: 07/173,311  
FILING DATE: 03/25/88  
APPLICATION NUMBER: 07/100,571  
FILING DATE: 09/24/87  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00537/00900D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The sequence contains at position 1 a pyroglutamate, rather than a glutamate, and has an methylester C-terminus (i.e., COOCH<sub>3</sub>), rather than a carboxyl C-terminus (i.e., COOH).  
US-08-337-127-9

Query Match 95.0%; Score 38; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
DB 2 QWVGH 8

RESULT 3

5217955-32  
Patent No. 5217955  
APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO: 32;  
LENGTH: 8  
5217955-32

Query Match 95.0%; Score 38; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
DB 2 QWVGH 8

RESULT 4

5217955-34  
Patent No. 5217955  
APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO: 34;  
LENGTH: 8  
5217955-34

Query Match 95.0%; Score 38; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 QMXVGH 8
      || ||||
Db      2 QWAVGH 8

RESULT      5
US-07-619-747B-1
; Sequence 1, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; APPLICANT: Schally, Andrew V.,
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BEPATDIN
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: Isostere of named aminoacid
US-07-619-747B-1

Query Match      95.0%; Score 38; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QMXVGH 8
      || ||||
Db      2 QWAVGH 8

RESULT      6
US-07-619-747B-2
; Sequence 2, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi

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; APPLICANT: Schally, Andrew V.,
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BEPATDIN
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: Position 1 is D-Trp
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: Isostere of named aminoacid
US-07-619-747B-2

Query Match      95.0%; Score 38; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY      2 QMXVGH 8
      || ||||
Db      2 QWAVGH 8

RESULT      7
US-07-619-747B-4
; Sequence 4, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; APPLICANT: Schally, Andrew V.,
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATDIN  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is 5F-D-Trp  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-4

Query Match 95.08; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXVGH 8  
|||  
DB 2 QWVXVGH 8

RESULT 8  
US-07-619-747B-5  
Sequence 5, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren zhi  
TITLE OF INVENTION: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e

FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATDIN  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Tpi  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-5

Query Match 95.08; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXVGH 8  
|||  
DB 2 QWVXVGH 8

RESULT 9  
US-07-619-747B-9  
Sequence 9, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren zhi  
TITLE OF INVENTION: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428

TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is NH2CO-Tip  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-9

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGHL 8  
DB 2 QWVGHL 8

RESULT 10  
US-07-619-747B-10  
; Sequence 10, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Trp  
; OTHER INFORMATION: Position 8 is a reduced

; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-10

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGHL 8  
DB 2 QWVGHL 8

RESULT 11  
US-07-619-747B-12  
; Sequence 12, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Tpi  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-12

QY 2 QWVGHL 8  
DB 2 QWVGHL 8

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

RESULT 12  
US-07-619-747B-14  
; Sequence 14, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is Hca  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
; OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-14

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

Qy 2 QWVXGHL 8  
Db 2 QWVXGHL 8

RESULT 13  
US-07-619-747B-15  
; Sequence 15, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin

; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-pGlu  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
; OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-15

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

Qy 2 QWVXGHL 8  
Db 2 QWVXGHL 8

RESULT 14  
US-07-619-747B-17  
; Sequence 17, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Phe  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-17

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGHL 8  
|||  
Db 2 QWVGHL 8

RESULT 15  
US-07-619-747B-18  
Sequence 18, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren zhi  
APPLICANT: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Trp  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-18  
Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 QWVGHL 8  
|||  
Db 2 QWVGHL 8

Search completed: October 25, 2001, 11:23:56  
Job time: 289 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:45 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-4  
Perfect score: 40  
Sequence: 1 XQXVGH L 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

al number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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- 2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT.\*
- 3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT.\*
- 4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT.\*
- 5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT.\*
- 6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT.\*
- 7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT.\*
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- 9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT.\*
- 10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT.\*
- 11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT.\*
- 12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT.\*
- 13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT.\*
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- 15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT.\*
- 16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT.\*
- 17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT.\*
- 18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT.\*
- 19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT.\*
- 20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT.\*
- 21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT.\*
- 22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	38	95.0	7 22 AAB48341	Bombesin/gastrin-r
2	38	95.0	8 11 AAR04531	Non-cyclic analogu
3	38	95.0	8 12 AAR11224	Linear litorin ana
4	38	95.0	8 12 AAR11240	Linear litorin ana
5	38	95.0	8 12 AAR14877	Peptide analogue #
6	38	95.0	8 13 AAR28456	Bombesin antagonis
7	38	95.0	8 13 AAR28459	Bombesin antagonis
8	38	95.0	8 16 AAW64910	Bombesin receptor
9	38	95.0	8 19 AAW50941	Bombesin antagonis
10	38	95.0	8 20 AAW92740	Bombesin peptide a
11	38	95.0	8 21 AAB08302	Amino acid sequenc

12	38	95.0	8 22 AAB72406	Bomb
13	38	95.0	9 11 AAR04526	Non-cyclic analogu
14	38	95.0	9 11 AAR04527	Non-cyclic analogu
15	38	95.0	9 11 AAR04529	Non-cyclic analogu
16	38	95.0	9 11 AAR04528	Non-cyclic analogu
17	38	95.0	9 11 AAR04530	Non-cyclic analogu
18	38	95.0	9 11 AAR08345	Example of peptid
19	38	95.0	9 12 AAR11520	Example of peptid
20	38	95.0	9 12 AAR11521	Example of peptid
21	38	95.0	9 12 AAR11522	Example of peptid
22	38	95.0	9 12 AAR11529	Example of peptid
23	38	95.0	9 12 AAR12033	Bombesin antagonis
24	38	95.0	9 12 AAR14860	Peptide analogue #
25	38	95.0	9 12 AAR14861	Peptide analogue #
26	38	95.0	9 12 AAR14862	Peptide analogue #
27	38	95.0	9 12 AAR14863	Peptide analogue #
28	38	95.0	9 12 AAR14864	Peptide analogue #
29	38	95.0	9 12 AAR14872	Peptide analogue #
30	38	95.0	9 12 AAR14876	Peptide analogue #
31	38	95.0	9 12 AAR14880	Cyclic analogue #
32	38	95.0	9 12 AAR15038	Cyclic analogue #
33	38	95.0	9 13 AAR24483	[psi8-4 pseudo] N
34	38	95.0	9 13 AAR24484	[psi8-4 pseudo] N
35	38	95.0	9 13 AAR24486	[psi8-4 pseudo] N
36	38	95.0	9 13 AAR24490	[psi8-4 pseudo] N
37	38	95.0	9 13 AAR24491	[psi8-4 pseudo] N
38	38	95.0	9 13 AAR24492	[psi8-4 pseudo] N
39	38	95.0	9 13 AAR24487	[psi8-4 pseudo] N
40	38	95.0	9 13 AAR24488	[psi8-4 pseudo] N
41	38	95.0	9 13 AAR24489	[psi8-4 pseudo] N
42	38	95.0	9 13 AAR24493	[psi8-4 pseudo] N
43	38	95.0	9 13 AAR28447	[psi8-4 pseudo] N
44	38	95.0	9 13 AAR28448	[psi8-4 pseudo] N
45	38	95.0	9 13 AAR28450	[psi8-4 pseudo] N

ALIGNMENTS

RESULT 1  
AAB48341  
ID AAB48341 standard; peptide; 7 AA.  
XX  
AC AAB48341;  
XX

20-APR-2001 (first entry)

DE Bombesin/gastrin-releasing peptide receptor-recognising peptide.  
XX Cancer; chemotherapy; heparin; thrombospondin; drug resistance;  
KW Toxicity; tumour; cytostatic; metalloprotease.  
XX Synthetic.

XX WO200078359-A2.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-US16955.

XX 21-JUN-1999; 99US-0140310.

XX (TUSZ/) TUSZYNSKI G.  
XX (WILL/) WILLIAMS T.  
XX (ACTO/) ACTOR P.

XX Tuszynski G, Williams T, Actor P;

XX WPI; 2001-080760/09.

XX Treating cancer involves administering chemotherapy agent containing a peptide or co-administering chemotherapy agent and the peptide.

PS Disclosure; Page 6; 44pp; English.  
 XX  
 CC The invention relates to a method of treating a patient suffering from  
 CC cancer that comprises administering a chemotherapy agent conjugated to a  
 CC peptide, or co-administering the agent and the peptide. The peptides can  
 CC be selected from heparin binding domains of the thrombospondin protein.  
 CC The method and compositions comprising the agent and the peptide are  
 CC useful for treating a patient with drug resistant cancer, and for  
 CC treating a patient with cancer to prevent drug resistance from occurring.  
 CC Toxic chemotherapeutic agent can also be used, as peptide conjugation and  
 CC co-administration can considerably reduce the toxicity of the agent and  
 CC allow less composition to be administered due to increased efficacy. More  
 CC effective treatment at lower doses is achieved by targeting the  
 CC chemotherapy agents to the tumour cells. The present sequence represents  
 CC bombesin/gastrin-releasing peptide receptor-recognising peptide.  
 XX  
 SQ Sequence 7 AA;

Query Match 95.0%; Score 38; DB 22; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGH 8  
 Db 1 qvagh 7

RESULT 2  
 AAR04531  
 ID AAR04531 standard; protein; 8 AA.  
 XX  
 AC AAR04531;  
 DT 24-SEP-1990 (first entry)  
 DE Non-cyclic analogue of amphibian bombesin and mammalian GRP.  
 DE Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
 KW therapeutic peptides.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= D-phenylalanine  
 XX  
 WO9003980-A.  
 19-APR-1990.  
 XX  
 PF 13-OCT-1989; 89WO-US00416.  
 XX  
 PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.  
 XX (TULA ) TULANE E FUND ADMINISTRA.  
 XX  
 PI Coy DH, Moreau J-P, Taylor JE, Kim SH;  
 DR WPI; 1990-147822/19.  
 XX  
 PT New non-cyclic analogues of mammalian gastrin releasing peptide -  
 PT and amphibian bombesin, used for cancer treatment eg small  
 PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.  
 XX  
 PS Claim 21; Page 55; 68pp; English.  
 XX  
 CC C-terminal = ethylamide or amide.  
 CC The peptide has an active site and a binding site for binding to a  
 CC target cell receptor, and has one of the following modifications:  
 CC (a) a deletion of a residue within the active site and a  
 CC modification of a residue outside of the active site; and  
 CC (b) a replacement of 1 or 2 residues within the active site with a

CC synthetic amino acid.  
 CC On binding to its receptor, the analogue acts as a competitive  
 CC inhibitor of the naturally occurring peptide but due to the  
 CC modifications, fails to exhibit the normal in vivo biological activity.  
 CC The peptides are useful for the treatment of benign or malignant  
 CC proliferation of tissues, eg cancers of the gastrointestinal  
 CC tract, pancreatic cancer, colon cancer, lung cancer or breast  
 CC cancer; for the treatment of atherosclerosis; and disorders of the  
 CC gastrointestinal tissues.  
 CC This peptide is a claimed example of a highly generic formula.  
 CC See also AAR04525-R04533.  
 XX  
 SQ Sequence 8 AA;

Query Match 95.0%; Score 38; DB 11; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGH 8  
 Db 2 qvagh 8

RESULT 3  
 AAR11224  
 ID AAR11224 standard; Protein; 8 AA.  
 XX  
 AC AAR11224;  
 DT 17-MAY-1991 (first entry)  
 DE Linear litorin analogue.  
 DE Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 KW diabetes.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..1  
 FT /label= D-p-chloro-phenylalanine  
 XX  
 PN WO9102746-A.  
 XX  
 PD 07-MAR-1991.  
 XX  
 PF 17-AUG-1990; 90WO-US04646.  
 XX  
 PR 21-AUG-1989; 89US-0397169.  
 PR 30-MAR-1990; 90US-0502438.  
 XX  
 PA (TULA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.  
 XX  
 PI Coy DH, Moreau JP, Kim SH;  
 DR WPI; 1991-087241/12.  
 XX  
 PT New linear peptide analogues of bombesin - modified to eliminate  
 PT biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.  
 XX  
 PS Claim 13; Page 53; 58pp; English.  
 XX  
 CC This peptide is a specifically claimed example of a generic  
 CC formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to an amide and Phe 8 has been replaced  
 CC by statine.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, atherosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological

CC activity.  
XX Sequence 8 AA;  
SQ

Query Match 95.0%; Score 38; DB 12; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8  
|| ||||  
Db 2 qwvghl 8

## RESULT 4

AAR11240  
ID AAR11240 standard; Protein; 8 AA.

XX AC AAR11240;

17-MAY-1991 (first entry)

Linear litorin analogue (II).

XX Bombesin; litorin analogue; linear; receptor affinity; cancer;  
KW diabetes.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1.1  
/label= D-p-chloro-phenylalanine

PN WO9102746-A.

XX PD 07-MAR-1991.

XX PF 17-AUG-1990; 90WO-US04646.

XX PR 21-AUG-1989; 89US-0397169.

XX PR 30-MAR-1990; 90US-0502438.

XX (TULA ) ADMIN TULANE EDUCATIONAL.

PA (BIOM-) BIOMEASURE INC.

XX PI Coy DH, Moreau JP, Kim SH;

XX WPI; 1991-087241/12.

New linear peptide analogues of bombesin - modified to eliminate biological activity while retaining receptor affinity, for treating cancer, diabetes, etc.

PS Claim 17; Page 53; 58pp; English.

XX This peptide is a specifically claimed example of a generic formula. The C-terminal amino acid (Met) of the naturally occurring peptide has been converted to an amide and Phe 8 has been replaced by beta-Ieu.

CC The peptide is useful for treating benign or malignant tissue proliferation, arteriosclerosis, gastrointestinal disorders and diabetes. They act as competitive inhibitors of natural peptides, since they bind to the cell receptors but have no biological activity.

CC The analogue may also be of a naturally occurring peptide terminating at the C-terminus with a Met residue, such as the 10 amino acid C-terminal region of mammalian GRP or amphibian bombesin.

XX See also AAR11239-242.

XX Sequence 8 AA;

Query Match 95.0%; Score 38; DB 12; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8  
|| ||||  
Db 2 qwvghl 8

## RESULT 5

AAR14877  
ID AAR14877 standard; Protein; 8 AA.

XX AC AAR14877;

XX DT 14-FEB-1992 (first entry)

XX DE Peptide analogue #18 of litorin, GRP, neuromedin or bombesin

XX KW tissue proliferation; gastrin related peptide; peptide hormone

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1  
/label= D-Phe

FT Modified-site 8  
/label= OTHER

FT /note= "Leu-propylamide"

XX WO9117181-A.

PN 14-NOV-1991.

XX PF 09-MAY-1991; 91WO-0003265.

XX PR 09-MAY-1990; 90US-0520226.

XX (TULA ) TULANE E FUND ADMINISTRA.

PA (BIOM-) BIOMEASURE INC.

XX PI Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

XX Peptide agonists of litorin, gastrin releasing peptide - neuromedin B or C or bombesin, for treating cancer, preventing smooth muscle proliferation and suppressing appetite and alcohol craving

XX Claim 20; Page 19; 25pp; English.

CC This peptide is one of 27 specific examples of a highly general formula. The peptides are all analogues of either litorin; the amino acid C-terminal region of mammalian GRP, neuromedin B, neuromedin C; or the 10 amino acid C-terminal region of amphibian bombesin. They act as at least partial agonists of the natural peptides. The peptide analogues are made by standard methods; synthesis and can be cyclised.

CC See AAR14860-R14880 and AAR15035-R15040.

XX Sequence 8 AA;

Query Match 95.0%; Score 38; DB 12; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8  
|| ||||  
Db 2 qwvghl 8

RESULT	7
AAAR28459	
ID	AAAR28459 standard; Protein; 8 AA.
XX	
AC	AAAR28459;
XX	
DT	09-DEC-1992 (first entry)
XX	
DE	Bombesin antagonist (27).
XX	
KW	Bombesin; GRP; gastrin releasing peptide.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1
FT	Modified-site
FT	/note= "Mpp-Glo; Mpp= 3-(4-methoxyphenyl) propionic acid"
FT	
FT	Modified-site
FT	7
FT	/label= psi
FT	/note= "residues 7-8 are linked via a pseudo peptide bond"
FT	
FT	Modified-site
FT	8
FT	/label= psi
FT	/note= "Trp(For), For= formyl; residues 7-8 are linked via a pseudo peptide bond"
XX	
XX	WO9209626-A.
XX	
PD	11-JUN-1992.
XX	
XX	
PF	15-NOV-1991; 91WO-US08534.
XX	
PR	29-NOV-1990; 90US-0619747.
XX	
PA	(TULA ) TULANE EDUCATIONAL FUND.
XX	
XX	Cai RZ, Schally AV;
XX	
XX	WPI; 1992-217019/26.
XX	
DR	
PT	New nona:peptide bombesin antagonists - used for treating
PT	hypergastrinaemic states, such as pernicious anaemia and
PT	Zollinger-Ellison syndrome and also used against lung and
PT	cancer, etc.
XX	
PS	Disclosure; Page 8; 50pp; English.
XX	
CC	The C-terminal is amidated. The peptide is an example of a high
CC	generic formula for bombesin antagonists which are [psi8-9 pseudo
CC	nonapeptides contg. D- or L-tryptophan or tryptophan analog
CC	2,3,4,9-tetrahydro-1H-pyrido[3,4-b]-indol-3-carboxylic acid (Tpt
CC	at the N- and/or C-terminal.
CC	The peptide is a bombesin/GRP (gastrin releasing peptide) antagonist
CC	and is useful for treatment of states of hypergastrinemia, e.g.
CC	pernicious anaemia, chronic atrophic gastritis, Zollinger-Ellison
CC	syndrome and vitiligo, associated with diffuse hyperplasia of
CC	gastric enterochromaffin-like cells, and with an increased risk
CC	developing multifocal gastric carcinoma tumours. The peptide can
CC	also be used to treat lung, colon and gastric cancers. Dosage 1
CC	1- 1000 microg/kg parenterally.
XX	
XX	Sequence 8 AA;
SQ	

```

Query Match          95.0%; Score 38; DB 13; Length 8;
Best Local Similarity 85.7%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY      2  QWXXVGH  8
        || ||| |
Db       1  qwavghl  7

```

RESULT 8  
AAW64910  
ID AAW64910 standard; peptide; 8 AA.  
XX AC AAW64910;  
XX DT 06-JUL-1999 (first entry)  
XX DE Bombesin receptor antagonist.  
XX KW Bombesin; antagonist; chlorambucil; peptic ulcer; pancreatitis;  
XX KW eating disorder; diabetes; acromegaly; enterocutaneous fistula;  
XX KW psoriasis; growth retardation; gastrointestinal motility disorder;  
XX KW antitumour.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1  
XX FT /note= "The amino terminal is acylated with acetyl,  
XX FT bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-amino]-  
XX FT L-phenylalanine or a chlorambucil group"  
XX FT Modified-site 8  
XX FT /note= "The carboxy terminal is in the form of an  
XX FT ethyl ester"  
XX FT  
XX FT W09500542-A1.  
XX PN  
XX PD 05-JAN-1995.  
XX PF 15-JUN-1994; 94WO-US06757.  
XX PR 17-DEC-1993; 93US-0168390.  
XX PR 18-JUN-1993; 93US-0078062.  
XX PA (PEPT-) PEPTIDE TECHNOLOGIES CORP.  
XX PI Chandrasekhar B, Knight M, Takahashi K;  
XX PI WPI; 1995-052004/07.  
XX DR  
XX PT New bombesin, gastrin releasing peptide or Neuromedin B or C derivs.  
XX PT - antagonists for treating conditions such as gastrointestinal  
XX PT disorders, psoriasis and cancers  
XX PS  
XX PS Claim 6; Page 34; 45pp; English.  
XX CC The patent discloses (1) the peptide sequence of bombesin (BBN),  
XX CC gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C,  
XX CC the peptide sequence having a chlorambucil group attached to the  
XX CC amino terminal; (2) a BBN receptor antagonist of formula  
XX CC R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
XX CC antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
XX CC In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
XX CC Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
XX CC amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His.  
XX CC The compounds act as potent BBN/GRP-like peptide antagonists. They  
XX CC can be used to inhibit the growth of cells that are sensitive to the  
XX CC growth-promoting effects of BBN, GRP or a related peptide such as  
XX CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
XX CC cancerous cells or tumours. They can also be used to inhibit the  
XX CC binding of BBN, GRP or a related peptide to cells capable of such  
XX CC binding. They can be used for treating e.g. peptic ulcer, pancreatitis,  
XX CC eating disorders, diabetes, acromegaly, enterocutaneous fistula,  
XX CC psoriasis, growth retardation, gastrointestinal motility disorders or  
XX CC tumours. The terminal structures of the compounds protect them from  
XX CC in vivo proteolysis and provide highly potent antagonist effects that  
XX CC persist for extended periods of time upon administration.  
XX SQ Sequence 8 AA;  
Query Match 95.0%; Score 38; DB 19; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0

Query Match 95.0%; Score 38; DB 16; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QWVXGHL 8  
DB 2 qwavghl 8  
RESULT 9  
AAW50941  
ID AAW50941 standard; peptide; 8 AA.  
XX AC AAW50941;  
XX DT 31-JUL-1998 (first entry)  
XX DE Bombesin antagonist (BOM1).  
XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;  
XX KW Substance P; cancer; inhibition.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 1  
XX FT /note= "D-form residue"  
XX FT Modified-site 8  
XX FT /note= "Leu-NHET"  
XX FT  
XX PN EP835662-A2.  
XX PD 15-APR-1998.  
XX PF 11-DEC-1996; 96EP-0309012.  
XX PR 08-OCT-1996; 96US-0727679.  
XX PR 16-AUG-1996; 96IN-0001822.  
XX PA (NAIM-) NAT INST IMMUNOLOGY.  
XX PI Jaggi M, Mukherjee R;  
XX PI WPI; 1998-208959/19.  
XX DR  
XX PT Composition containing analogues of vasoactive intestinal peptide,  
XX PT somatostatin - bombesin and substance P, for treatment of tumours  
XX PT and for inhibiting over-expression of these peptide(s)  
XX PS  
XX PS Claim 1; Page 4; 49pp; English.  
XX CC The invention relates to a new composition which comprises: (i) the  
XX CC somatostatin analogue SOM2 AGCRNFWKPTSDC (3-14 disulphide bridge),  
XX CC and (ii) at least 4 of the peptides: antagonist of vasoactive  
XX CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIPRI);  
XX CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin  
XX CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are  
XX CC more general compositions containing peptide analogues of somatostatin,  
XX CC VIP, bombesin and substance P. The compositions are used in human or  
XX CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour  
XX CC or cancer cells, particularly for treatment of leukaemia, lymphoma,  
XX CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,  
XX CC breast, kidney or particularly rectum and colon, and (b) to prevent  
XX CC inhibit or modulate over-expression of, e.g. VIP. A wide range of can-  
XX CC cells express receptors for VIP, somatostatin, bombesin and/or substance  
XX CC P. The present sequence represents bombesin antagonist (BOM1).  
XX SQ Sequence 8 AA;  
Query Match 95.0%; Score 38; DB 19; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0

QY 2 QWVXGHL 8  
 II IIII  
 Db 2 qvavghl 8

## RESULT 10

AAW92740  
 ID AAW92740 standard; peptide; 8 AA.

XX  
 AC AAW92740;

XX 30-APR-1999 (first entry)

DE Bombesin peptide analogue #6.

XX Bombesin; gastrin releasing peptide; GRP; GRF; litorin; proliferation;  
 KW growth hormone releasing factor; treatment; benign; malignant; tissue;  
 KW small-cell lung carcinoma; atherosclerosis; gastrointestinal disorder;  
 KW diabetes; diabetes related retinopathy.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Residue is pyroglutamate"

FT Modified-site 8 /note= "methyl ester C-terminus"

FT  
 FT  
 FT  
 FT  
 PN US5877277-A.

XX 02-MAR-1999.

XX 10-NOV-1994; 94US-0337127.

XX 18-OCT-1991; 91US-0779039.

XX 24-SEP-1987; 87US-0100571.

XX 25-MAR-1988; 88US-0173311.

XX 08-JUN-1988; 88US-0204171.

XX 16-JUN-1988; 88US-0207759.

XX 23-SEP-1988; 88US-0248771.

XX 14-OCT-1988; 88US-0257998.

XX 09-DEC-1988; 88US-0282328.

XX 02-MAR-1989; 89US-0317941.

XX 07-JUL-1989; 89US-0376555.

XX 30-MAR-1990; 90US-0502438.

XX 10-NOV-1994; 94US-0337127.

(BIOM-) BIOMEASURE INC.

(TULA ) TULANE EDUCATIONAL FUND.

XX Coy DH, Kim SH, Moreau J;

XX WPI; 1999-189718/16.

XX New peptides - useful for treating benign or malignant tissue  
 proliferation, gastrointestinal disorders and diabetes

XX Disclosure; Column 29-30; 22pp; English.

XX This invention describes novel peptides which are analogues of litorin  
 or the 10 amino acid carboxy-terminal region of mammalian gastrin  
 releasing peptide or the 10 amino acid carboxy-terminal region of  
 amphibian bombesin of formula (R1)(R2)A1-A2-Trip-A4-A5-A6-A7-W where A1 =  
 D-isomer of p-X-Phe, Trip or beta-Nal; X = F, Cl, Br, NO2, OH, H or Me;  
 A2 = Gly, Ala, Val, Gln, Asn, Leu, Ile, Met, p-X-Phe, Trp, Cys,  
 beta-Nal, His, 1-methyl-His or 3-methyl-His; A4 = Ala, Val, Gln, Asn,  
 Gly, Leu, Ile, Nle, alpha-aminobutyric acid, Met, p-X-Phe, Trp, Cys or  
 beta-Nal; A5 = Gln, Asn, Gly, Ala, Leu, Ile, Nle, alpha-aminobutyric  
 acid, Met, Val, p-X-Phe, Trp, Thr or beta-Nal; A6 = Sar, Gly or D-isomer  
 of Ala, N-methyl-Ala, Val, Gln, Asn, Leu, Ile, Met, p-X-Phe, Trp, Cys or  
 beta-Nal; A7 = His or 1-methyl or 3-methyl-His; W = -N(R3)-CH(z1)-R4-  
 , (CH2)-C(-O)V; R4 = CH2NH; Z1, Z2 = Gly, Ala, Val, Leu, Ile, Ser, Asp,

CC Asn, Glu, Gln, p-X-Phe, Trp, Cys, Met, Pro, Hyp or cyclohexylalanine;  
 CC OR5 or NR6R7; R3, R5, R6, R7 = H, lower alkyl, phenyl(lower alkyl) or  
 CC naphthyl(lower alkyl); R1, R2 = H, 112C alkyl, 7-10C phenylalkyl or  
 CC COEt; where R1 and R2 are bonded to the N-terminal amino acid of the  
 CC peptide; E1 = 1-20C alkyl, 3-20C alkenyl, 3-20C alkynyl, Ph, na; lhy;  
 CC or 7-10C phenylalkyl; provided that when 1 of R1 and R2 is COEt, the  
 CC other must be H. The peptides can be used for treating benign or  
 CC malignant proliferation of tissue e.g. small-cell lung carcinoma, or  
 CC atherosclerosis, gastrointestinal disorders, and diabetes or diabetes  
 CC related retinopathy. AAW92735-W92742 represent bombesin peptide  
 CC analogues used in the method of the invention.

XX Sequence 8 AA;

Query Match 95.0%; Score 38; DB 20; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 2 QWVXGHL 8  
 II IIII  
 Db 2 qvavghl 8

## RESULT 11

AAW08302

ID AAW08302 standard; peptide; 8 AA.

XX AAW08302;

XX 04-DEC-2000 (first entry)

XX Amino acid sequence of bombesin analogue BOM1.

XX Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;  
 KW VIP1; VIP2; VIP3; BOM1; bombesin; SP1; substance P; MuJ-7; tumour growth.  
 KW tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma,  
 KW leukaemia; lymphoma.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Modified-site 8

FT /note= "residue is Leu-NHET"

XX WC2000047221-A1.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03559.

XX 11-FEB-1999; 99US-0248381.

XX (NAIM-) NAT INST IMMUNOLOGY.

XX (DABU-) DABUR RES FOUND.

XX (CORD/) CORD J I.

XX Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A,  
 PI Singh AP;

XX WPI; 2000-549083/50.

XX Novel therapeutically active composition comprising at least 5  
 PT peptides, useful for treating angiogenesis especially as a result of  
 PT adenocarcinomas -

XX Disclosure; Page 8; 42pp; English.

XX The present sequence represents an analogue of bombesin. The  
 CC specification describes therapeutically active compositions comprising  
 CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), etc.

CC at least four analogues chosen from vasoactive intestinal peptide (VIP) 1  
 CC (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a VIP  
 CC receptor antagonist), BOM1 (a bombesin antagonist), and SP1 (a substance  
 CC P antagonist). The combination of these 7 analogues is known as MuJ-7.  
 CC MuJ-7 is used as an anticancer drug to restrict tumour growth and spread  
 CC by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits  
 CC metastasis through its antiangiogenic activity in all cancers. The  
 CC peptides are useful for the treatment and prevention of angiogenesis,  
 CC especially as a result of adenocarcinomas of the colon, breast, lung,  
 CC prostate, kidney, leukemias or lymphomas.  
 XX  
 SQ Sequence 8 AA;

Query Match 95.0%; Score 38; DB 21; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
 || ||||  
 2 qvavghl 8

RESULT 12  
 AAB72406  
 ID AAB72406 standard; peptide; 8 AA.  
 XX  
 AC AAB72406;

DT 03-MAY-2001 (first entry)

XX Bombesin analogue.

KW Gene therapy; gene transfer; gastrin releasing peptide receptor; GRPr;  
 KW bombesin analogue; BBN.

XX Unidentified.

PN WO200112234-A1.

XX 22-FEB-2001.

PF 16-AUG-2000; 2000WO-US22456.

XX 16-AUG-1999; 99US-0374972.

PR 01-JUN-2000; 2000US-0585194.

XX (UABR-) UAB RES FOUND.

PA Buchsbaum DJ, Curiel DT, Zinn KR, Rogers BE;

XX WPI; 2001-218310/22.

XX Monitoring therapeutic gene transfer and expression into a subject, by  
 PT administering vector encoding the gene and gene for membrane expressed  
 PT targeting molecule, and a radiolabelled ligand, and imaging gene  
 PT transfer -

XX Example 10; Page 33; 107pp; English.

PS The present invention relates to a method for monitoring therapeutic gene  
 XX transfer and expression into a subject, comprising administering a vector  
 CC encoding a therapeutic gene and a gene for a membrane expressed targeting  
 CC molecule (TM), and a radiolabelled ligand (RL) having high affinity for  
 CC TM, and detecting the binding of RL with TM. The binding is directly  
 CC proportional to the transfer and expression of the therapeutic gene.  
 CC Preferably, the TM is gastrin releasing peptide receptor (GRPr). A  
 CC technique was developed to image GRPr expression using a 99mTc-labelled  
 CC bombesin (BBN) analogue (the present sequence).  
 XX  
 SQ Sequence 8 AA;

Query Match 95.0%; Score 38; DB 22; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels

QY 2 QWVGH 8  
 || ||||  
 Db 1 qvavghl 7

RESULT 13

AAR04526  
 ID AAR04526 standard; protein; 9 AA.

XX  
 AC AAR04526;

DT 24-SEP-1990 (first entry)

XX Non-cyclic analogue of amphibian bombesin and mammalian GRP-  
 DE Mammalian gastrin releasing peptide; amphibian bombesin; cat  
 XX therapeutic peptides.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1

FT /label= OTHER

FT /note= "D-p-Cl"

FT Modified-site 8

FT /label=beta-homoleucine

XX WO9003980-A.

XX 19-APR-1990.

XX 13-OCT-1989; 89WO-US00416.

PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.

XX (TULA ) TULANE E FUND ADMINISTRA.

XX Coy DH, Moreau J-P, Taylor JE, Kim SH;

XX WPI; 1990-147822/19.

XX New non-cyclic analogues of mammalian gastrin releasing pe  
 PT and amphibian bombesin, used for cancer treatment eg small  
 PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.

XX Claim 8; Page 49; 68pp; English.

PS C-terminal = NH2.

XX The peptide has an active site and a binding site for binding  
 CC target cell receptor, and has one of the following modification  
 CC (a) a deletion of a residue within the active site and a  
 CC modification of a residue outside of the active site; and  
 CC (b) a replacement of 1 or 2 residues within the active site with  
 CC synthetic amino acid.

XX On binding to its receptor, the analogue acts as a competitor;  
 CC inhibitor of the naturally occurring peptide but due to the  
 CC modifications, fails to exhibit the normal in vivo biological activity.  
 CC The peptides are useful for the treatment of benign or malignant  
 CC proliferation of tissues, eg cancers of the gastrointestinal  
 CC tract, pancreatic cancer, colon cancer, lung cancer or breast  
 CC cancer; for the treatment of atherosclerosis; and disorders of the  
 CC gastrointestinal tissues.  
 CC This peptide is a claimed example of a highly generic formula.  
 CC See also AAR04525-R04533.

XX Sequence 9 AA;

Query Match 95.0%; Score 38; DB 11; Length 9;



Qy 2 QWVGHl 8  
I I I I I  
Db 2 qvavghl 8

Search completed: October 25, 2001, 11:22:45  
Job time: 218 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:45 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-5  
Perfect score: 28  
Sequence: 1 QXAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Full number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT.*
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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	85.7	9	14 AAR40907	Bombesin analogue
2	23	82.1	7	10 AAP91147	Sequence of new ne
3	23	82.1	7	13 AAR20585	Antagonist of bomb
4	23	82.1	7	13 AAR32998	[D-Ala11]-bombesin
5	23	82.1	7	20 AAW94610	Bombesin/gastrin r
6	23	82.1	8	3 AAP20294	Bombesin analog pe
7	23	82.1	8	12 AAR11241	Linear litorin ana
8	23	82.1	8	12 AAR11242	Linear litorin ana
9	23	82.1	8	13 AAR29155	Bombesin analogue
10	23	82.1	8	13 AAR29157	Bombesin analogue
11	23	82.1	8	16 AAW64911	Bombesin receptor

12	23	82.1	9	11 AAR09335	Seque of bomb
13	23	82.1	9	12 AAR11522	Exam of peptide
14	23	82.1	9	12 AAR14865	Peptide analogue
15	23	82.1	9	12 AAR14866	Peptide analogue
16	23	82.1	9	12 AAR14867	Peptide analogue
17	23	82.1	9	12 AAR14873	Peptide analogue
18	23	82.1	9	14 AAR40903	Bombesin analogue
19	23	82.1	9	19 AAW51195	Peptide derived f
20	23	82.1	9	19 AAW51201	Peptide derived f
21	23	82.1	10	10 AAP96113	Sequence of new m
22	23	82.1	24	19 AAW75003	Human secreted pro
23	23	82.1	180	20 AAY37918	Amino acid sequenc
24	23	82.1	218	21 AAB58984	Breast and ovarian
25	23	82.1	396	21 AAY75289	Neisseria gonorrhoe
26	23	82.1	500	20 AAY00207	Enterococcus faec
27	23	82.1	531	21 AAY59404	Human RICK protein
28	23	82.1	540	20 AAY31140	Human CARD-3 prote
29	23	82.1	540	20 AAW92795	Human R1 protein
30	23	82.1	540	21 AAY68774	Amino acid sequenc
31	23	82.1	540	22 AAB20079	Human CARD-3 prote
32	23	82.1	544	21 AAB43570	Human cancer associ
33	23	82.1	768	20 AAW98108	Caenorhabditis
34	23	82.1	935	21 AAB07570	Protein encoding
35	23	82.1	1074	20 AAY00206	Enterococcus faec
36	23	82.1	1074	20 AAY00188	Enterococcus faec
37	22	78.6	7	22 AAB48341	Bombesin/gastrin r
38	22	78.6	8	11 AAR04531	Non-cyclic analog
39	22	78.6	8	12 AAR11224	Linear litorin an
40	22	78.6	8	12 AAR11240	Linear litorin an
41	22	78.6	8	12 AAR14877	Peptide analogue
42	22	78.6	8	13 AAR28456	Bombesin antagonist
43	22	78.6	8	13 AAR28459	Bombesin antagonist
44	22	78.6	8	16 AAW64910	Bombesin receptor
45	22	78.6	8	22 AAB72406	Bombesin analogue

#### ALIGNMENTS

RESULT 1

AAR40907

ID AAR40907 standard; peptide; 9 AA.

XX AAR40907;

AC AAR40907;

DT 10-FEB-1994 (first entry)

XX Bombesin analogue #9.

DE Bombesin analogue #9.

XX Bombesin; analogue; antagonist; agonist; antimitotic; anti-secretory;

KW activity; digestion; food intake; tissue growth; lung; pancreas;

KW intestine; ulcer; cancer.

XX Synthetic.

OS Synthetic.

XX Key

FH Modified-site 1

FT Location/Qualifiers

FT /label= OTHER

FT /note= "Glp"

XX W09316105-A.

XX 19-AUG-1993.

XX 07-JAN-1993; 93WO-US00183.

XX 07-FEB-1992; 92US-0833834.

XX (RICH ) MERRELL DOW PHARM INC.

XX Edwards JV, Fanger BO;

XX WPI; 1993-272830/34.

XX Bombesin analogues contg. modified phenylalanine derivs. - used  
PT for stimulating digestion, decreasing food intake and stimulating  
PT growth of organ tissues  
XX Example 1; Page 43; 54pp; English.  
XX The sequences given in AAR40899-908 are bombesin analogues. These  
CC peptides were prepared by solid phase sequential or block  
CC synthesis. These peptides act as bombesin antagonists or agonists  
CC and have antimitotic and/or anti-secretory activity. They may be  
CC used for stimulating digestion in patients, decreasing food intake  
CC in patients or stimulating growth of organ tissue of lung, pancreatic  
CC or intestinal origin in patients. They can be used for the treatment  
CC of gastrointestinal and pancreatic ulcers and for the treatment of  
CC cancers.  
XX Sequence 9 AA;  
SQ  
XX Query Match 85.7%; Score 24; DB 14; Length 9;  
CC Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
CC Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX QY 2 QXAVXHL 8  
DB 3 qtavghl 9  
XX  
XX RESULT 2  
XX ID AAR91147 standard; protein; 7 AA.  
XX AC AAR91147;  
XX DT 13-MAY-1990 (first entry)  
XX DT 22-DEC-1990 (corrected)  
XX DE Sequence of new neuromedin C deriv.  
XX KW Bombesin antagonist; malignant disease; therapy; gastric acid secretion.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 1 /label=OTHER  
XX FT /note="Ac-D-Gln"  
XX FT Misc-difference 5 /label=OTHER  
XX FT /note="D-Ala"  
XX FT Misc-difference 7 /label=OTHER  
XX FT /note="Leu-Ome"  
XX EP315367-A.  
XX PN 10-MAY-1989.  
XX PD 27-OCT-1988; 88EP-0310094.  
XX PF 06-JUN-1988; 88GB-0013355.  
XX PR (ICIL ) IMPERIAL CHEM INDS PLC.  
XX PA Camble R, Cotton R, Dutta AS, Hayward CF;  
XX PI WPI; 1989-139341/19.  
XX DR New Neuromedin C polypeptide derivs. -  
XX PT are potent bombesin antagonist used for treating malignant  
XX PT disease and conditions associated with gastrin or gastric acid  
XX PT secretion  
XX PS Disclosure; Page 929; 49pp; English.

XX It is a potent bombesin antagonist. It may be used for the treatment of  
CC e.g. malignant disease, conditions associated with the over-production of  
CC bombesin and conditions associated with failure of normal physiological  
CC control of the regulation of gastric acid secretion.  
XX Sequence 7 AA;  
SQ  
XX Query Match 82.1%; Score 23; DB 10; Length 7;  
CC Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
CC Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX QY 2 QXAVXHL 8  
DB 1 qvavahl 7  
XX  
XX RESULT 3  
XX AAR20585  
XX ID AAR20585 standard; Peptide; 7 AA.  
XX AC AAR20585;  
XX DT 07-MAY-1992 (first entry)  
XX DE Antagonist of bombesin/GRP.  
XX KW Antitumour agent; leukaemia.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 5 /note="D-Ala"  
XX PN EP468497-A.  
XX PD 29-JAN-1992.  
XX PF 25-JUL-1991; 91EP-0112504.  
XX PR 26-JUL-1990; 90US-0558031.  
XX PA (RICH ) MERRELL DOW PHARM INC.  
XX PI Krstenansky JL;  
XX DR WPI; 1992-034251/05.  
XX PT New peptide bombesin-GRP antagonists - used as antitumour agents  
XX PT to treat e.g. leukaemia, small cell lung and prostatic carcinoma  
XX PT and to inhibit gastric acid secretion.  
XX PS Claim 7; Page 12; 14pp; English.  
XX The peptide is modified at the N-terminal with a lauryl, palmitoyl  
CC or esp. an octanoyl gp. The Leu at position 7 may be absent. The  
CC C-terminal (Leu or His) is amidated. The peptides and derived  
CC salts can be used to treat small cell lung carcinoma, prostatic  
CC carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-  
CC ciated conditions, and to effect antagonism of bombesin/gastrin  
CC releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at  
CC 5-200 mg/dose.  
XX Sequence 7 AA;  
SQ  
XX Query Match 82.1%; Score 23; DB 13; Length 7;  
CC Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
CC Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX QY 2 QXAVXHL 8

Db 1 ||||  
1 qvavahl 7

## RESULT 4

AAR32998  
ID AAR32998 standard; peptide; 7 AA.

AC AAR32998;  
XX

DT 13-APR-1993 (first entry)  
XX

DE [D-Ala11]-bombesin(7-13)amide derivs.  
XX

KW Intracellular signal; inhibition; gastrointestinal tract;  
KW litorin; Gastrin Releasing Peptide; GRP.  
XX

OS Synthetic.  
XX

Key Location/Qualifiers  
Modified-site 1

FT /label= OTHER  
FT /note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,  
FT N-alpha-lauryl-Gln or N-alpha-palmityl-Gln"

FT Misc-difference 5

FT /note= "D-Ala"

FT Modified-site 7  
FT /note= "amidated"

XX WO9220707-A.  
XX

PN 26-NOV-1992.  
XX

PD 21-APR-1992; 92WO-US03287.  
XX

PF 23-MAY-1991; 91US-0704863.  
XX

PR (RICH ) MERRELL DOW PHARM INC.  
XX

PI Edwards JV, Fanger BO;  
XX

PS WPI; 1992-415707/50.  
XX

DR New bombesin peptide agonists and antagonists - stimulate or  
XX inhibit digestion, increase susceptibility of tumours to  
XX chemotherapeutic agents, treat gastric ulcers and tumours etc.

PS Example; Page 40; 64pp; English.

CC The peptides in this example are bombesin analogues. The peptides  
CC were tested in a competitive binding assay and a Phosphatidyl Inositol  
CC (PI)-turnover assay in mouse pancreas. None of the peptides  
CC demonstrated agonist activity but all inhibited PI-turnover (c.f.  
CC stimulation produced by 100nM GRP). Analogues of bombesin are  
CC potentially useful for growth therapy and the treatment of digestive  
CC disorders, e.g. for stimulating digestion, stimulating growth of  
CC tissue in the lung, pancreas and intestine, stimulating NK cell  
CC activity against tumour cells and stimulating growth of tumours to  
CC increase susceptibility to chemotherapeutic agents.

XX Sequence 7 AA;

Query Match 82.1%; Score 23; DB 13; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

Db 1 qvavahl 7

## RESULT 5

AAW94610

ID AAW94610 standard; peptide; 7 AA.

AC AAW94610;  
XX

DT 27-APR-1999 (first entry)  
XX

DE Bombesin/gastrin releasing peptide type inhibitor peptide #.  
XX

KW Bombesin; gastrin releasing peptide; GRP; inhibitor; antagonist;  
KW small cell lung carcinoma; tumour; frog; antimitotic; antisecretory;  
KW peptic ulcer.  
XX

OS Synthetic.  
XX

OS Bombina bombina.  
XX

Key Location/Qualifiers  
Modified-site 1

FT /note= "optionally modified by octanoyl, lauroyl or  
FT palmitoyl"

FT Modified-site 7  
FT /note= "amidated"

XX US5834433-A.  
XX

PN 10-NOV-1998.  
XX

PD 23-FEB-1996; 96US-0960130.  
XX

PF 24-JUL-1991; 91US-0735402.  
XX

PR 26-JUL-1990; 90US-0558031.  
XX

PR 21-JUL-1994; 94US-0278692.  
XX

PR 23-MAY-1995; 95US-047528.  
XX

PR 23-FEB-1996; 96US-0960130.  
XX

XX (RICH ) MERRELL PHARM INC.  
XX

PI Krstenansky JL;  
XX

DR WPI; 1999-141255/12.  
XX

XX New peptide antagonists of bombesin or gastrin releasing peptide -  
XX are useful as antimitotic and antisecretory agents in treating,  
XX e.g., small cell lung carcinoma or peptic ulcers

PS Claim 5; Column 14; 9pp; English.

XX The present sequence represents a bombesin/gastrin releasing peptide  
XX type inhibitor peptide. The peptide may be used as an antimitotic and  
XX antisecretory peptide. It can control growth of small cell lung and  
XX prostatic carcinomas, and it can also inhibit gastric secretions which  
XX are causative and symptomatic of peptic ulcers. Administration may be  
XX oral but is preferably subcutaneous, intravenous, intramuscular or  
XX intraperitoneal, by depot injection, by implant preparation or by  
XX application to the mucous membranes (e.g. of the nose or bronchial  
XX tubes) by aerosol.

XX Sequence 7 AA;

Query Match 82.1%; Score 23; DB 20; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

Db 1 qvavahl 7

## RESULT 6

AAP20294

ID AAP20294 standard; peptide; 8 AA.

XX

[illegible]

PF 17-AUG-1990; 90WO-US04646.  
 XX  
 PR 21-AUG-1989; 89US-0397169.  
 PR 30-MAR-1990; 90US-0502438.  
 XX  
 PA (TULA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.

XX  
 PI Coy DH, Moreau JP, Kim SH;  
 XX WPI; 1991-087241/12.  
 XX

XX New linear peptide analogues of bombesin - modified to eliminate  
 PT biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.

XX Claim 20+21; Page 54; 58pp; English.

XX These peptides are specifically claimed examples of a generic  
 CC formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to a methylester.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, arteriosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological  
 CC activity.

CC The analogue may also be of a naturally occurring peptide  
 CC terminating at the C-terminus with a Met residue, such as the  
 CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
 CC bombesin.

CC See also AAR11239-242.

XX Sequence 8 AA;

Query Match 82.1%; Score 23; DB 12; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qwavahl 8

RESULT 9  
 AAR29155  
 ID AAR29155 standard; peptide; 8 AA.

XX AAR29155;

DE 16-APR-1993 (first entry)

XX Bombesin analogue (5).

XX Hepatoma; liver cancer; antagonist.

XX Synthetic.

XX Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Modified-site 6 /note= "NMe-D-Ala"  
 FT Modified-site 8 /note= "Leu-OMe"

XX WO9220363-A.

XX 26-NOV-1992.

XX 11-MAY-1992; 92WO-US03916.

XX 10-MAY-1991; 91US-0698681.

XX (BIOM-) BIOMEASURE INC.  
 PA (TULA ) TULANE EDUCATIONAL FUND.  
 XX  
 PI Bodgen AE, Coy DH, Kim SH, Moreau J;  
 XX WPI; 1992-415466/50.  
 XX

XX Treatment of hepatoma - by admin. of admixed bombesin analogue  
 PT with carrier  
 XX

XX Claim 14; Page 48; 54pp; English.

XX The peptide is an example of a highly generic formula. It is used  
 CC in a medicament for treating hepatoma. The cpd. acts as antagonist  
 CC to bombesin, which has been detected in a number of human cancer  
 CC lines.

XX Sequence 8 AA;

Query Match 82.1%; Score 23; DB 13; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qwavahl 8

RESULT 10

AAR29157  
 ID AAR29157 standard; peptide; 8 AA.

XX AAR29157;

DT 16-APR-1993 (first entry)

DE Bombesin analogue (6).

XX Hepatoma; liver cancer; antagonist.

XX Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "D-F5-Phe"  
 FT Misc-difference 6 /note= "D-form residue"  
 FT Modified-site 8 /note= "Leu-OMe"

XX WO9220363-A.

XX 26-NOV-1992.

XX 11-MAY-1992; 92WO-US03916.

XX 10-MAY-1991; 91US-0698681.

XX (BIOM-) BIOMEASURE INC.  
 PA (TULA ) TULANE EDUCATIONAL FUND.

XX Bodgen AE, Coy DH, Kim SH, Moreau J;  
 XX WPI; 1992-415466/50.

XX Treatment of hepatoma - by admin. of admixed bombesin analogue  
 PT with carrier

XX Claim 15; Page 48; 54pp; English.

XX The peptide is an example of a highly generic formula. It

CC in a medicament for treating hepatoma. The cpd. acts as antagonist  
 CC to bombesin, which has been detected in a number of human cancer  
 CC lines.  
 XX  
 SQ Sequence 8 AA;

Query Match 82.1%; Score 23; DB 13; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 | | | | |  
 Db 2 qwavahl 8

RESULT 11  
 AAW64911  
 ID AAW64911 standard; peptide; 8 AA.  
 XX AAW64911;  
 DT 06-JUL-1999 (first entry)  
 XX Bombesin receptor antagonist.  
 DE Bombesin; antagonist; chlorambucil; peptic ulcer; pancreatitis;  
 KW eating disorder; diabetes; acromegaly; enterocutaneous fistula;  
 KW psoriasis; growth retardation; gastrointestinal motility disorder;  
 KW antitumour.  
 XX Synthetic.

Key Location/Qualifiers  
 FT Modified-site 1  
 /note= "The amino terminal is acylated with acetyl,  
 bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-amino]-  
 L-phenylalanine or a chlorambucil group"  
 FT Modified-site 8  
 /note= "The carboxy terminal is in the form of an  
 ethyl ester"

WO9500542-A1.  
 XX  
 XX 05-JAN-1995.  
 XX  
 XX 15-JUN-1994; 94WO-US06757.  
 XX  
 XX 17-DEC-1993; 93US-0168390.  
 XX 18-JUN-1993; 93US-0078062.  
 XX (PEPT-) PEPTIDE TECHNOLOGIES CORP.  
 XX Chandrasekhar B, Knight M, Takahashi K;  
 XX WPI; 1995-052004/07.

XX New bombesin, gastrin releasing peptide or Neuromedin B or C derivs.  
 PT - antagonists for treating conditions such as gastrointestinal  
 PT disorders, psoriasis and cancers  
 XX  
 XX Claim 6; Page 34; 45pp; English.

XX The patent discloses (1) the peptide sequence of bombesin (BBN),  
 CC gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C,  
 CC the peptide sequence having a chlorambucil group attached to the  
 CC amino terminal; (2) a BBN receptor antagonist of formula  
 CC R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
 CC antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
 CC In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
 CC Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
 CC amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His.  
 CC The compounds act as potent BBN/GRP-like peptide antagonists. They

CC can be used to inhibit the growth of cells that are sensitive to the  
 CC growth-promoting effects of BBN, GRP or a related peptide such as  
 CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
 CC cancerous cells or tumours. They can also be used to inhibit the  
 CC binding of BBN, GRP or a related peptide to cells capable of such  
 CC binding. They can be used for treating e.g. peptic ulcer, pancreati-  
 CC eating disorders, diabetes, acromegaly, enterocutaneous fistula  
 CC psoriasis, growth retardation, gastrointestinal motility disorders or  
 CC tumours. The terminal structures of the compounds protect them from  
 CC in vivo proteolysis and provide highly potent antagonist effects that  
 CC persist for extended periods of time upon administration.

XX Sequence 8 AA;

Query Match 82.1%; Score 23; DB 16; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 2 qwavahl 8

RESULT 12  
 AAR09335  
 ID AAR09335 standard; peptide; 9 AA.  
 XX AAR09335;  
 AC AAR09335;  
 XX 30-MAR-1992 (first entry)  
 DT  
 XX Sequence of Bombesin receptor peptide ligand with irreversible  
 DE effects.  
 DE  
 DE Bombesin receptor; agonist; antagonist.

Key Location/Qualifiers  
 FT Modified-site 1  
 /label= H-pMel  
 /note= "pMel= p-bis (2-chloroethyl)  
 amino-L-phenylalanine"  
 FT Modified-site 9  
 /label= Met-NH2  
 FT  
 FT WO9001037-A.  
 XX  
 XX 08-FEB-1990.  
 PD  
 XX 19-JUL-1989; 89WO-EP00842.  
 PF  
 XX 28-MAR-1989; 89GB-0006900.  
 PR  
 XX 21-JUL-1988; 88GB-0017379.  
 PR  
 XX (FARM ) FARMITALIA C ERBA SPA.

XX de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciomei M;  
 PI Molinari I;  
 PI WPI; 1990-067161/09.  
 DR  
 XX Bombesin receptor peptide ligands with irreversible effects - as  
 PT agonists and antagonists both weak and strong  
 PT Claim 2; Page 26; 32pp; English.  
 PS  
 XX The inventors claim 36 peptides. Also claimed are:  
 CC (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.  
 CC of the peptides.

XX Sequence 9 AA;

Query Match 82.1%; Score 23; DB 11; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qvavahl 8

RESULT 13  
 AAR11522  
 ID AAR11522 standard; Protein; 9 AA.  
 XX  
 AC AAR11522;  
 XX  
 DT 13-JUN-1991 (first entry)  
 XX  
 DE Example of peptide agonist of GRP, neuromedin, bombesin and litorin.  
 XX  
 KW Non-malignant proliferative disease; cancer.

Key Location/Qualifiers  
 Modified-site 1..1  
 /label= OTHER  
 /note= "D-p-chlorophenylalanine"

XX W09104040-A.  
 XX  
 PD 04-APR-1991.  
 XX  
 PF 17-SEP-1990; 90WO-US05271.  
 XX  
 PR 05-MAY-1990; 90US-0520225.  
 PR 15-SEP-1989; 89US-0408125.  
 PR 21-NOV-1989; 89US-0440039.  
 XX  
 PA (BIOM-) BIOMEASURE INC.  
 XX  
 PI Bogden AE, Moreau J-P;  
 XX  
 DR WPI; 1991-117320/16.  
 XX  
 PT Treatment of non malignant proliferative disease and cancer - by  
 PT administration of natural peptide or fragment selected from  
 PT gastrin-releasing peptide, neuromedin, amphibian bombesin or  
 PT litorin  
 XX  
 PS Claim 22; page 54; 73pp; English.

This is a peptide analogue of mammalian gastrin releasing peptide  
 (GRP), neuromedin-B or -C, amphibian bombesin and litorin.  
 It is an agonist of these cpds. and is used to treat smooth muscle  
 CC proliferation and cancer of the prostate, breast or lung.  
 CC Residue 6 (Ala) is D-alanine.  
 CC See also AAR11519-21 and AAR11523-30.  
 XX  
 SQ Sequence 9 AA;

Query Match 82.1%; Score 23; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qvavahl 8

RESULT 14  
 AAR14865  
 ID AAR14865 standard; Protein; 9 AA.  
 XX  
 AC AAR14865;

Query Match 82.1%; Score 23; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qvavahl 8

RESULT 15  
 AAR14866  
 ID AAR14866 standard; Protein; 9 AA.  
 XX  
 AC AAR14866;  
 XX  
 DT 14-FEB-1992 (first entry)  
 XX  
 DE Peptide analogue #7 of litorin, GRP, neuromedin or bombesin.  
 XX  
 KW tissue proliferation; gastrin related peptide; peptide hor  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers

XX 14-FEB-1992 (first entry)  
 DT  
 XX Peptide analogue #6 of litorin, GRP, neuromedin or bombesin;  
 DE  
 XX tissue proliferation; gastrin related peptide; peptide hormone.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /label= D-Phe  
 FT Modified-site 6  
 FT /label= D-Ala  
 FT  
 XX W09117181-A.  
 PN  
 XX 14-NOV-1991.  
 PD  
 XX 09-MAY-1991; 91WO-0003265.  
 PF  
 XX 09-MAY-1990; 90US-0520226.  
 PR  
 XX (TULA ) TULANE E FUND ADMINISTRATRA.  
 PA (BIOM-) BIOMEASURE INC.  
 FT  
 XX Coy DH, Kim SH, Moreau JP;  
 PI  
 XX WPI; 1991-353721/48.  
 DR  
 XX Peptide agonists of litorin, gastrin releasing peptide  
 PT neuromedin B or C or bombesin, for treating cancer, prevent  
 PT smooth muscle proliferation and suppressing appetite and alcohol  
 PT craving  
 PT  
 XX Claim 8; Page 18; 25pp; English.  
 PS  
 XX The C-terminal residue is amidated. This peptide is one of 2  
 CC specific examples of a highly generic formula. The peptides are  
 CC analogues of either litorin; the 10 amino acid C-terminal region of  
 CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 CC C-terminal region of amphibian bombesin. They act as at least partial  
 CC agonists of the natural peptides. The peptide analogues are made by  
 CC standard methods of synthesis and can be cyclised.  
 CC See AAR14860-R14880 and AAR15035-R15040.  
 XX  
 SQ Sequence 9 AA;

Query Match 82.1%; Score 23; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qvavahl 8

RESULT 15  
 AAR14866  
 ID AAR14866 standard; Protein; 9 AA.  
 XX  
 AC AAR14866;  
 XX  
 DT 14-FEB-1992 (first entry)  
 XX  
 DE Peptide analogue #7 of litorin, GRP, neuromedin or bombesin.  
 XX  
 KW tissue proliferation; gastrin related peptide; peptide hor  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers

FT Modified-site 1  
 FT /label= D-Phe  
 FT Modified-site 6  
 FT /label= D-Ala  
 XX  
 PN WO9117181-A.  
 XX  
 PD 14-NOV-1991.  
 XX  
 PF 09-MAY-1991; 91WO-0003265.  
 XX  
 PR 09-MAY-1990; 90US-0520226.  
 XX  
 PA (TULA ) TULANE E FUND ADMINISTRA.  
 PA (BIOM-) BIOMEASURE INC.  
 XX  
 PI Coy DH, Kim SH, Moreau JP;  
 XX  
 DP WPI; 1991-353721/48.  
 CC Peptide agonists of litorin, gastrin releasing peptide -  
 PT neuromedin B or C or bombesin, for treating cancer, preventing  
 PT smooth muscle proliferation and suppressing appetite and alcohol  
 PT craving  
 XX  
 PS Claim 9; Page 18; 25pp; English.  
 XX  
 CC The C-terminal residue is amidated. This peptide is one of 27  
 CC specific examples of a highly generic formula. The peptides are all  
 CC analogues of either litorin; the 10 amino acid C-terminal region of  
 CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 CC C-terminal region of amphibian bombesin. They act as at least partial  
 CC agonists of the natural peptides. The peptide analogues are made by  
 CC standard methods of synthesis and can be cyclised.  
 CC See AAR14860-R14880 and AAR15035-R15040.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 82.1%; Score 23; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2 OXAVXHL 8  
 Db 2 qvavahl 8  
 Search completed: October 25, 2001, 11:22:46  
 Job time: 219 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-5

Perfect score: 28

Sequence: 1 QXAVXHL 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	85.7	9	1	US-08-263-905-12
2	24	85.7	9	5	PCT-US93-00183-12
3	23	82.1	8	1	US-08-168-390-12
4	23	82.1	8	6	5217955-35
5	23	82.1	8	6	5217955-36
6	23	82.1	9	6	5217955-13
7	23	82.1	9	6	5217955-14
8	23	82.1	9	6	5217955-15
9	23	82.1	9	6	5217955-22
10	23	82.1	540	3	US-09-019-942-1
11	23	82.1	910	4	US-08-460-269C-2
12	22	78.6	8	1	US-08-168-390-11
13	22	78.6	8	2	US-08-337-127-9
14	22	78.6	8	6	5217955-32
15	22	78.6	8	6	5217955-34
16	22	78.6	9	1	US-07-619-747B-1
17	22	78.6	9	1	US-07-619-747B-2
18	22	78.6	9	1	US-07-619-747B-4
19	22	78.6	9	1	US-07-619-747B-5
20	22	78.6	9	1	US-07-619-747B-9
21	22	78.6	9	1	US-07-619-747B-10
22	22	78.6	9	1	US-07-619-747B-12
23	22	78.6	9	1	US-07-619-747B-14
24	22	78.6	9	1	US-07-619-747B-15
25	22	78.6	9	1	US-07-619-747B-17
26	22	78.6	9	1	US-07-619-747B-18
27	22	78.6	9	1	US-07-619-747B-22

28 22 78.6 9 1 US-07-619-747B-23  
29 22 78.6 9 1 US-07-619-747B-24  
30 22 78.6 9 1 US-07-619-747B-25  
31 22 78.6 9 1 US-07-619-747B-26  
32 22 78.6 9 1 US-07-619-747B-27  
33 22 78.6 9 1 US-07-619-747B-28  
34 22 78.6 9 1 US-07-619-747B-29  
35 22 78.6 9 1 US-07-619-747B-30  
36 22 78.6 9 1 US-07-619-747B-31  
37 22 78.6 9 1 US-07-619-747B-32  
38 22 78.6 9 1 US-07-619-747B-33  
39 22 78.6 9 1 US-07-619-747B-34  
40 22 78.6 9 1 US-07-619-747B-35  
41 22 78.6 9 1 US-07-619-747B-36  
42 22 78.6 9 1 US-07-619-747B-37  
43 22 78.6 9 1 US-07-619-747B-38  
44 22 78.6 9 1 US-07-619-747B-39  
45 22 78.6 9 1 US-07-619-747B-40

#### ALIGNMENTS

RESULT 1  
US-08-263-905-12  
; Sequence 12, Application US/08263905  
; Patent No. 5428018  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Judson V  
; APPLICANT: Fanger, Bradford D  
; TITLE OF INVENTION: Phenylalanine Analogs of Bombesin  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marion Merrell Dow Inc.  
; STREET: 2110 East Galbraith Rd.  
; CITY: Cincinnati P. O. Box 156300  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45215-6300  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/263,905  
; FILING DATE: 22-JUN-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/833,834  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collier, Kenneth J  
; REGISTRATION NUMBER: 34,982  
; REFERENCE/DOCKET NUMBER: M01614 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (513) 948-7834  
; TELEFAX: (513) 948-7961  
; TELEX: 214320  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-263-905-12

Query Match 85.7%; Score 24; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels

QY 2 QXAVXHL 8

Db 3 QXAVGHL 9

RESULT 2  
PCT-US93-00183-12  
; Sequence 12, Application PC/TUS9300183  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Judson V  
; APPLICANT: Fanger, Bradford D  
; TITLE OF INVENTION: Phenylalanine Analogs of Bombesin  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marion Merrell Dow Inc.  
; STREET: 2110 East Galbraith Rd.  
; CITY: Cincinnati P. O. Box 156300  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45215-6300  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00183  
; FILING DATE: 19930107  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collier, Kenneth J  
; REGISTRATION NUMBER: 34,982  
; REFERENCE/DOCKET NUMBER: M01614 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (513) 948-7834  
; TELEFAX: (513) 948-7961  
; TELEX: 214320  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-00183-12

Query Match 85.7%; Score 24; DB 5; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |  
Db 3 QXAVGHL 9

RESULT 3  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Blaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "The alanine at position 6  
; OTHER INFORMATION: is dextrorotatory alanine."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-12

Query Match 82.1%; Score 23; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |  
Db 2 QXAVGHL 8

RESULT 4  
5217955-35  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 35;  
; LENGTH: 8  
5217955-35

Query Match 82.1%; Score 23; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |

Db 2 QWAV AHL 8

## RESULT 5

5217955-36

; Patent No. 5217955

; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

; NUMBER OF SEQUENCES: 42

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/520,225

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 440,039

; FILING DATE: 21-NOV-1989

; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989

; SEQ ID NO:36:

LENGTH: 8

5217955-36

Query Match 82.1%; Score 23; DB 6; Length 8;

Best Local Similarity 71.4%; Pred. No. 1.5e+05;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QXAVXHL 8

Db 2 QWAV AHL 8

## RESULT 6

5217955-13

; Patent No. 5217955

; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

; NUMBER OF SEQUENCES: 42

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/520,225

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 440,039

; FILING DATE: 21-NOV-1989

; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989

; SEQ ID NO:13:

LENGTH: 9

5217955-13

Query Match 82.1%; Score 23; DB 6; Length 9;

Best Local Similarity 71.4%; Pred. No. 1.5e+05;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QXAVXHL 8

Db 2 QWAV AHL 8

## RESULT 7

5217955-14

; Patent No. 5217955

; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

; NUMBER OF SEQUENCES: 42

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/520,225

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 440,039

; FILING DATE: 21-NOV-1989

; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989

; SEQ ID NO:14:

LENGTH: 9

5217955-14

Query Match

Best Local Similarity 82.1%; Score 23; DB 6; Length 9;

Matches 5; Conservative 0; Mismatches 2; Indels

Qy 2 QXAVXHL 8

Db 2 QWAV AHL 8

## RESULT 8

5217955-15

; Patent No. 5217955

; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

; NUMBER OF SEQUENCES: 42

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/520,225

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 440,039

; FILING DATE: 21-NOV-1989

; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989

; SEQ ID NO:15:

LENGTH: 9

5217955-15

Query Match

Best Local Similarity 82.1%; Score 23; DB 6; Length 9;

Matches 5; Conservative 0; Mismatches 2; Indels

Qy 2 QXAVXHL 8

Db 2 QWAV AHL 8

## RESULT 9

5217955-22

; Patent No. 5217955

; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

; NUMBER OF SEQUENCES: 42

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/520,225

; FILING DATE: 09-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 440,039

; FILING DATE: 21-NOV-1989

; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989

; SEQ ID NO:22:

LENGTH: 9

5217955-22

Query Match

Best Local Similarity 82.1%; Score 23; DB 6; Length 9;

Matches 5; Conservative 0; Mismatches 2; Indels

Qy 2 QXAVXHL 8

Db 2 QWAV AHL 8

RESULT 10  
US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-019-942-1

Query Match 82.1%; Score 23; DB 3; Length 540;  
Best Local Similarity 71.4%; Pred. No. 3.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 43 QVAVKHL 49

RESULT 11  
US-08-460-269C-2  
; Sequence 2, Application US/08460269C  
; Patent No. 6197548  
; GENERAL INFORMATION:  
; APPLICANT: CLARE, JEFFREY J.  
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
; STREET: 2200 Clarendon Blvd., Suite 1400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,269C  
; FILING DATE: 02-Jun-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lebovitz, Richard M.  
; REGISTRATION NUMBER: 37,067  
; REFERENCE/DOCKET NUMBER: Popov-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 243-6333  
; TELEFAX: (703) 243-6410  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 910 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-460-269C-2

Query Match 82.1%; Score 23; DB 4; Length 910;  
Best Local Similarity 71.4%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 247 QGAVVHL 253

RESULT 12  
US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "The amino-terminal residue
; OTHER INFORMATION: comprises one of several chemical end caps."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "The carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-11

Query Match 78.6%; Score 22; DB 1; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QXAVXHL 8
Db 2 QWAVGHL 8

ULT 13
US-08-337-127-9
; Sequence 9, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/009000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an methylester C-terminus (i.e., -COOCH3).
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., -COOH).
US-08-337-127-9

Query Match 78.6%; Score 22; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QXAVXHL 8
Db 2 QWAVGHL 8

RESULT 14
5217955-32
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:32:
; LENGTH: 8
5217955-32

Query Match 78.6%; Score 22; DB 6; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QXAVXHL 8
Db 2 QWAVGHL 8

RESULT 15
5217955-34
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
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; APPLICATION NUMBER: 408,125  
 ; FILING DATE: 15-SEP-1989  
 ; SEQ ID NO:34:  
 ; LENGTH: 8  
 5217955-34

Query Match 78.6%; Score 22; DB 6; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 Db 2 QWAVGHL 8

Search completed: October 25, 2001, 11:23:56  
 Time: 269 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:28:28 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-5  
Perfect score: 28  
Sequence: 1 QXAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	85.7	1510	1 MUKB_HAEIN	P45187 haemophilus
2	23	82.1	85	1 PPHP_ECOLI	P07006 escherichia
3	23	82.1	85	1 PPHP_HAEIN	P43921 haemophilus
4	23	82.1	85	1 PPHP_KLEPN	P16481 klebsiella
5	23	82.1	276	1 ENDB_TRYBC	O86820 streptomyces
6	23	82.1	320	1 VSIO_TRYBB	P06013 trypanosoma
7	23	82.1	420	1 PHE_THETH	P37250 thermus aqu
8	23	82.1	432	1 HEM1_CYAPA	P48077 cyanophora
9	23	82.1	434	1 HEM1_PASMU	P95525 pasteurella
10	23	82.1	472	1 IFT2_MOUSE	Q64112 mus musculus
11	23	82.1	495	1 THDF_TREPA	O83561 treponema p
12	23	82.1	496	1 RECO_BACSU	P50729 bacillus su
13	23	82.1	546	1 TCPE_SCHPO	O90244 schizosach
14	23	82.1	768	1 EP2K_CABEL	O01991 caenorhabdi
15	23	82.1	910	1 PERT_BORPE	P14283 bordetella
16	23	82.1	936	1 MSH4_HUMAN	O15457 homo sapien
17	23	82.1	1206	1 FM14_MOUSE	Q05859 mus musculus
18	23	82.1	1213	1 FNN_CHICK	Q05858 gallus gall
19	23	82.1	1468	1 FNN1_MOUSE	Q05860 mus musculus
20	23	82.1	1741	1 RPL1_GIALA	P25022 giardia lam
21	23	82.1	2347	1 KROS_HUMAN	P08922 homo sapien
22	23	82.1	4447	1 PKSQ_BACSU	P40803 bacillus su
23	22	78.6	14	1 ALYT_ALYOB	P08944 alytes obst
24	22	78.6	101	1 SMD3_YEAST	P43321 saccharomyc
25	22	78.6	107	1 BOMB_BOMVA	P01296 bombyx mori
26	22	78.6	119	1 BOMB_BOMOR	P21591 bombyx mori
27	22	78.6	246	1 PS61_ARATH	O81146 arabidopsis
28	22	78.6	246	1 PS62_ARATH	O81147 arabidopsis
29	22	78.6	246	1 PS66_TOBAC	Q9XG77 nicotiana t
30	22	78.6	261	1 YPSA_CAEEL	Q09247 caenorhabdi
31	22	78.6	310	1 PURU_MYCTU	Q50453 mycobacteri
32	22	78.6	358	1 MTG2_HAEGA	P25283 haemophilus
33	22	78.6	361	1 RUVB_SYNY3	Q57396 synechocyst

34	22	78.6	391	1 EDA_HUMAN	Q92838 human, sal
35	22	78.6	391	1 EDA_MOUSE	O54693 mus mus.
36	22	78.6	393	1 XYLA_ACTMI	P12851 actinoplanar
37	22	78.6	394	1 XYLA_AMSP	P10854 ampicillin
38	22	78.6	394	1 XYLA_ARTS7	P12070 actinoplanar
39	22	78.6	446	1 CLPX_HELPY	O25926 helicobacter
40	22	78.6	452	1 CLPX_HELPJ	P87671 ebola virus
41	22	78.6	676	1 VGP_EBOEC	O11457 ebola virus
42	22	78.6	676	1 VGP_EBOG4	P87866 ebola virus
43	22	78.6	676	1 VGP_EBOZ5	Q05320 ebola virus
44	22	78.6	676	1 VGP_EBOZM	P47190 saccharomyc
45	22	78.6	753	1 PMT3_YEAST	

ALIGNMENTS

RESULT 1

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ID MUKB\_HAEIN STANDARD; PRT; 1510 AA.

AC P45187;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE CELL DIVISION PROTEIN MUKB HOMOLOG.

GN MUKB OR H11374.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OC Haemophilus.

OX NCBI\_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RD / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon P.,

RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;

RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

RL Science 269:496-512(1995).

CC -!- FUNCTION: ESSENTIAL FOR CHROMOSOME PARTITIONING (BY SIMILARITY).

CC -!- SIMILARITY: CONTAINS A COILED COIL MYOSIN-LIKE STRUCTURE.

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CC EMBL: U32817; AAC23022.1; -

DR TIGR: H11374; -

KW ATP-binding; Coiled coil.

FT DOMAIN 1 345 GLOBULAR (POTENTIAL).

FT DOMAIN 346 469 COILED COIL (POTENTIAL).

FT DOMAIN 552 637 COILED COIL (POTENTIAL).

FT DOMAIN 677 706 COILED COIL (POTENTIAL).

FT DOMAIN 750 770 COILED COIL (POTENTIAL).

FT DOMAIN 821 1065 COILED COIL (POTENTIAL).

FT DOMAIN 1112 1154 COILED COIL (POTENTIAL).

FT DOMAIN 1155 1247 GLOBULAR (POTENTIAL).

FT DOMAIN 1248 1304 COILED COIL (POTENTIAL).

FT DOMAIN 1305 1510 GLOBULAR (POTENTIAL).

FT NP\_BIND 75 82 ATP (POTENTIAL).

FT NP\_BIND 1447 1454 ATP (POTENTIAL).

FT SEQUENCE 1510 AA; 173285 MW; 173EBC4198E3184F CRC64;

Query Match 85.7%; Score 24; DB 1; Length 1510;  
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAYXHL 8  
 | | | | |  
 Db 371 QSAVDHL 377

RESULT 2  
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AC P07006; P05525;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
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 Escherichia coli, and Salmonella typhimurium.  
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 Escherichia.  
 NCBI\_TaxID=562, 602;  
 [1]  
 SEQUENCE FROM N.A.  
 SPECIES=E.coli; STRAIN=K12;  
 MEDLINE=88314869; PubMed=2457575;  
 de Reuse H., Danchin A.;  
 "The ptsH, ptsI, and crr genes of the Escherichia coli  
 phosphoenolpyruvate-dependent phosphotransferase system: a complex  
 operon with several modes of transcription.";  
 J. Bacteriol. 170:3827-3837(1988).  
 [2]  
 SEQUENCE FROM N.A.  
 SPECIES=E.coli; STRAIN=K12;  
 MEDLINE=85286351; PubMed=2411636;  
 de Reuse H., Roy A., Danchin A.;  
 "Analysis of the ptsH-ptsI-crr region in Escherichia coli K-12:  
 nucleotide sequence of the ptsH gene.";  
 Gene 35:199-207(1985).  
 [3]  
 SEQUENCE FROM N.A.  
 SPECIES=E.coli;  
 MEDLINE=88038992; PubMed=2960675;  
 Saffen D.W., Presper K.A., Doering T.L., Roseman S.;  
 "Sugar transport by the bacterial phosphotransferase system.  
 Molecular cloning and structural analysis of the Escherichia coli  
 ptsH, ptsI, and crr genes.";  
 J. Biol. Chem. 262:16241-16253(1987).  
 [4]  
 SEQUENCE FROM N.A.  
 SPECIES=E.coli, and S.typhimurium; STRAIN=K12, AND LT2;  
 RX MEDLINE=88257033; PubMed=3290198;  
 Byrne C.R., Monroe R.S., Ward K.A., Kredich N.M.;  
 "DNA sequences of the cysK regions of Salmonella typhimurium and  
 Escherichia coli and linkage of the cysK regions to ptsH.";  
 J. Bacteriol. 170:3150-3157(1988).  
 [5]  
 SEQUENCE FROM N.A.  
 SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 Mau B., Shao Y.;  
 "The complete genome sequence of Escherichia coli K-12.";  
 Science 277:1234-1238(1997).  
 [6]  
 SEQUENCE FROM N.A.  
 SPECIES=E.coli; STRAIN=K12;  
 RX MEDLINE=97349980; PubMed=9205837;  
 Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,

RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi T.,  
 RA Mochizuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,  
 RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubramanian S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
 RA Yanagata S., Horiuchi T.;  
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
 RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and  
 RT analysis of its sequence features.";  
 RL DNA Res. 4:91-113(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium; STRAIN=LT2;  
 RX MEDLINE=89237892; PubMed=2497295;  
 RA Schnierow B.J., Yamada M., Saler M.H. Jr.;  
 RT "Partial nucleotide sequence of the pts operon in Salmonella  
 RT typhimurium: comparative analyses in five bacterial genera.";  
 RL Mol. Microbiol. 3:113-118(1989).  
 RN [8]  
 RP SEQUENCE.  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=83056997; PubMed=6754732;  
 RA Weigel N., Powers D.A., Roseman S.;  
 RT "Sugar transport by the bacterial phosphotransferase system. Primary  
 RT structure and active site of a general phosphocarrier protein (HPr)  
 RT from Salmonella typhimurium.";  
 RL J. Biol. Chem. 257:14499-14509(1982).  
 RN [9]  
 RP REVISIONS  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=85080006; PubMed=6392295;  
 RA Powers D.A., Roseman S.;  
 RT "The primary structure of Salmonella typhimurium HPr, a  
 RT phosphocarrier protein of the phosphoenolpyruvate:glycose  
 RT phosphotransferase system. A correction.";  
 RL J. Biol. Chem. 259:15212-15214(1984).  
 RN [10]  
 RP SEQUENCE OF 1-12.  
 RC SPECIES=E.coli; STRAIN=K12 / EMG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 RT in the genome of Escherichia coli K-12.";  
 RL Electrophoresis 18:1259-1313(1997).  
 RN [11]  
 RP SEQUENCE OF 1-12.  
 RC STRAIN=K12 / W3110;  
 RA Frutiger S., Hughes G.J., Pasquali C., Hochstrasser D.F.;  
 RL Submitted (FEB-1996) to the SWISS-PROT data bank.  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=94043003; PubMed=8226757;  
 RA Jia Z., Quail J.W., Waygood E.B., Delbaere L.T.J.;  
 RT "The 2.0-A resolution structure of Escherichia coli  
 RT histidine-containing phosphocarrier protein HPr. A redetermination.";  
 RL J. Biol. Chem. 268:22490-22501(1993).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RX MEDLINE=96378616; PubMed=8784179;  
 RA Napper S., Anderson J.W., Georges F., Quail J.W., Delbaere L.T.J.,  
 RA Waygood E.B.;  
 RT "Mutation of serine-46 to aspartate in the histidine-containing  
 RT protein of Escherichia coli mimics the inactivation by  
 RT phosphorylation of serine-46 in Hprs from gram-positive bacteria.";  
 RL Biochemistry 35:11260-11267(1996).  
 RN [14]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=87101066; PubMed=3542036;  
 RA Kleit R.E., Waygood E.B.;  
 RT "Two-dimensional 1H NMR studies of histidine-containing protein from  
 RT Escherichia coli. 3. Secondary and tertiary structure as determined  
 RT by NMR.";  
 RL Biochemistry 25:7774-7781(1986).  
 RN [15]

RP STRUCTURE BY NMR.  
RX MEDLINE-92089095; PubMed=1751501;  
RA Hammen P.K., Waygood E.B., Klevit R.E.;  
RT "Reexamining of the secondary and tertiary structure of histidine-  
RT containing protein from Escherichia coli by homonuclear and  
RT heteronuclear NMR spectroscopy.";  
RL Biochemistry 30:11842-11850(1991).  
RN [16]  
RP STRUCTURE BY NMR.  
RX MEDLINE-93130914; PubMed=1483471;  
RA van Nuland N.A.J., Groetzing J., Dijkstra K., Scheek R.M.,  
RA Robillard G.T.;  
RT "Determination of the three-dimensional solution structure of the  
RT histidine-containing phosphocarrier protein HPr from Escherichia coli  
RT using multidimensional NMR spectroscopy.";  
RL Eur. J. Biochem. 210:881-891(1992).  
RN [17]  
RP STRUCTURE BY NMR.  
RX MEDLINE-94210480; PubMed=8158637;  
RA van Nuland N.A.J., Hangyi I.W., van Schaik R.C., Berendsen H.J.,  
RA van Gunsteren W.F., Scheek R.M., Robillard G.T.;  
RT "The high-resolution structure of the histidine-containing  
RT phosphocarrier protein HPr from Escherichia coli determined by  
RT restrained molecular dynamics from nuclear magnetic resonance nuclear  
RT Overhauser effect data.";  
RL J. Mol. Biol. 237:544-559(1994).  
RN [18]  
RP STRUCTURE BY NMR.  
RX MEDLINE-95156481; PubMed=7853396;  
RA van Nuland N.A.J., Boelens R., Scheek R.M., Robillard G.T.;  
RT "High-resolution structure of the phosphorylated form of the  
RT histidine-containing phosphocarrier protein HPr from Escherichia  
RT coli determined by restrained molecular dynamics from NMR-NOE data.";  
RL J. Mol. Biol. 246:180-193(1995).  
RN [19]  
RP STRUCTURE BY NMR.  
RX MEDLINE-9702120; PubMed=8868480;  
RA van Nuland N.A.J., Wiersma J.A., van der Spoel D., de Groot B.L.,  
RA Scheek R.M., Robillard G.T.;  
RT "Phosphorylation-induced torsion-angle strain in the active center of  
RT HPr, detected by NMR and restrained molecular dynamics refinement.";  
RL Protein Sci. 5:442-446(1996).  
RN [20]  
RP STRUCTURE BY NMR.  
RX MEDLINE-99140298; PubMed=10048929;  
RA Garrett D.S., Seok Y.-J., Peterkofsky A., Gronenborn A.M., Clore G.M.;  
RT "Solution structure of the 40,000 Mr phosphoryl transfer complex  
RT between the N-terminal domain of enzyme I and HPr.";  
RL Nat. Struct. Biol. 6:166-173(1999).  
RN [21]  
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT  
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE  
CC -TRANSPORT SYSTEM. THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE  
CC (PEP) IS TRANSFERRED TO THE PHOSPHORYL CARRIER PROTEIN HPR BY  
CC ENZYME I. PHOSPHO-HPR THEN TRANSFERS IT TO THE PERMEASE (ENZYMES  
CC II/III). HPR IS COMMON TO ALL PTS.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- SIMILARITY: TO ALL OTHER HPR OR HPR DOMAINS.  
CC -----  
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CC -----  
CC EMBL; M10425; AAA24438.1; -.  
DR EMBL; M10425; AAA24438.1; -.  
DR HSSP; P07006; 1PFH.  
DR TIGR; H11713; -.  
DR InterPro; IPR001020; -.  
DR Pfam; PF00381; PTS-HPR; 1.  
DR PRINTS; PR00107; PHOSPHOPHR.  
DR PROSITE; PS00369; PTS\_HPR\_HIS; 1.  
DR PROSITE; PS00589; PTS\_HPR\_SER; 1.  
DR Phosphotransferase system; Sugar transport; Phosphorylation.  
KW MOD\_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).  
FT SEQUENCE 85 AA; 9004 MW; 3D8D599742311830 CRC64;  
SQ

Query Match 82.1%; Score 23; DB 1; Length 85;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

Db 71 QXAVEHL 77

RESULT 4

Db 71 QXAVEHL 77

RESULT 3

PTHP\_HAEIN STANDARD; PRT; 85 AA.

AC P43921;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN).  
GN PTHP OR H11713.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae.  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Li L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.,  
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
RT influenzae Rd.";  
RL Science 269:496-512(1995).  
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT  
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE  
CC -TRANSPORT SYSTEM. THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE  
CC (PEP) IS TRANSFERRED TO THE PHOSPHORYL CARRIER PROTEIN HPR BY  
CC ENZYME I. PHOSPHO-HPR THEN TRANSFERS IT TO THE PERMEASE (ENZYMES  
CC II/III). HPR IS COMMON TO ALL PTS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
CC -!- SIMILARITY: TO ALL OTHER HPR OR HPR DOMAINS.  
CC -----  
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CC -----  
CC EMBL; U32844; AAC23358.1; -.  
DR EMBL; U32844; AAC23358.1; -.  
DR HSSP; P07006; 1PFH.  
DR TIGR; H11713; -.  
DR InterPro; IPR001020; -.  
DR Pfam; PF00381; PTS-HPR; 1.  
DR PRINTS; PR00107; PHOSPHOPHR.  
DR PROSITE; PS00369; PTS\_HPR\_HIS; 1.  
DR PROSITE; PS00589; PTS\_HPR\_SER; 1.  
DR Phosphotransferase system; Sugar transport; Phosphorylation.  
KW MOD\_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).  
FT SEQUENCE 85 AA; 9004 MW; 3D8D599742311830 CRC64;  
SQ

Query Match 82.1%; Score 23; DB 1; Length 85;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

Db 71 QXAVEHL 77

RESULT 4

PTHP\_KLEPN STANDARD; PRT; 85 AA.  
ID P16481;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-NOV-1991 (Rel. 20, Last annotation update)  
DE PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN).  
GN PTPH.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1033-5P14 / KAY2026;  
RX MEDLINE=90245592; PubMed=2186369;  
RA Titzmeyer F., Eisermann R., Hengstenberg W., Lengeler J.W.;  
RT "The nucleotide sequence of pth gene from Klebsiella pneumoniae.";  
Nucleic Acids Res. 18:1898-1898(1990).  
-|- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT  
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE  
-TRANSPORT SYSTEM. THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE  
(PEP) IS TRANSFERRED TO THE PHOSPHORYL CARRIER PROTEIN HPR BY  
CC ENZYME I. PHOSPHO-HPR THEN TRANSFERS IT TO THE PERMEASE (ENZYMES  
CC II/III). HPR IS COMMON TO ALL PTS.  
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X51452; CAA35818.1; -;  
DR PIR; S12749; S12749.  
DR HSSP; P07006; LPFH.  
DR InterPro; IPR001020; -;  
DR Pfam; PF00381; PTS-HPR; 1.  
DR PRINTS; PR00107; PHOSPHOPHPR.  
DR PROSITE; PS00369; PTS\_HPR\_HIS; 1.  
DR PROSITE; PS00589; PTS\_HPR\_SER; 1.  
KW Phosphotransferase system; Sugar transport; Phosphorylation.  
FT MOD\_RES 15 15 PHOSPHORYLATION.  
FT SEQUENCE 85 AA; 9119 MW; 10C8879C0A95ABF7 CRC64;  
Query Match 82.1%; Score 23; DB 1; Length 95;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 71 QKAVEHL 77  
RESULT 5  
END8\_STRCO  
ID END8\_STRCO STANDARD; PRT; 276 AA.  
AC O86820;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).  
GN NEI OR SC7C7.15C.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);

RA Harris D., Taylor K., Parkhill J., Barrell B.G., Rajandram M.A.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
CC -|- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED  
CC FOR THE REPAIR OF OXIDATIVE DNA DAMAGE (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO THE FPG FAMILY.  
CC  
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CC  
CC EMBL; AL031031; CAA19861.1; -;  
DR InterPro; IPR000191; -;  
DR Pfam; PF01149; Fapy-DNA\_glyco; 1.  
DR PROSITE; PS01242; FPG; 1.  
KW DNA repair; Hydrolyase; Glycosidase; Endonuclease; Zinc.  
FT ZN\_FING 231 258 POTENTIAL.  
SQ SEQUENCE 276 AA; 30408 MW; 01106CD65EF94DE9 CRC64;  
Query Match 82.1%; Score 23; DB 1; Length 276;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 118 QKAVGHL 124  
RESULT 6  
VS10\_TRYBB STANDARD; PRT; 320 AA.  
ID VS10\_TRYBB  
AC P06013;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 01-MAY-1992 (Rel. 22, Last annotation update)  
DE VARIANT SURFACE GLYCOPROTEIN ILTAT 1.2 (VSG) (FRAGMENT).  
OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rice-Ficht A.C., Chen K.K., Donelson J.E.;  
RT "Sequence homologues near the C-termini of the variable surface  
RT glycoproteins of Trypanosoma brucei.";  
RL Nature 294:53-57(1981).  
CC -|- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE  
CC TYRANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING  
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000  
CC VSG GENES.  
CC -|- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.  
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A  
CC PI-PLC.  
CC  
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CC  
CC EMBL; J01220; AAA30286.1; -;  
DR PIR; S09639; S09639.  
DR Pfam; PF00913; Trypan\_glycop; 1.  
KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane.  
FT NON\_TER 1  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)

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Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 QXAVXHL 8
      |  |  |  |
Db      318 QFAVKHL 324

RESULT 8
HEMI_CYAPA STANDARD; PRT; 432 AA.
AC      P48077;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR).
GN      HEMA.
OS      Cyanophora paradoxa.
OC      Cyanelle.
OC      Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
NCBI_TaxID=2762;
[1]
SEQUENCE FROM N.A.
STRAIN=LB555 / PRINGSHEIM;
Stirewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H. J
Bryant D.A.;
Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE OF 407-432 FROM N.A.
STRAIN=LB555 UTEX;
MEDLINE=90092562; PubMed=2403527;
Bryant D.A., Stirewalt V.L.;
"The cyanelle genome of Cyanophora paradoxa encodes ribosomal
proteins not encoded by the chloroplast genomes of higher plants. ";
FEBS Lett. 259:273-280(1990)
CC      -1- CATALYTIC ACTIVITY: GLUTAMYL-TRNA(GLU) + NADPH -> GLUTAMATE +
      SEMIALDEHYDE + NADP(+) + TRNA(GLU).
CC      -1- PATHWAY: FIRST STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY.
      INVOLVED IN CHLOROPHYLL BIOSYNTHESIS.
CC      -1- SIMILARITY: BELONGS TO THE GLUTAMYL-TRNA REDUCTASE FAMILY.
      -----
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      or send an email to license@isb-sib.ch).
      -----
CC      EMBL; U30821; AAA81194.1; -.
CC      DR      EMBL; X17063; CAA34909.1; -.
CC      InterPro: IPR000343; -.
CC      Pfam: PF00745; GlutR; 1.
CC      PROSITE; PS00747; GLUTR; 1.
KW      Porphyrin biosynthesis; Chlorophyll biosynthesis; Oxidoreductase;
      NADP; Cyanelle.
KW      NADP; Cyanelle.
KW      NADP; Cyanelle.
SQ      SEQUENCE 432 AA; 48542 MW; F14378FC72FFD05B CRC64;

Query Match 82.1%; Score 23; DB 1; Length 432;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 QXAVXHL 8
      |  |  |  |
Db      94 QDAVXHL 100

RESULT 9
HEMI_PASMA STANDARD; PRT; 434 AA.
ID      HEMI_PASMA
AC      P95525;
DT      01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR).  
 GN HEMA.  
 OS Pasteurella multocida.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Pasteurella.  
 OC NCBI\_TaxID=747;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2.5;  
 RA Castillon R.T.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: GLUTAMYL-TRNA (GLU) + NADPH = GLUTAMATE-1-  
 CC SEMIALDEHYDE + NADP(+) + TRNA (GLU).  
 CC -1- PATHWAY: FIRST STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMYL-TRNA REDUCTASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; Y10430; CAA71452.1; -.  
 DR InterPro: IPR00343; -.  
 DR Pfam: PF00745; Glutr; 1.  
 DR PROSITE: PS00747; GLUTR; 1.  
 DR Porphyrin biosynthesis; Oxidoreductase; NADP.  
 KW PORPHYRIN BIOSYNTHESIS; Oxidoreductase; NADP.  
 SQ SEQUENCE 434 AA; 48460 MW; D4FF92E52CFFB2B3 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 434;  
 Best Local Similarity 71.4%; Pred. No. 78;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I  
 DB 99 QQAVLHL 105

RESULT 10  
 IFT2\_MOUSE  
 ID IFT2\_MOUSE STANDARD; PRT; 472 AA.  
 AC Q64112; Q62385;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE INTERFERON-INDUCED PROTEIN WITH TETRATRICOPEPTIDE REPEATS 2 (IFI-2)  
 DE (INTERFERON-INDUCED 54 KDA PROTEIN) (IFI-54K) (GLUCOCORTICOID-  
 DE ATTENUATED RESPONSE GENE 39 PROTEIN) (GARG-39).  
 GN IFI2 OR IFI54 OR GARG39.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95203869; PubMed=7896268;  
 RA Bluyssen H.A., Vlietstra R.J., Faber P.W., Smit E.M., Hagemeljer A.,  
 RA Trapman J.;  
 RT "Structure, chromosome localization, and regulation of expression of  
 RT the interferon-regulated mouse Ifi54/Ifi56 gene family";  
 RL Genomics 24:137-148(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96239145; PubMed=8660659;  
 RA Smith J.B., Herschman H.R.;  
 RT "The glucocorticoid attenuated response genes GARG-16, GARG-39, and  
 RT GARG-49/IRG2 encode inducible proteins containing multiple  
 RT tetratrico peptide repeat domains";

RL Arch. Biochem. Biophys. 330:290-300(1996).  
 CC -1- SIMILARITY: BELONGS TO THE IFIT FAMILY.  
 CC -1- SIMILARITY: CONTAINS TPR REPEATS.  
 CC -----  
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 CC -----  
 CC EMBL; S77713; AAB33830.1; -.  
 DR EMBL; S77710; AAB33830.1; JOINED.  
 DR EMBL; U43085; AAC52626.1; -.  
 DR MGD: MGI:99449; Ifit2  
 KW Repeat; TPR repeat; Interferon induction.  
 FT REPEAT 51 85 TPR 1.  
 FT REPEAT 87 128 TPR 2.  
 FT REPEAT 157 172 TPR 3B.  
 FT REPEAT 175 209 TPR 4.  
 FT REPEAT 210 244 TPR 5.  
 FT REPEAT 245 278 TPR 6.  
 FT REPEAT 279 289 TPR 7A.  
 FT REPEAT 317 332 TPR 7B.  
 FT REPEAT 333 366 TPR 8.  
 FT REPEAT 369 404 TPR 9.  
 FT REPEAT 428 461 TPR 10.  
 FT CONFLICT 10 11 VC -> ES (IN REF. 2).  
 FT CONFLICT 182 182 F -> N (IN REF. 2).  
 FT CONFLICT 223 224 MISSING (IN REF. 2).  
 FT CONFLICT 468 468 D -> A (IN REF. 2).  
 SQ SEQUENCE 472 AA; 55020 MW; 0C76034B1C0B2C41 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 472;  
 Best Local Similarity 71.4%; Pred. No. 86;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I  
 DB 315 QLVNHL 321

RESULT 11  
 THDF\_TREPA  
 ID THDF\_TREPA STANDARD; PRT; 495 AA.  
 AC O83561;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.  
 GN THDF OR TP0550.  
 OS Treponema pallidum  
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.  
 OC NCBI\_TaxID=160;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NICHOLS;  
 RX MEDLINE=98332770; PubMed=9665876;  
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.  
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,  
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Petersen J.,  
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,  
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
 RA Venter J.C.;  
 RT "Complete genome sequence of Treponema pallidum, the syphilis  
 RT spirochete";  
 RL Science 281:375-388(1998).  
 CC -1- FUNCTION: INVOLVED IN THIOPHENE OXIDATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ERA/THDF FAMILY OF GTP-BINDING  
 CC PROTEINS.

```
CC -----
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CC -----
DR EMBL; AE001230; AAC65535.1; -
DR TIGR; TP0550; -
DR InterPro; IPR002086; -
DR InterPro; IPR002106; -
DR InterPro; IPR002917; -
DR Pfam; PF01926; MMR_HSR1.1.
KW GTP-binding.
FT NP_BIND 230 237 GTP (BY SIMILARITY).
FT NP_BIND 277 281 GTP (BY SIMILARITY).
FT NP_BIND 337 340 GTP (BY SIMILARITY).
SQ SEQUENCE 495 AA; 53781 MW; C40681269E7AFD2F CRC64;

Query Match 82.1%; Score 23; DB 1; Length 495;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8
DB 150 QQAVLHL 156

RESULT 12
RECO_BACSU STANDARD; PRT; 496 AA.
AC P50729;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATP-DEPENDENT DNA HELICASE RECO (EC 3.6.1.-) (RECOMBINATION PROTEIN
DE S).
GN RECO OR RECS.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MARBURG;
MEDLINE=96349105; PubMed=8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
Serron P.;
"Sequence analysis of the Bacillus subtilis chromosome region between
the serA and kds loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
[2]
CHARACTERIZATION.
MEDLINE=98317281; PubMed=9642195;
Fernandez S., Sorokin A., Alonso J.C.;
"Genetic recombination in Bacillus subtilis 168: effects of recU and
recS mutations on DNA repair and homologous recombination.";
J. Bacteriol. 180:3405-3409(1998).
CC -!- FUNCTION: PROBABLE DNA HELICASE. REQUIRED FOR DNA REPAIR AND
CC INTRAMOLECULAR RECOMBINATION.
CC -!- SIMILARITY: BELONGS TO THE RECO SUBFAMILY OF HELICASES.
CC -----
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CC -----
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DR EMBL; L47648; AAC83947.1; -
DR EMBL; Z99115; CAB14218.1; -
DR EMBL; Z99116; CAB14234.1; -
DR Subtilist; BG11407; recU.
DR InterPro; IPR001410; -
DR InterPro; IPR001650; -
DR InterPro; IPR002464; -
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW Hydrolase; Helicase; DNA-binding; ATP-binding.
FT NP_BIND 38 45 ATP (POTENTIAL).
FT SITE 136 139 DEAH BOX.
SQ SEQUENCE 496 AA; 56508 MW; DDC2FED715875F2D CRC64;

Query Match 82.1%; Score 23; DB 1; Length 496;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8
DB 189 QNAVRL 195

RESULT 13
TCPE_SCHPO STANDARD; PRT; 546 AA.
AC Q9UTM4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSI, 1)
GN CCT5 OR SPAC1420.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Aert R., Voickaert G., McDougall R.C., Rajandream M.A., Barral, H.G.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
CC ACTIN AND TUBULIN (BY SIMILARITY).
CC -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KDA THAT
CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL121732; CAB57321.1; -
DR InterPro; IPR001844; -
DR InterPro; IPR002194; -
DR InterPro; IPR002423; -
DR Pfam; PF00118; cpn60_TCP1; 1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00750; TCP1_1; 1.
DR PROSITE; PS00751; TCP1_2; 1.
DR PROSITE; PS00995; TCP1_3; 1.
KW Chaperone; ATP-binding; Multigene family.
SQ SEQUENCE 546 AA; 59377 MW; DAB279CF67BFD94 CRC64;
```

Query Match 82.1%; Score 23; DB 1; Length 546;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |  
DB 144 QVAVKHL 150

RESULT 14  
EF2K\_CABEL STANDARD; PRT; 768 AA.  
AC 001991; 001992; Q20309;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE ELONGATION FACTOR 2 KINASE (EC 2.7.1.-) (EEF-2 KINASE) (EEF-2K)  
(CALCIUM/CALMODULIN-DEPENDENT EUKARYOTIC ELONGATION FACTOR-2 KINASE).  
EFK-1 OR F42A10.4.  
Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=BRISTOL N2;  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=97289688; PubMed=9144159;  
RA Ryazanov A.G., Ward M.D., Mendola C.E., Pavur K.S., Dorovkov M.V.,  
Wiedmann M., Erfjument-Bromage H., Tempst P., Farmer T.G.,  
RA Prostko C.R., Germino F.J., Hait W.N.;  
RT "Identification of a new class of protein kinases represented by  
eukaryotic elongation factor-2 kinase".  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4884-4889(1997).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=BRISTOL N2;  
RC STRAIN=BRISTOL N2;  
RA LaReille P.;  
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PHOSPHORYLATES TWO ADJACENT THREONINE RESIDUES, THR-57  
AND THR-59, IN THE N-TERMINUS OF EUKARYOTIC ELONGATION FACTOR-2.  
CC BINDS CALMODULIN (BY SIMILARITY).  
CC -1- ENZYME REGULATION: UNDERGOES CALCIUM/CALMODULIN-DEPENDENT  
INTRAMOLECULAR AUTOPHOSPHORYLATION, AND THIS RESULTS IN IT  
BECOMING PARTIALLY CALCIUM/CALMODULIN-INDEPENDENT (BY SIMILARITY).  
CC -1- SUBUNIT: MONOMER OR HOMODIMER (POTENTIAL).  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; EFK-1A (SHOWN HERE) AND EFK-  
1B/CEFK-2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: BELONGS TO THE MHCK / EF-2 PROTEIN KINASE FAMILY.  
-----  
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-----  
DR EMBL; U93846; AAB58268.1; -;  
DR EMBL; U93847; AAB58269.1; -;  
DR EMBL; U10414; AAA19075.1; ALT\_SEQ.  
DR WormPep; F42A10.4; CE01295.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Calcium;  
FT Calmodulin-binding; Phosphorylation; Alternative splicing.  
FT DOMAIN 690 693 POLY-GLU.  
FT NP-BIND 279 284 ATP (POTENTIAL).  
FT VARSPPLIC 625 632 MISSING (IN ISOFORM EFK-1B).  
SQ SEQUENCE 768 AA: 87825 MW: 93333F3B13F0C14C5 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 768;  
Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |  
DB 570 QSAIFHL 576

RESULT 15  
PERT\_BORPE STANDARD; PRT; 910 AA.  
AC P14283;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE PERTACTIN PRECURSOR (OUTER MEMBRANE PROTEIN P.69) (P.93).  
GN PRN OR OMP69A.  
OS Bordetella pertussis.  
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;  
OC Bordetella.  
OX NCBI\_TaxID=520;  
[1]  
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RP STRAIN=ISOLATE CN2992;  
RX MEDLINE=89264462; PubMed=2542937;  
RA Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M.,  
RA Novotny P., Morrissey P., Fairweather N.F.;  
RT "Molecular cloning and characterization of protective outer membrane  
protein P.69 from Bordetella pertussis".  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).  
[2]  
RN REVISIONS TO 264 AND 332.  
RP MEDLINE=92407514; PubMed=1527510;  
RA Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;  
RT "Cloning, nucleotide sequence and heterologous expression of the  
protective outer-membrane protein P.68 pertactin from Bordetella  
bronchiseptica".  
RL J. Gen. Microbiol. 138:1697-1705(1992).  
[3]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RP MEDLINE=96196517; PubMed=8609998;  
RA Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.;  
RT "Structure of Bordetella pertussis virulence factor P.69 pertactin".  
RL Nature 381:90-92(1996).  
CC -1- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS  
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN  
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.  
CC -1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.  
CC -1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)  
CONCENTRATION.  
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-----  
DR EMBL; J04560; AAA22980.1; ALT\_SEQ.  
DR PIR; A32560; A32560.  
KW Outer membrane; Signal; Virulence; Repeat.  
FT SIGNAL 1 34  
FT CHAIN 35 910 P.93.  
FT CHAIN 35 711 PERTACTIN (P.69).  
FT PROPEP 712 910 POTENTIAL.  
FT SITE 260 262  
FT DOMAIN 266 290 5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.  
FT REPEAT 266 270 1.  
FT REPEAT 271 275 2.  
FT REPEAT 276 280 3.

FT REPEAT 281 285 4 (APPROXIMATE).  
 FT REPEAT 286 290 5 (APPROXIMATE).  
 FT DOMAIN 579 593 5 X 3 AA TANDEM REPEATS OF P-Q-P.  
 SQ SEQUENCE 910 AA; 93452 MW; A169871E20A2E7DB CRC64;

Query Match 82.1%; Score 23; DB 1; Length 910;  
 Best Local Similarity 71.4%; Pred. NO. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 247 QGAVVHL 253

Search completed: October 25, 2001, 11:28:29  
 Job time: 477 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:42 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-5

Perfect score: 28

Sequence: 1 QXAVXHL 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

1 number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16.\*

1: sp.archaea.\*

2: sp.bacteria.\*

3: sp.fungi.\*

4: sp.human.\*

5: sp.invertebrate.\*

6: sp.mammal.\*

7: sp.mhc.\*

8: sp.organelle.\*

9: sp.phage.\*

10: sp.plant.\*

11: sp.rodent.\*

12: sp.unclassified.\*

13: sp.vertebrate.\*

14: sp.virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	89.3	264	2 O07048	O07048 aeromonas h
2	25	89.3	424	11 Q92023	Q92023 mus musculus
3	25	89.3	432	3 O42654	O42654 schizosacch
4	24	85.7	179	2 Q92316	Q92316 rhizobium s
5	24	85.7	237	2 Q9WZ25	Q9WZ25 thermotoga
6	24	85.7	257	2 Q9PPN8	Q9PPN8 ureaplasma
7	24	85.7	265	2 Q9RA67	Q9RA67 thermomonos
8	24	85.7	302	2 Q55655	Q55655 synechocyst
9	24	85.7	328	2 Q9L296	Q9L296 streptomyce
10	24	85.7	347	4 Q9HAF9	Q9HAF9 homo sapien
11	24	85.7	363	2 Q52936	Q52936 calothrix v
12	24	85.7	476	10 Q9M318	Q9M318 arabidopsis
13	24	85.7	513	5 Q9N8N9	Q9N8N9 trypanosoma
14	24	85.7	614	1 Q9HSB1	Q9HSB1 halobacteri
15	24	85.7	796	5 Q9VAP3	Q9VAP3 drosophila
16	24	85.7	929	2 O08235	O08235 erwinia car
17	24	85.7	1467	10 Q9M033	Q9M033 arabidopsis
18	24	85.7	2051	5 Q9NAW9	Q9NAW9 anopheles g
19	23	82.1	160	2 Q9K5G3	Q9K5G3 alcaligenes

20	23	82.1	161	2	Q9K5G2	Q9K5G2 alcaligenes
21	23	82.1	166	2	Q9RV36	Q9RV36 innococcus
22	23	82.1	174	2	O84729	O84729 camydia t
23	23	82.1	211	5	Q9VQF0	Q9VQF0 drosophila
24	23	82.1	228	5	Q9VKY4	Q9VKY4 drosophila
25	23	82.1	241	2	Q9X899	Q9X899 streptomyce
26	23	82.1	316	5	Q94483	Q94483 dictyostell
27	23	82.1	340	2	Q9KZU3	Q9KZU3 streptomyce
28	23	82.1	355	5	Q9VDL6	Q9VDL6 drosophila
29	23	82.1	366	1	O93715	O93715 sulfolobus
30	23	82.1	387	2	Q9S3M9	Q9S3M9 bordetella
31	23	82.1	404	5	Q9WI70	Q9WI70 drosophila
32	23	82.1	419	2	Q9KQ24	Q9KQ24 vibrio chol
33	23	82.1	453	5	Q9VLJ8	Q9VLJ8 drosophila
34	23	82.1	475	2	O52506	O52506 pseudomonas
35	23	82.1	475	2	P96956	P96956 pseudomonas
36	23	82.1	497	2	O9I751	O9I751 pseudomonas
37	23	82.1	540	4	O43353	O43353 homo sapien
38	23	82.1	573	2	Q9EWH6	Q9EWH6 streptomyce
39	23	82.1	595	14	Q84421	Q84421 paramecium
40	23	82.1	714	2	O9EY99	O9EY99 klebsiella
41	23	82.1	822	5	O00901	O00901 klebsiella
42	23	82.1	851	4	Q9ULM4	Q9ULM4 homo sapien
43	23	82.1	879	14	Q9WIU9	Q9WIU9 human immu
44	23	82.1	890	5	Q9VWI2	Q9VWI2 drosophila
45	23	82.1	905	2	Q9S6N0	Q9S6N0 bordetella

#### ALIGNMENTS

RESULT 1  
O07048 PRELIMINARY; PRT; 264 AA.  
AC O07048;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE SIMILARITY WITH KNOWN PROKARYOTIC OR EUKARYOTIC PROTEINS.  
OS Aeromonas hydrophila.  
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;  
OC Aeromonas.  
OX NCBI\_TaxID=644;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A6.  
RX MEDLINE=97315206; PubMed=9171380;  
RA Wong C.Y.F., Heuzenroeder M.W., Quinn D.M., Flower R.L.P.;  
RT "Cloning and characterization of two immunophilin-like genes, p1pA and  
RT fkpA, on a single 3.9-kilobase fragment of Aeromonas hydrophila  
RT genomic DNA."  
RL J. Bacteriol. 179:3397-3403(1997).  
DR EMBL; U56832; AAC45361.1; -.  
SQ SEQUENCE 264 AA; 26815 MW; 8D2A5AB9CDD9681 CRC64;

Query Match 89.3%; Score 25; DB 2; Length 264;  
Best Local Similarity 71.4%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 QXAVXHL 8  
| | | | |  
Db 10 QXAVXHL 16

RESULT 2  
Q92023 PRELIMINARY; PRT; 424 AA.  
ID Q92023  
AC Q92023;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE SCF COMPLEX PROTEIN SKP2.

GN SKP2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F1(C57/BL6XCB); TISSUE=THYMUS;  
RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,  
RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,  
RA Nakayama K.-I.;  
RT "Ubiquitin-dependent degradation of IKB is mediated by a novel  
RT ubiquitin ligase SCFFWD1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1999).  
DR EMBL: AF083215; AAD16037.1; -.  
DR MGD: MGI:1351663; Skp2.  
DR InterPro: IPR001810; -.  
DR InterPro: IPR003592; -.  
DR Pfam: PF00646; F-box; 1.  
DR PROSITE: PSS0181; FBOX; 1.  
DR SMART: SMO0370; LRR; 1.  
SQ SEQUENCE 424 AA; 47766 MW; 5B7945C979D26AF9 CRC64;  
Query Match 89.3%; Score 25; DB 11; Length 424;  
Best Local Similarity 71.4%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 275 QAAVAHL 281  
RESULT 3  
ID 042654 PRELIMINARY; PRT; 432 AA.  
AC 042654;  
DT 01-JAN-1999 (TrEMBLrel. 09, Created)  
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
DE HYPOTHETICAL 49.4 KDA PROTEIN C10F6.15 IN CHROMOSOME I.  
GN SPAC10F6.15.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: SOME, TO S.POMBE SPAC4G9.07.  
DR EMBL: AL009197; CAA15728.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 432 AA; 49448 MW; C6CAEBB860CCFDE9F CRC64;  
Query Match 89.3%; Score 25; DB 3; Length 432;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 142 QTAVSHL 148  
RESULT 4  
ID 0923L6 PRELIMINARY; PRT; 179 AA.  
AC 0923L6;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE NODULATION PROTEIN B (FRAGMENT).  
OS Rhizobium sp. USDA 2061.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group.  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=87208;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA 2061;  
RX MEDLINE=99261640; PubMed=10331255;  
RA Wernegreen J.J., Riley M.A.;  
RT "Comparison of the evolutionary dynamics of symbiotic and housekeeping  
RT loci: a case for the genetic coherence of rhizobial lineages.";  
RL Mol. Biol. Evol. 16:98-113(1999).  
DR EMBL: AF063486; AAD11384.1; -.  
DR InterPro: IPR002509; -.  
DR Pfam: PF01522; Polysac\_deacet; 1.  
DR NON\_TER 1 1  
FT SEQUENCE 179 AA; 19262 MW; F66FA52E61942F13 CRC64;  
Query Match 85.7%; Score 24; DB 2; Length 179;  
Best Local Similarity 71.4%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 73 QAAVOHL 79  
RESULT 5  
ID 09WZZ5 PRELIMINARY; PRT; 237 AA.  
AC 09WZZ5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE BACITRACIN RESISTANCE PROTEIN.  
GN TM0893.  
OS Thermotoga maritima.  
OC Bacteria; Thermotogales; Thermotoga.  
OX NCBI\_TaxID=2336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MSB / DSM 3109;  
RX MEDLINE=99287316; PubMed=10360571;  
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
RT genome sequence of Thermotoga maritima.";  
RL Nature 399:323-329(1999).  
DR EMBL: AE001754; AAD35974.1; -.  
DR TIGR: TM0893; -.  
SQ SEQUENCE 237 AA; 26036 MW; 759239335C5FE10F CRC64;  
Query Match 85.7%; Score 24; DB 2; Length 237;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 38 QTAVLHL 44  
RESULT 6  
ID 09PPN8 PRELIMINARY; PRT; 257 AA.  
AC 09PPN8;

DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE DIMETHYLADENOSINE TRANSFERASE.  
 GN KSGA.  
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SERVAR 3;  
 RX MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;  
 RT "The complete sequence of the mucosal pathogen Ureaplasma  
 urealyticum";  
 RL Nature 407:757-762(2000).  
 DR EMBL; AE002158; AAF31015.1; -;  
 DR InterPro; IPR000051; -;  
 DR InterPro; IPR001737; -;  
 PFam; PF00398; RnaAD; 1.  
 DR PROSITE; PS01131; RNA\_A\_DIMETH; 1.  
 SQ SEQUENCE 257 AA; 29781 MW; 85F54A69404ECC4C CRC64;

Query Match 85.7%; Score 24; DB 2; Length 257;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QXAVXHL 8  
 | | | |  
 Db 177 QSAVIHL 183

RESULT 7  
 Q9RA67 PRELIMINARY; PRT; 265 AA.  
 AC Q9RA67;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE PUTATIVE DIENELACTONE HYDROLASE.  
 GN DLHA.  
 OS Thermomonospora fusca.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptosporangineae; Thermomonosporaceae;  
 OC Thermobifida.  
 OX NCBI\_TaxID=2021;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Spiridonov N.A., Wilson D.B.;  
 RT "PepA and dlhA genes from Thermobifida fusca";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF218823; AAF25687.1; -;  
 DR InterPro; IPR000379; -;  
 DR InterPro; IPR002925; -;  
 DR Pfam; PF01738; DLH; 2.  
 KW Hydrolase.  
 SQ SEQUENCE 265 AA; 29069 MW; 06C5A8E364BCDF8F CRC64;

Query Match 85.7%; Score 24; DB 2; Length 265;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QXAVXHL 8  
 | | | |  
 Db 97 QTAVDHL 103

RESULT 8  
 Q55655

ID Q55655 PRELIMINARY; PRT; 302 AA.  
 AC Q55655;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE HYPOTHETICAL 33.8 KDA PROTEIN.  
 GN SLL0310.  
 OS Synecocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC6803;  
 RA Tabata S.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 RA Suglura M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 region from map positions 64% to 92% of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hiroseawa M., Suglura M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura;  
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL; D64000; BAA10175.1; -;  
 DR InterPro; IPR000182; -;  
 DR Pfam; PF00583; Acetyltransf; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 302 AA; 33760 MW; 62D74D7F5B74564E CRC64;

Query Match 85.7%; Score 24; DB 2; Length 302;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 QXAVXHL 8  
 | | | |  
 Db 90 QTAIHL 96

RESULT 9  
 Q9L296 PRELIMINARY; PRT; 328 AA.  
 ID Q9L296  
 AC Q9L296;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE HYPOTHETICAL 37.4 KDA PROTEIN (FRAGMENT).  
 GN SCL2.01.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetaceae;  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Seeger K.J., Harris D.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);

RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kleser H.M., Denapalate D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb streptomyces coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 DR EMBL; ALI37778; CAB70913.1; -;  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 328 AA; 37352 MW; D60E937C5C48321F CRC64;

Query Match 85.7%; Score 24; DB 2; Length 328;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 43 QTAVDHL 49

RESULT 10  
 Q9HAF9 PRELIMINARY; PRT; 347 AA.  
 AC Q9HAF9;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE CDNA FLJ11703 FIS, CLONE HEMBA1005075.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=WHOLE EMBRYO, MAINLY HEAD;  
 RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
 RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;  
 RT "NEDO human cDNA sequencing project.";  
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 EMBL; AK021765; BAB13890.1; -;  
 SQ SEQUENCE 347 AA; 37973 MW; DF68202D85E6EC48 CRC64;

Query Match 85.7%; Score 24; DB 4; Length 347;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 86 QAAVLHL 92

RESULT 11  
 O52936 PRELIMINARY; PRT; 363 AA.  
 AC O52936;  
 DT 01-JUN-1998 (TRENBLrel. 06, Created)  
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
 DT 01-AUG-1998 (TRENBLrel. 07, Last annotation update)  
 DE HYPOTHETICAL 43.1 KDA PROTEIN (FRAGMENT).  
 OS Calothrix viguieri.  
 OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Calothrix.  
 OX NCBI\_TaxID=57746;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=D254;  
 RA Evans I.M., Bown D., Gupta A., Morby A.P., Whitton B.A.,  
 RA Gatehouse J.A.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y09899; CAA71029.1; -;  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT NON\_TER 363 363  
 SQ SEQUENCE 363 AA; 43113 MW; FAE7DB281D7E1BC9 CRC64;

Query Match 85.7%; Score 24; DB 2; Length 363;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 221 QEAVSHL 227

RESULT 12  
 Q9M318 PRELIMINARY; PRT; 476 AA.  
 AC Q9M318;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE HYPOTHETICAL 51.9 KDA PROTEIN.  
 GN FZA19.90.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X., Quetier F., Salanoubat M.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; ALI32962; CAB71079.1; -;  
 DR InterPro; IPR000743; -;  
 DR InterPro; IPR001066; -;  
 DR Pfam; PF00295; Glyco\_hydro\_28; 1.  
 DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 476 AA; 51939 MW; 48233D8B48A4BEDD CRC64;

Query Match 85.7%; Score 24; DB 10; Length 476;  
 Best Local Similarity 71.4%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 65 QSAVDHL 71

RESULT 13  
 Q9N8N9 PRELIMINARY; PRT; 513 AA.  
 AC Q9N8N9;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE PROBABLE AXONEMAL CENTRAL APPARATUS PROTEIN.  
 GN CHRI.235.  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

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OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TRE0927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359782; CAB95504.1; -.
DR InterPro; IPR00225; -.
DR Pfam; PF00514; Armadillo_seg; 8.
DR SMART; SM00185; ARM; 1.
SQ SEQUENCE 513 AA; 56126 MW; 40BB4546A1B390C3 CRC64;

Query Match 85.7%; Score 24; DB 5; Length 513;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8
1 1 1 1 1
208 QDAVTHL 214

RESULT 14
QHSHB1 PRELIMINARY; PRT; 614 AA.
AC Q9HSHB1;
DT 01-WAR-2001 (TREMBLrel. 16, Created)
DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-WAR-2001 (TREMBLrel. 16, Last annotation update)
DE DOLICHOL-P-GLUCOSE SYNTHETASE.
GN DPG OR VNG03186.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weitz R., Goo Y.A.,
RA Leitchauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RA "Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AF004992; AAG18896.1; -.
DR InterPro; IPR001173; -.
DR Pfam; PF00535; Glycos.transf.2; 1.
SQ SEQUENCE 614 AA; 54802 MW; DAD585C50B14DAB2 CRC64;

Query Match 85.7%; Score 24; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8
1 1 1 1 1
65 QSAVRHL 71

RESULT 15
Q9VAP3 PRELIMINARY; PRT; 796 AA.
AC Q9VAP3;
DT 01-WAY-2000 (TREMBLrel. 13, Created)
DT 01-WAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-WAR-2001 (TREMBLrel. 16, Last annotation update)
DE CG11880 PROTEIN.

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GN CG11880.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscivora; plin...
OC Ephyridae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Thewissen C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spiers R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
RL
DR EMBL; AE003768; AAF56859.1; -.
DR FlyBase; FBgn0039637; CG11880.
DR InterPro; IPR001662; -.
DR ProDom; PD006217; -.
SQ SEQUENCE 796 AA; 90628 MW; 20961DD889A3EB3B CRC64;

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Query Match 85.7%; Score 24; DB 5; Length 796;  
Best Local Similarity 71.4%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
1 1 1 1 1  
Db 587 QTAVYHL 593

Search completed: October 25, 2001, 11:27:43  
Job time: 446 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:20 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-5

Perfect score: 28

Sequence: 1 QXAVXHL 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

11 number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	89.3	432	2 T37509	hypothetical prote
2	24	85.7	237	2 F72321	bacitracin resista
3	24	85.7	257	2 E82871	dimethyladenosine
4	24	85.7	302	2 S76323	hypothetical prote
5	24	85.7	476	2 T47941	hypothetical prote
6	24	85.7	614	2 D84191	dolichol-P-glucose
7	24	85.7	1467	2 T48162	hypothetical prote
8	24	85.7	1510	2 D64120	cell division prot
9	23	82.1	85	1 WQECPH	phosphotransferase
10	23	82.1	85	1 WQEBPH	phosphotransferase
11	23	82.1	85	1 S12749	phosphotransferase
12	23	82.1	85	1 I64137	phosphotransferase
13	23	82.1	85	2 B85884	PTS system protein
14	23	82.1	166	2 A75426	hypothetical prote
15	23	82.1	174	2 T71478	hypothetical prote
16	23	82.1	241	2 T36164	hypothetical prote
17	23	82.1	276	2 T35693	DNA glycosylase -
18	23	82.1	320	2 S09639	variant surface gl
19	23	82.1	366	2 T44937	glucose 1-dehydrog
20	23	82.1	419	2 C82109	glutamyl-tRNA redu
21	23	82.1	432	2 T06851	glutamyl-tRNA redu
22	23	82.1	470	2 S71355	glucocorticoid-att
23	23	82.1	472	2 A55088	interferon alpha I
24	23	82.1	475	2 D83202	arginate biosynthe
25	23	82.1	495	2 B71311	probable thiophene
26	23	82.1	496	2 A69691	ATP-dependent DNA
27	23	82.1	497	2 F83634	hypothetical prote
28	23	82.1	546	2 T37665	probable t-complex
29	23	82.1	595	2 T17590	probable glutamine

## ALIGNMENTS

### RESULT 1

T37509

hypothetical protein SPAC10F6.15 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03 Dec-1999

C:Accession: T37509

R:Connor, R.; Church, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, November 1997

A:Reference number: Z21719

A:Accession: T37509

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-432 <CON>

A:Cross-references: EMBL:AL009197; PIDN:CAA15728.1; GSPDB:GN000066; JIB:SPAC10

A:Experimental source: strain 972h-; cosmid c10F6

C:Genetics:

A:Gene: SPDB:SPAC10F6.15

A:Map position: 1

Query Match 89.3%; Score 25; DB 2; Length 432;

Best Local Similarity 71.4%; Pred. No. 44;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 2 QXAVXHL 8

DB 142 QTAVSHL 148

### RESULT 2

F72321

bacitracin resistance protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C:Accession: F72321

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.; Hart, D.

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richar

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from

A:Reference number: A72200; MUID:99287316

A:Accession: F72321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <ARN>

A:Cross-references: GB:AE001754; GB:AE000512; NID:g4981417; PIDN:CAA15974.1; P

A:Experimental source: strain MSB8

C:Genetics:

C:Superfamily: Escherichia coli bacitracin resistance protein baci

Query Match 85.7%; Score 24; DB 2; Length 237;  
 Best Local Similarity 71.4%; Pred. No. 42;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I | | | |  
 Db 38 QTAVALHL 44

## RESULT 3

E82871  
 dimethyladenosine transferase UU601 [imported] - Ureaplasma urealyticum  
 C:Species: Ureaplasma urealyticum  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: E82871  
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 Submitted to GenBank, February 2000  
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
 A:Reference number: A82870  
 A:Accession: E82871  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-257 <GLA>  
 A:Cross-references: GB:AE002158; GB:AF222894; MID:g6899599; PIDN:AAF31015.1; GSPDB:GN001  
 A:Experimental source: serovar 3; biovar 1  
 C:Genetics:  
 A:Gene: ksqA; UU601  
 A:Genetic code: SGC3  
 C:Superfamily: rRNA (adenine-N6-)-methyltransferase

Query Match 85.7%; Score 24; DB 2; Length 257;  
 Best Local Similarity 71.4%; Pred. No. 46;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I | | | |  
 Db 177 QSAVHL 183

## RESULT 4

S76323  
 hypothetical protein sl10310 - Synechocystis sp. (strain PCC 6803)  
 C:Species: Synechocystis sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76323  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
 s.  
 A:Reference number: S74322; MUID:97061201  
 A:Accession: S76323  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-302 <KAN>  
 A:Cross-references: EMBL:D64000; GB:AB001339; MID:g1001484; PIDN:BAAL0175.1; PID:g100154  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 85.7%; Score 24; DB 2; Length 302;  
 Best Local Similarity 57.1%; Pred. No. 56;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I | | | |  
 Db 90 QTAIAHL 96

## RESULT 5

T47941  
 hypothetical protein F2A19.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: T47941  
 R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.  
 Submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z24480  
 A:Accession: T47941  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-476 <DEH>  
 A:Cross-references: EMBL:AL132962  
 A:Experimental source: cultivar Columbia; BAC clone F2A19  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 155/1; 213/2; 237/1  
 A:Note: F2A19.90

Query Match 85.7%; Score 24; DB 2; Length 476;  
 Best Local Similarity 71.4%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I | | | |  
 Db 65 QSAVDHL 71

## RESULT 6

D84191  
 dolichol-P-glucose synthetase [imported] - Halobacterium sp. NRC 1  
 C:Species: Halobacterium sp. NRC-1  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: D84191  
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.;  
 Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.;  
 Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, J.  
 A:Title: Genome sequence of Halobacterium species NRC-1.  
 A:Reference number: A84160; MUID:20504483  
 A:Accession: D84191  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-614 <STO>  
 A:Cross-references: GB:AE004437; MID:g10579946; PIDN:AAG18896.1; GSPDB:GN00118  
 C:Genetics:  
 A:Gene: dpq

Query Match 85.7%; Score 24; DB 2; Length 614;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I | | | |  
 Db 65 QSAVRHL 71

## RESULT 7

T48162  
 hypothetical protein T1008.110 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: T48162  
 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer,  
 Submitted to the Protein Sequence Database, March 2000  
 A:Reference number: Z24486  
 A:Accession: T48162  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1467 <BEV>  
 A:Cross-references: EMBL:AL161746  
 A:Experimental source: cultivar Columbia; BAC clone T1008

A;Residues: 1-85 <SAFE>  
A/Cross-references: GB:J02796; NID:g147397; PIDN:AAA2440.1; PID:g147398  
R;De Reuse, H.; Roy, A.; Danchin, A.  
Gene 35, 199-207, 1985  
A/Title: Analysis of the ptsH-ptsI-crr region in *Escherichia coli* K-12: nucleotide sequence  
A/Reference number: A24035; MUID:85286351  
A/Accession: A24035  
A/Molecule type: DNA

A:Title: Mutation of serine-46 to aspartate in the histidine-containing protein of *Escherichia coli* HPr  
 A:Reference number: A58915; MUID:96378616  
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms  
 C:Comment: This protein is phosphorylated by the phosphotransferase system enzyme I (see systems).

C:Genetics:  
 A:Gene: ptsH  
 A:Map position: 52 min  
 C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system  
 F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H  
 F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I) #s  
 F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
 I I I I I  
 71 QKAVEHL 77

## RESULT 10

WQEBPH  
 phosphotransferase system phosphohistidine-containing protein - *Salmonella typhimurium*  
 N:Alternate names: phosphocarrier protein HPr  
 C:Species: *Salmonella typhimurium*

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Jul-1999

C:Accession: C28181; S04159; A22849  
 R:Byrne, C.R.; Monroe, R.S.; Ward, K.A.; Kredich, N.M.  
 J. Bacteriol. 170, 3150-3157, 1988  
 A:Title: DNA sequences of the cysK regions of *Salmonella typhimurium* and *Escherichia coli*  
 A:Reference number: A28181; MUID:88257033

A:Accession: C28181  
 A:Molecule type: DNA  
 A:Residues: 1-85 <BYR>  
 A:CROSS-references: GB:M21450; NID:g153933; PIDN:AAA27052.1; PID:g153936  
 R:Schlirow, B.J.; Yamada, M.; Salier Jr., M.H.  
 Mol. Microbiol. 3, 113-118, 1989

A:Title: Partial nucleotide sequence of the pts operon in *Salmonella typhimurium*: comparison of the pts operon in *Salmonella typhimurium* and *Escherichia coli*  
 A:Reference number: S04159; MUID:89237892

A:Accession: S04159  
 A:Molecule type: DNA  
 A:Residues: 1-85 <SCH>  
 A:CROSS-references: EMBL:X14737; NID:g47844; PIDN:CAA32865.1; PID:g47845

R:Powells, D.A.; Roseman, S.  
 J. Biol. Chem. 259, 15212-15214, 1984  
 A:Title: The primary structure of *Salmonella typhimurium* HPr, a phosphocarrier protein of the phosphotransferase system  
 A:Reference number: A22849; MUID:85080006

A:Accession: A22849  
 A:Molecule type: protein  
 A:Residues: 1-20, 'G', 22-84, 'Z' <POW>  
 C:Comment: The phosphoenolpyruvate-glycose phosphotransferase system (PTS) comprises two parts (II-A/II-B or III/III), lipid, and divalent cation. The phosphoryl group is transferred to the substrate as it crosses the cell membrane.

C:Genetics:  
 A:Gene: ptsH  
 A:Map position: 49 min  
 C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system  
 F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H  
 F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I) #s  
 F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
 I I I I I

Db 71 QKAVEHL 77

## RESULT 11

S12749

phosphotransferase system phosphohistidine-containing protein - *Klebsiella pneumoniae*  
 C:Species: *Klebsiella pneumoniae*

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S12749  
 R:Ritgemeyer, F.; Eisermann, R.; Hengstenberg, W.; Lengeler, J.W.

Nucleic Acids Res. 18, 1898, 1990

A:Title: The nucleotide sequence of ptsH gene from *Klebsiella pneumoniae*.

A:Reference number: S12749; MUID:90245592

A:Accession: S12749

A:Molecule type: DNA

A:Residues: 1-85 <TIT>

A:CROSS-references: EMBL:X51452; NID:g43910; PIDN:CAA35818.1; PID:g43911

C:Genetics:

A:Gene: ptsH

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system  
 F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H  
 F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I)  
 F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

I I I I I

Db 71 QKAVEHL 77

## RESULT 12

I64137

phosphotransferase system phosphohistidine-containing protein - *Haemophilus influenzae*  
 C:Species: *Haemophilus influenzae*

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: I64137

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ketchum, K.A.; Binkley, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Whitehead, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, S.M.  
 Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; White

A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae*

A:Reference number: A64000; MUID:95350630

A:Accession: I64137

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-85 <TIGR>

A:CROSS-references: GB:U32844; GB:L42023; NID:g1574563; PIDN:AAC23358.1; PID:g1568

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system  
 F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H  
 F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I)  
 F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

I I I I I

Db 71 QKAVEHL 77

## RESULT 13

B85684

PTS system protein Hpr [imported] - *Escherichia coli* (strain O157:H7)  
 C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
C:Accession: B05884  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B05884  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-85 <STO>  
A:Cross-references: GB:AE005174; NID:gt12516791; PIDN:AAG57534.1; GSPDB:GN00145; UNGP:236  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ptsH

Query Match 82.1%; Score 23; DB 2; Length 85;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
| | | | |  
Db 71 QKAVEHL 77

RESULT 14  
A75426  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
C:Accession: A75426  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896  
A:Accession: A75426  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-166 <WHI>  
A:Cross-references: GB:AE001968; GB:AE000513; NID:g6458930; PIDN:AAF10769.1; PID:g645893  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1194  
A:Map position: 1  
C:Superfamily: Deinococcus radiodurans hypothetical protein DR1194

Query Match 82.1%; Score 23; DB 2; Length 166;  
Best Local Similarity 71.4%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 144 QYAVIHL 150

RESULT 15  
G71478  
hypothetical protein CT724 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C>Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 08-Oct-1999  
C:Accession: G71478  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
Science 282, 754-759, 1998  
A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac  
A:Reference number: A71570; MUID:99000809  
A:Accession: G71478  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-174 <ARN>

A:Cross-references: GB:AE001343; GB:AE001273; NID:g3329176; PIDN:AA:58319.1; 1;  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: CT724

Query Match 82.1%; Score 23; DB 2; Length 174;  
Best Local Similarity 71.4%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 113 QEAVQHL 119

Search completed: October 25, 2001, 11:25:21  
Job time: 334 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:43 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-6

Perfect score: 40

Sequence: 1 QXWVGH1 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_unclassified:\*

13: sp\_vertebrate:\*

14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	35	87.5	266	5 Q9VZF7	Q9vzf7 drosophila
2	35	87.5	399	5 Q9U0V1	Q9u0v1 leishmania
3	34	85.0	119	13 Q90253	Q90253 bombina ori
4	34	85.0	224	4 Q9UI28	Q9ui28 homo sapien
5	34	85.0	232	3 Q9UVE4	Q9uve4 zygosacchar
6	34	85.0	256	3 Q9P6Y1	Q9p6y1 neurospora
7	33	82.5	211	2 Q9WMT3	Q9wmt3 pseudomonas
8	33	82.5	252	10 Q9VFI20	Q9vfi20 arabidopsis
9	33	82.5	387	2 Q9VN79	Q9vn79 streptomyce
10	33	82.5	539	2 P72284	P72284 rhizobium l
11	33	82.5	540	2 O06656	O06656 rhizobium l
12	33	82.5	540	2 P72288	P72288 rhizobium l
13	33	82.5	540	2 Q9FDG4	Q9fdg4 rhizobium e
14	32	80.0	276	5 Q9V5C9	Q9v5c9 drosophila
15	32	80.0	406	2 Q9Z7L5	Q9z7l5 chlamydia p
16	32	80.0	494	11 Q08612	Q08612 mus musculus
17	32	80.0	540	2 P93600	P93600 rhizobium e
18	32	80.0	920	10 Q9SSD5	Q9ssd5 arabidopsis
19	32	80.0	949	4 Q9ULH1	Q9ulh1 homo sapien

20	32	80.0	1006	4	O43150	O43150 homo sapien
21	32	80.0	1090	11	Q9Z2B6	Q9z2b6 mus musculu
22	32	80.0	1129	6	O97902	O97902 bos taurus
23	32	80.0	1147	11	Q9QWY8	Q9qwY8 mus musculu
24	31	77.5	23	13	Q9PS30	Q9ps30 oncorhynch
25	31	77.5	91	5	Q9XVR9	Q9xvr9 caenorhabdi
26	31	77.5	119	5	Q9NH76	Q9nh76 naegleria f
27	31	77.5	157	13	Q9I829	Q9i829 carassius
28	31	77.5	279	2	P73885	P73885 synechocysti
29	31	77.5	350	8	Q32721	Q32721 nicotiana t
30	31	77.5	372	2	Q9HVL9	Q9hvl9 pseudomonas
31	31	77.5	375	10	Q9SY04	Q9sy04 arabidopsi
32	31	77.5	396	4	Q99986	Q99986 homo sapien
33	31	77.5	423	4	Q15114	Q15114 homo sap
34	31	77.5	426	5	Q9N4Q4	Q9n4q4 caenorhabd
35	31	77.5	475	2	Q9I3G3	Q9i3g3 pseudomonas
36	31	77.5	475	2	Q9I3G0	Q9i3g0 pseudomonas
37	31	77.5	475	2	Q9HWP8	Q9hwp8 pseudomonas
38	31	77.5	477	2	Q9K519	Q9k519 vibrio chol
39	31	77.5	480	2	Q9I2N9	Q9i2n9 pseudomonas
40	31	77.5	481	10	Q9M3J5	Q9m3j5 stinacia o
41	31	77.5	484	2	Q9WVB7	Q9wvb7 thermotoga
42	31	77.5	498	2	Q9ZHR7	Q9zhr7 asospirill
43	31	77.5	532	2	Q30727	Q30727 rhodobacter
44	31	77.5	535	2	O53111	O53111 rhodobacter
45	31	77.5	539	2	Q51679	Q51679 paracoccus

## ALIGNMENTS

RESULT 1

ID	Q9VZF7	PRELIMINARY;	PRT;	266 AA.
AC	Q9VZF7			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
DE	IMPL2 PROTEIN.			
GN	IMPL2 OR CG15009.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=107311132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preli			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos J.G.,			
RA	Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Chun P.			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketch K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.			

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,  
RA Pallazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
DR EMBL: AE003480; AAF47866.2; -.  
DR HSSP: P56276; 1TLK.  
DR Flybase: FBgn0001257; Impl2.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; Ig; 4.  
SQ SEQUENCE 266 AA; 29823 MW; FC97694BDFE60F33 CRC64;

Query Match 87.5%; Score 35; DB 5; Length 266;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWYVGH 8  
|||:  
DB 90 QWVVGHL 96

RESULT 2  
Q9U0V1 PRELIMINARY; PRT; 399 AA.  
AC Q9U0V1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE MITOCHONDRIAL CARRIER PROTEIN.  
GN L8342.02  
OS Leishmania major.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Masny D., Purnelle B., Goffeau A., Ivens A.C., Lawson D., Quail M.,  
RA Rajandream M.A., Barrell B.G.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Smith D.F.;  
RC STRAIN=FRIEDLIN;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome."  
RL Genome Res. 8:135-145(1998).  
DR EMBL: AL122012; CAB58416.1; -.  
DR InterPro: IPR000847; -.  
DR InterPro: IPR001993; -.  
DR Pfam: PF00153; mito\_carr; 3.  
DR PROSITE: PS00044; HTH\_LYSR\_FAMILY; UNKNOWN.1.  
DR PROSITE: PS00215; MITOCH\_CARRIER; UNKNOWN.2.  
SQ SEQUENCE 399 AA; 43755 MW; A3D4E510517865C8 CRC64;

Query Match 87.5%; Score 35; DB 5; Length 399;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWYVGH 8  
|||:  
DB 90 QWVVGHL 96

Db 131 QWTLGHI 137  
|||:  
RESULT 3  
Q90253 PRELIMINARY; PRT; 119 AA.  
AC Q90253;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE PHE-13 BOMBESIN PREPROHORMONE.  
OS Bombina orientalis (Oriental fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina  
OX NCBI\_TaxID=8346;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96205965; PubMed=8631814;  
RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,  
RA Dong J.Z., Spindel E.R.;  
RT "There are three distinct forms of bombesin. Identification of  
RT [Leu13]bombesin, [Phe13]bombesin, and [Ser3,Arg10,Phe13]bombesin in  
RT the frog *Bombina orientalis*."  
RL J. Biol. Chem. 271:7731-7737(1996).  
DR EMBL: U49450; AAC59784.1; -.  
DR InterPro: IPR000874; -.  
DR Pfam: PF02044; Bombesin; 1.  
DR PROSITE: PS00257; BOMBESIN; 1.  
FT CHAIN 45 59 PHE-13 BOMBESIN.  
SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 85.0%; Score 34; DB 13; Length 119;  
Best Local Similarity 83.3%; Pred. No. 9.8;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWYVGH 7  
|||:  
DB 51 QWAVGH 56

RESULT 4  
Q9UI28 PRELIMINARY; PRT; 224 AA.  
AC Q9UI28;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE ADRENAL GLAND PROTEIN AD-003.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADRENAL GLAND;  
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,  
RA Han Z., Wang Y., Chen Z., Fu G.;  
RT "A novel gene expressed in human adrenal gland."  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF10776; AAF14859.1; -.  
DR InterPro: IPR000051; -.  
DR InterPro: IPR001601; -.  
SQ SEQUENCE 224 AA; 25474 MW; 8BB11B3FA7804CD3 CRC64;

Query Match 85.0%; Score 34; DB 4; Length 224;  
Best Local Similarity 57.1%; Pred. No. 19;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWYVGH 8  
|||:  
DB 2 QWYVGH 8

Db 136 QWVIGHL 142

RESULT 5  
Q9UVE4 PRELIMINARY; PRT; 232 AA.  
AC Q9UVE4; (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE HYPOTHETICAL 26.4 KDA PROTEIN.  
OS Zygocaccharomyces rouxii (Candida mogii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Zygocaccharomyces.  
OX NCBI\_TaxID=4956;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS 732;  
RA Sychrova H., Braun V., Potler S., Souciet J.L.;  
RT "Genomic organization of Pichia sorbitophila and Zygocaccharomyces  
rouxii genomes: comparison with Saccharomyces cerevisiae.";  
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y18560; CAB62288.1; -;  
DR InterPro: IPR001601; -;  
KW Hypothetical protein.  
SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 232;  
Best Local Similarity 71.4%; Pred. No. 19;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVIGHI 8  
Db 140 QWCVGHL 146

RESULT 6  
Q9P6Y1 PRELIMINARY; PRT; 256 AA.  
AC Q9P6Y1;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE CONSERVED HYPOTHETICAL PROTEIN.  
GN 13E11.350.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariiales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA German Neurospora genome project;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL353820; CAB88603.1; -;  
DR InterPro: IPR001601; -;  
SQ SEQUENCE 256 AA; 27789 MW; 5251FBC58B6BDD9 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 256;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVIGHI 8  
Db 162 QWCVGHL 168

RESULT 7  
Q9WWT3 PRELIMINARY; PRT; 211 AA.  
AC Q9WWT3;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE HYPOTHETICAL 23.6 KDA PROTEIN (FRAGMENT).  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PRS2000;  
RA Nichols N.N., Harwood C.S.;  
RT "Aerotaxis receptor of Pseudomonas putida PRS2000.";  
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF079997; AAD22404.1; -;  
DR InterPro: IPR000014; -;  
DR InterPro: IPR000160; -;  
DR InterPro: IPR000700; -;  
DR InterPro: IPR001610; -;  
DR Pfam: PF00785; PAC; 1.  
DR Pfam: PF00989; PAS; 1.  
DR Pfam: PF00990; DUF9; 1.  
DR SMART: SM00267; DUF1; 1.  
KW Hypothetical protein.  
FT NON\_TER 211  
SQ SEQUENCE 211 AA; 23566 MW; F113AF955610BBE5 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 211;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 7  
Db 125 QWVGH 130

RESULT 8  
Q9FI20 PRELIMINARY; PRT; 252 AA.  
AC Q9FI20;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE GENOMIC DNA, CHROMOSOME 5, PI CLONE:MFC16.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eudicots II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=99397451; PubMed=10470850;  
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotai,  
RA Miyajima N., Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I  
Sequence features of the regions of 1,011,550 bp covered by seventeen  
PI and TAC clones.";  
RL DNA Res. 6:183-195(1999).  
DR EMBL: AB017065; BAB09152.1; -;  
SQ SEQUENCE 252 AA; 28622 MW; F93F8EB657D284B2 CRC64;

Query Match 82.5%; Score 33; DB 10; Length 252;  
Best Local Similarity 57.1%; Pred. No. 34;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVIGHI 8

Db 147 QWCIHGL 153  
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RESULT 9  
Q9JN79 PRELIMINARY; PRT; 387 AA.  
AC Q9JN79;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE PUTATIVE ENOYL REDUCTASE.  
GN MYE.  
OS Streptomyces coelicolor.  
OC Plasmid pSCP1.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
SEQUENCE FROM N.A.  
STRAIN=A3(2);  
RA Bruton C.J., Wietzorrek A., Hartley N., Woodburn L., Chater K.F.;  
RT "Genes involved in methylenomycin biosynthesis from plasmid SCP1 of  
Streptomyces coelicolor A3(2).";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
SEQUENCE FROM N.A.  
STRAIN=A3(2);  
RA Neal R.J., Chater K.F.;  
RT "Nucleotide sequence analysis reveals similarities between proteins  
determining methylenomycin A resistance in Streptomyces and  
tetracycline resistance in eubacteria.";  
RL Gene 58:229-241(1987).  
RN [3]  
SEQUENCE FROM N.A.  
STRAIN=A3(2);  
RA Chater K.F., Bruton C.J.;  
RT "Resistance, regulatory and production genes for the antibiotic  
methylenomycin are clustered.";  
RL EMO J. 4:1893-1897(1985);  
DR EMBL; AJ276673; CAB82878.1; -;  
DR InterPro; IPR001155; -;  
DR Pfam; PF00724; oxidored\_FMN; 1.  
KW Plasmid.  
SQ SEQUENCE 387 AA; 40974 MW; 0149B42D0F6B90A3 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 387;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWXYVGH 7  
||:|:

Db 246 QWKVGH 251  
PRELIMINARY; PRT; 539 AA.  
ID P72284 Q52826;  
AC P72284; Q52826;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE FIXNC (EC 1.9.3.1).  
GN FIXNC.  
OS Rhizobium leguminosarum.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=384;  
RN [1]  
SEQUENCE FROM N.A.

RC STRAIN=VF39;  
RX MEDLINE=97348582; PubMed=9204566;  
RA Schluter A., Patschkowski T., Quandt J., Selinger L.B., Weidner S.,  
RA Kramer M., Zhou L., Hynes M., Priefer U.;  
RT "Functional and regulatory analysis of the two copies of the fixNOQP  
operon of Rhizobium leguminosarum strain VF39.";  
RL Mol. Plant Microbe Interact. 10:605-616(1997).  
RN [2]  
SEQUENCE OF 1-187 FROM N.A.  
RC STRAIN=VF39;  
RX MEDLINE=97011572; PubMed=8858582;  
RA Patschkowski T., Schluter A., Priefer U.;  
RT "Rhizobium leguminosarum bv. viciae contains a second fnr/fixK-like  
gene and an unusual fixL homologue.";  
RL Mol. Microbiol. 21:267-280(1996).  
CC -|- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4  
FERROCYTOCHROME C.  
CC -|- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).  
CC -|- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
DR EMBL; Z80340; CAB02453.1; -;  
DR EMBL; Z70305; CAA94321.1; -;  
DR InterPro; IPR000883; -;  
DR Pfam; PF00115; COX1; 1.  
DR PROSITE; PS00077; COX1; 1.  
KW Copper; Heme; Oxidoreductase; Respiratory chain; Transmembrane.  
SQ SEQUENCE 539 AA; 60883 MW; 886DC41633BF8307 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 539;  
Best Local Similarity 42.9%; Pred. No. 74;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWXYVCHI 8  
:|:|:

Db 398 EWTIGHV 404  
PRELIMINARY; PRT; 540 AA.  
ID O06656  
AC O06656;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE CB3-TYPE CYTOCHROME OXIDASE COMPONENT FIXN (EC 1.9.3.1).  
OS Rhizobium leguminosarum.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=384;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=UPM791;  
RA Gutierrez D., Hernando Y., Palacios J., Imperial J., Ruiz-Argueso T.  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
CC -|- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4  
FERROCYTOCHROME C.  
CC -|- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).  
CC -|- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
DR EMBL; U90521; AAB58264.1; -;  
DR InterPro; IPR000883; -;  
DR Pfam; PF00115; COX1; 1.  
DR PROSITE; PS00077; COX1; 1.  
KW Copper; Heme; Oxidoreductase; Respiratory chain; Transmembrane.  
SQ SEQUENCE 540 AA; 61003 MW; 0BF0CA019C798BD2 CRC64; ?

Query Match 82.5%; Score 33; DB 2; Length 540;  
Best Local Similarity 42.9%; Pred. No. 74;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 2 QMXVGH1 8
Db 399 EWTIGHV 405

RESULT 12
ID P72288 PRELIMINARY; PRT; 540 AA.
AC P72288;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FIXND (EC 1.9.3.1).
GN FIXND.
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=384;
RN [1]
SEQUENCE FROM N.A.
STRAIN=VF39;
MEDLINE=97348582; PubMed=9204566;
RA Schluter A., Patschkowski T., Quandt J., Selinger L.B., Weidner S.,
RA Kramer M., Zhou L., Hynes M., Pfeifer U.;
RT "Functional and regulatory analysis of the two copies of the fixNOOP
operon of Rhizobium leguminosarum strain VF39.";
RL Mol. Plant Microbe Interact. 10:605-616(1997).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC -!- FERROCYTOCHROME C.
CC -!- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; Z80339; CAB02448.1; -.
DR InterPro; IPR000983; -.
DR Pfam; PF00115; COX1; 1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Oxidoreductase; Respiratory chain; Transmembrane.
SQ SEQUENCE 540 AA; 60969 MW; 7F287AC24B83F99C CRC64;

Query Match 82.5%; Score 33; DB 2; Length 540;
Best Local Similarity 42.9%; Pred. No. 74;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QMXVGH1 8
Db 399 EWTIGHV 405

RESULT 13
ID Q9FDG4 PRELIMINARY; PRT; 540 AA.
AC Q9FDG4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FIXNF.
GN FIXNF.
OS Rhizobium etli.
OG Plasmid pCFN42f.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
SEQUENCE FROM N.A.
STRAIN=CFN42;
RA Girard L., Brom S., Davalos A., Lopez O., Soberon M., Romero D.;
RT "Differential regulation of fixN reiterated genes in Rhizobium etli by
a novel fixL-fixK cascade.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF273679; AAG00947.1; -.
SQ SEQUENCE 276 AA; 30601 MW; 917222EFC544A385 CRC64;
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KW Plasmid.
SQ SEQUENCE 540 AA; 60778 MW; 1B6984488887CFBE CRC64;

Query Match 82.5%; Score 33; DB 2; Length 540;
Best Local Similarity 42.9%; Pred. No. 74;
Matches 3; Conservative 3; Mismatches 1; Indels 0;

QY 2 QMXVGH1 8
Db 399 EWTIGHV 405

RESULT 14
ID Q9V5C9 PRELIMINARY; PRT; 276 AA.
AC Q9V5C9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG1675 PROTEIN.
GN CG1675.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer J.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen L.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003831; AAF58883.1; -.
DR FlyBase; FBgn0033457; CG1675.
DR InterPro; IPR001601; -.
SQ SEQUENCE 276 AA; 30601 MW; 917222EFC544A385 CRC64;
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Search completed: October 25, 2001, 11:27:44  
Job time: 447 sec

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Query Match      80.0%; Score 32; DB 5; Length 276;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGVGH 8
   |||
Db 182 QWVGLHL 188

RESULT 15
Q9Z7L5 PRELIMINARY; PRT; 406 AA.
AC Q9Z7L5;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
NIFS-RELATED AMINOTRANSFERASE.
YFHO_1 OR CP0057.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
[1]
SEQUENCE FROM N.A.
STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
[2]
SEQUENCE FROM N.A.
STRAIN=J138;
MEDLINE=20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
[3]
SEQUENCE FROM N.A.
STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Unayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J.,
McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL: AE001651; AAD18828.1; -
EMBL: AP002547; BRA98896.1; -
EMBL: AE002169; AAF73623.1; -
TIGR: CP0057; -
InterPro: IPR000192; -
Pfam: PF00266; aminotran_5; 1.
PROSITE: PS00595; AA_TRANSFER_CLASS_5; UNKNOWN_1.
Transferase; Aminotransferase.
SQ SEQUENCE 406 AA; 44600 MW; 2180F627878A0F96 CRC64;

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Query Match      80.0%; Score 32; DB 2; Length 406;
Best Local Similarity 57.1%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGVGH 8
   |||
Db 370 RNVGVHV 376

```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:28:29 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-6  
Perfect score: 40  
Sequence: 1 QWXXVGH 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	90.0	14	1	ALYT_ALYOB
2	36	90.0	107	1	BOMB_BOMVA
3	36	90.0	119	1	BOMB_BOMOR
4	35	87.5	263	1	IML2_DROME
5	34	85.0	9	1	LITO_LITAU
6	34	85.0	13	1	BOML_PSEGU
7	34	85.0	82	1	RANA_RANPI
8	34	85.0	232	1	YB9H_YEAST
9	33	82.5	120	1	NEUB_XENLA
10	33	82.5	308	1	LIVH_ECOLI
11	32	80.0	551	1	FIXN_AZOCA
12	31	77.5	10	1	GRP_RANRI
13	31	77.5	25	1	GRP_SCYCA
14	31	77.5	27	1	GRP_CANFA
15	31	77.5	27	1	GRP_CHICK
16	31	77.5	27	1	GRP_PIG
17	31	77.5	28	1	GRP_ALLMI
18	31	77.5	134	1	GRP_SHEEP
19	31	77.5	147	1	GRP_RAT
20	31	77.5	148	1	GRP_HUMAN
21	31	77.5	155	1	GRP_BOMOR
22	31	77.5	276	1	SACT_BACSU
23	31	77.5	366	1	YBAB_BACCI
24	31	77.5	391	1	HERP_HUMAN
25	31	77.5	532	1	COX1_RHOCA
26	31	77.5	539	1	FIXN_AGRTU
27	31	77.5	539	1	FIXN_RHIME
28	31	77.5	549	1	FIXN_BRAJA
29	31	77.5	1005	1	YCF1_OENBE
30	31	77.5	1122	1	EX5C_ECOLI
31	31	77.5	1738	1	YCF1_EPIVI
32	31	77.5	1786	1	YCF1_ARATH
33	31	77.5	1901	1	YCF1_TOBAC

34 30 75.0 11 1 RANC\_RANPI  
35 30 75.0 17 1 RANR\_RANRU  
36 30 75.0 195 1 VMT2\_INBAC  
37 30 75.0 195 1 VMT2\_INBAD  
38 30 75.0 195 1 VMT2\_INBLE  
39 30 75.0 195 1 VMT2\_INBST  
40 30 75.0 278 1 YGLI\_YEAST  
41 30 75.0 390 1 CBL\_MLVCN  
42 30 75.0 392 1 PO14\_NASVI  
43 30 75.0 474 1 CBL\_C\_HUMAN  
44 30 75.0 732 1 YAGR\_ECOLI  
45 30 75.0 896 1 CBL\_MOUSE

## ALIGNMENTS

RESULT 1

ALYT\_ALYOB  
ID ALYT\_ALYOB STANDARD; PRT; 14 AA.  
AC P08944;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE ALYTESIN.  
OS Alytes Obsteetricans (Midwife toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.  
OX NCBI\_TaxID=8443;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84131098; PubMed=6141890;  
RA Ersamer V., Ersamer G.F., Mazzanti G., Engdean R.;  
RT "Active peptides in the skins of one hundred amphibian species from  
RT Australia and Papua New Guinea";  
RL Comp. Biochem. Physiol. 77C:99-108(1984).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR InterPro; IPR000874; .  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT MOD\_RES 1 1  
FT MOD\_RES 14 14  
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 14;  
Best Local Similarity 71.4%; Pred. No. 0.19;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0.

QY 2 QWXXVGH 8  
DB 7 QWAVGHL 13

RESULT 2

BOMB\_BOMVA  
ID BOMB\_BOMVA STANDARD; PRT; 107 AA.  
AC P01296;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE BOMBESIN PRECURSOR.  
OS Bombina variegata (Yellow-bellied toad), and  
OS Bombina bombina (Fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8348, 8345;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.variegata; TISSUE=Skin;  
RX MEDLINE=90242964; PubMed=2335218;

RA Richter K., Egger R., Krell G.;  
RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
of Bombina variegata.";  
RL FEBS Lett. 262:353-355(1990).  
RN [2]  
RP SEQUENCE OF 42-55.  
RC SPECIES=B.variegata, and B.bombina;  
RX MEDLINE=72163516; PubMed=4537042;  
RA Anastasi A., Erspamer V., Buccì M.;  
RT "Isolation and amino acid sequences of altyesin and bombesin, two  
analogous active tetradecapeptides from the skin of European  
discoglossid frogs.";  
RT Arch. Biochem. Biophys. 148:443-446(1972).  
RL Arch. Biochem. Biophys. 148:443-446(1972).  
CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
GASTROINTESTINAL HORMONES.  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
FAMILY.  
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CC -----  
DR EMBL; X52447; CAA36686.1; -;  
DR PIR; A01564; BSTD.  
DR PIR; B01564; BSTDY.  
DR PIR; S09095; S09095.  
DR InterPro; IPR000874; -;  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT PEPTIDE 42 55 BOMBESIN.  
FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;  
Query Match 90.0%; Score 36; DB 1; Length 107;  
Best Local Similarity 71.4%; Pred. No. 1.3;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 2 QWVGVGHI 8  
|||  
48 QWVGVGHL 54  
RESULT 3  
ID BOMB\_BOMOR STANDARD; PRT; 119 AA.  
AC P21591;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE BOMBESIN PRECURSOR.  
OS Bombina orientalis (Oriental fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8346;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91088602; PubMed=2263631;  
RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;  
RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
relationship between bombesin and gastrin-releasing peptide.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
CC -!- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN  
THE SKIN AND THE BRAIN.  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
FAMILY.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M55255; AAA48551.1; -;  
DR PIR; A39261; A39261.  
DR InterPro; IPR000874; -;  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 2 BOMBESIN.  
FT PEPTIDE 45 58 BOMBESIN.  
FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2445A44A CRC64;  
Query Match 90.0%; Score 36; DB 1; Length 119;  
Best Local Similarity 71.4%; Pred. No. 1.4;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 2 QWVGVGHI 8  
|||  
51 QWVGVGHL 57  
RESULT 4  
ID IML2\_DROME STANDARD; PRT; 263 AA.  
AC Q09024;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2 PRECURSOR.  
GN IML2.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscidae; Muscidae; Muscidae;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON-S; TISSUE=Embryo;  
RX MEDLINE=94139565; PubMed=8306886;  
RA Garbe J.C., Yang E., Fristrom J.W.;  
RT "IMP-L2: an essential secreted immunoglobulin family member  
implicated in neural and ectodermal development in Drosophila";  
RL Development 119:1237-1250(1993).  
CC -!- FUNCTION: ESSENTIAL DEVELOPMENTAL ROLE DURING EMBRYOGENESIS, IN  
PARTICULAR THE NORMAL DEVELOPMENT OF THE NERVOUS SYSTEM. MAY BE  
INVOLVED IN SOME ASPECT OF CELL ADHESION.  
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
CC -!- TISSUE SPECIFICITY: DETECTED IN SEVERAL SITES INCLUDING THE  
VENTRAL NEUROECTODERM, THE TRACHEAL PITS, THE PHARYNX AND  
OESOPHAGUS, AND SPECIFIC NEURONAL CELL BODIES, WHERE IT IS  
PRIMARILY EXPRESSED.  
CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT THE CELLULAR BLASTODERM  
STAGE AND CONTINUES TO BE EXPRESSED THROUGH SUBSEQUENT  
DEVELOPMENT.  
CC -!- INDUCTION: BY 20-HYDROXYECYDSONE.  
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -----  
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DR EMBL; L23066; AAB59251.1; -;  
 DR HSSP; P56276; ITLK.  
 DR FlyBase; FBgn0001257; Impl2.  
 DR InterPro; IPR003006; -;  
 DR Pfam; PF00047; ig; 2;  
 KW Immunoglobulin domain; Cell adhesion; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 263  
 FT DOMAIN 69 142  
 FT DOMAIN 184 247  
 FT DISULFID 76 135  
 FT DISULFID 191 240  
 FT VARIANT 173 173  
 SEQUENCE 263 AA; 29421 MW; 44AADB1B22DD1804 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 263;  
 Best Local Similarity 71.4%; Pred. No. 4.6;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHI 8  
 || |||  
 Db 87 QWVVGHL 93

RESULT 5  
 LITO\_LITAU STANDARD; PRT; 9 AA.  
 AC P08945;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LITORIN.  
 OS Litoria aurea (Australian frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 CC Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE.  
 MEDLINE=75187011; PubMed=1140241;  
 Anastasi A., Erspamer V., Endean R.;  
 "Aminoacid composition and sequence of litorin, a bombesin-like  
 nonapeptide from the skin of the Australian leptodactylid frog  
 Litoria aurea."  
 RT Litoria aurea.  
 RL Experientia 31:510-511(1975).  
 RN [2]  
 RP SEQUENCE (METHYLATED VARIANT).  
 RX MEDLINE=78003546; PubMed=908397;  
 RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;  
 "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in  
 RT methanol extracts of the skin of the Australian frog Litoria aurea."  
 RL Experientia 33:1289-1289(1977).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR; S07204; S07204.  
 DR PIR; S07205; S07205.  
 DR InterPro; IPR0000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN;  
 KW Bombesin family; Amidation; Methylation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 2 2  
 FT MOD\_RES 9 9  
 SEQUENCE 9 AA; 1103 MW; D7CCC1E8G2CDC366 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+04;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0.

QY 2 QWVVGHI 7  
 || |||  
 Db 2 QWAVGH 7

RESULT 6  
 BOML\_PSEGU STANDARD; PRT; 13 AA.  
 ID AC P42991;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE BOMBESIN-LIKE PEPTIDE L (PG-L).  
 OS Pseudophryne guentheri (Frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 CC Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 TISSUE=Skin;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 "Six novel tachykinin- and bombesin-related  
 RT peptides from the Australian frog Pseudophryne guntheri."  
 RL Peptides 11:299-304(1990).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR; A60409; A60409.  
 DR InterPro; IPR0000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN;  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 13 13  
 FT MOD\_RES 13 13  
 SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 13;  
 Best Local Similarity 83.3%; Pred. No. 0.45;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVVGHI 7  
 || |||  
 Db 6 QWAVGH 11

RESULT 7  
 RANA\_RANPI STANDARD; PRT; 82 AA.  
 ID AC P08550;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE RANATENSIN PRECURSOR.  
 OS Rana pipiens (Northern leopard frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88330837; PubMed=2458345;  
 RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel  
 RT "Molecular cloning of cDNAs encoding the human bombesin-11  
 RT neuromedin B. Chromosomal localization and comparison to clon-  
 RT encoding its amphibian homolog ranatensin.";

```
RL J. Biol. Chem. 263:13317-13323(1988).
RN [2]
RP SEQUENCE OF 48-58.
RA Nakajima T., Tanimura T., Pisano J.J.;
RT "Isolation and structure of a new vasoactive polypeptide.";
RL Fed. Proc. 29:282-282(1970).
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M21552; AAA49533.1; -.
DR PIR; B28945; B28945.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
DR Bombesin family; Amidation; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL. 1 27 POTENTIAL.
FT PROPEP 28 47
FT PEPTIDE 48 58
FT MOD_RES 58 58
FT SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 85.0%; Score 34; DB 1; Length 82;
Best Local Similarity 83.3%; Pred. No. 2.5;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 7
DB 51 QWAVGH 56

RESULT 8
YB9H_YEAST
ID YB9H_YEAST STANDARD; PRT; 232 AA.
AC P38340;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT HYPOTHEICAL 26.1 KDA PROTEIN IN POP4-SH1 INTERGENIC REGION.
DT YBR261C OR YBR1729.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93220397; PubMed=8465606;
RA Doignon F., Biteau N., Crouzet M., Aigle M.;
RT "The complete sequence of a 19,482 bp segment located on the right
RL arm of chromosome II from Saccharomyces cerevisiae.";
RL Yeast 9:189-199(1993).
CC -1- SIMILARITY: TO S.POMBE SPAC16E8.14C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70529; CAA49926.1; -.
DR EMBL; Z36130; CAA85224.1; -.

J. Biol. Chem. 263:13317-13323(1988).
RN [2]
RP SEQUENCE OF 48-58.
RA Nakajima T., Tanimura T., Pisano J.J.;
RT "Isolation and structure of a new vasoactive polypeptide.";
RL Fed. Proc. 29:282-282(1970).
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; M21552; AAA49533.1; -.
DR PIR; B28945; B28945.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
DR Bombesin family; Amidation; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL. 1 27 POTENTIAL.
FT PROPEP 28 47
FT PEPTIDE 48 58
FT MOD_RES 58 58
FT SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 85.0%; Score 34; DB 1; Length 82;
Best Local Similarity 83.3%; Pred. No. 2.5;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 7
DB 51 QWAVGH 56

RESULT 8
YB9H_YEAST
ID YB9H_YEAST STANDARD; PRT; 232 AA.
AC P38340;
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT HYPOTHEICAL 26.1 KDA PROTEIN IN POP4-SH1 INTERGENIC REGION.
DT YBR261C OR YBR1729.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93220397; PubMed=8465606;
RA Doignon F., Biteau N., Crouzet M., Aigle M.;
RT "The complete sequence of a 19,482 bp segment located on the right
RL arm of chromosome II from Saccharomyces cerevisiae.";
RL Yeast 9:189-199(1993).
CC -1- SIMILARITY: TO S.POMBE SPAC16E8.14C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70529; CAA49926.1; -.
DR EMBL; Z36130; CAA85224.1; -.

J. Biol. Chem. 263:13317-13323(1988).
RN [2]
RP SEQUENCE OF 48-58.
RA Nakajima T., Tanimura T., Pisano J.J.;
RT "Isolation and structure of a new vasoactive polypeptide.";
RL Fed. Proc. 29:282-282(1970).
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; M21552; AAA49533.1; -.
DR PIR; B28945; B28945.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
DR Bombesin family; Amidation; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL. 1 27 POTENTIAL.
FT PROPEP 28 47
FT PEPTIDE 48 58
FT MOD_RES 58 58
FT SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 85.0%; Score 34; DB 1; Length 232;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 8
DB 139 QWCVGHL 145

RESULT 9
NEUB_XENLA
ID NEUB_XENLA STANDARD; PRT; 120 AA.
AC P43443;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEUROMEDIN B PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93028554; PubMed=1409705;
RA Wechselberger C., Kreil G., Richter K.;
RT "Isolation and sequence of a cDNA encoding the precursor of a
RT bombesin-like peptide from brain and early embryos of Xenopus
RT laevis.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9819-9822(1992).
CC -1- FUNCTION: MAY BE A GROWTH FACTOR REQUIRED FOR THE HIGH RATE OF
CC CELL DIVISION ENSUING AFTER FERTILIZATION, OR MAY HAVE A ROLE AS A
CC SECRETAGOGUE THAT TRIGGERS THE RELEASE OF STORED COMPONENTS.
CC -1- TISSUE SPECIFICITY: BRAIN, INTESTINE, AND OVARIES AND EARLY
CC EMBRYOS (STAGES 2 AND 10).
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; L01530; AAA49912.1; -.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
DR Bombesin family; Amidation; Cleavage on pair of basic residues;
KW Signal. 1 29 POTENTIAL.
FT SIGNAL. 30 44
FT PROPEP 45 54
FT PEPTIDE 54 54
FT MOD_RES 54 54
FT SEQUENCE 120 AA; 14384 MW; 2CB146BA082A2442 CRC64;
SQ SEQUENCE 120 AA; 14384 MW; 2CB146BA082A2442 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 120;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 7
DB 47 QWAIGH 52
```

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RESULT 10
LIVH_ECOLI STANDARD; PRT; 308 AA.
AC P08340;
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM PERMEASE
GN PROTEIN LIVH (LIV-I PROTEIN H).
LN LIVH.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86193847; PubMed=3009409;
RA Nazos P.M., Antonucci T.K., Landick R., Oxender D.L.;
DE "Cloning and characterization of livH, the structural gene encoding a
component of the leucine transport system in Escherichia coli.";
J. Bacteriol. 166:565-573(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90307651; PubMed=2195019;
RA Adams M.D., Wagner L.M., Graddis T.J., Landick R., Antonucci T.K.,
Gibson A.L., Oxender D.L.;
DE "Nucleotide sequence and genetic characterization reveal six
essential genes for the LIV-I and LS transport systems of Escherichia
coli.";
J. Biol. Chem. 265:11436-11443(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
DE "Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
BRANCHED-CHAIN AMINO ACIDS. PROBABLY RESPONSIBLE FOR THE
TRANSLLOCATION OF THE SUBSTRATES ACROSS THE MEMBRANE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
CC -!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE LIVHM
SUBFAMILY.
CC -----
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CC -----
DR EMBL; J05519; AAA83884.1; -.
DR EMBL; U00039; AAB18432.1; -.
DR EMBL; AE000421; AAC76482.1; -.
DR PIR; A24548; QRECLH.
DR PIR; D37074; D37074.
DR EcoGene; EG10538; livH.
DR InterPro; IPR000515; -.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; FALSE_NEG.
KW Transport; Amino-acid transport; Transmembrane; Inner membrane.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 155 175 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
FT TRANSMEM 246 266 POTENTIAL.
FT TRANSMEM 281 301 POTENTIAL.

FT CONFLICT 253 253 G -> S (IN REF. 3).
FT CONFLICT 288 288 P -> L (IN REF. 3).
SQ SEQUENCE 308 AA; 32936 MW; C88A5FC17319E4A5 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 308
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 6; Gaps 0.

QY 2 QWVGVGH 7
| | | | |
DB 140 QWVGVGH 145

RESULT 11
FIXN_AZOCA STANDARD; PRT; 551 AA.
AC P98056;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I HOMOLOG (EC 1.9.3.1).
GN FIXN.
OS Azorhizobium caulinodans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae;
OC Hyphomicrobium group; Azorhizobium.
OX NCBI_TaxID=7;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ORS571;
RX MEDLINE=94109675; PubMed=8282187;
RA Mandon K., Kaminski P.A., Mougel C., Desnoues N., Elmerich C.,
RT "Role of the fixGHI region of Azorhizobium caulinodans in free living
and symbiotic nitrogen fixation.";
FEMS Microbiol. Lett. 114:185-189(1993).
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C OR A QUINOL ARE TRANSFERRED TO THE BIMETALLIC CENTRE
FORMED BY A HIGH-SPIN HEME AND COPPER B.
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
4 FERRICYTOCHROME C.
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 13 OR 14
POTENTIAL TRANSMEMBRANE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; X74410; CAA52429.1; -.
DR InterPro; IPR000883; -.
DR Pfam; PF00115; COX1; 1.
DR PROSITE; PS00077; COX1; 1.
KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain.
FT METAL 132 132
FT METAL 281 281 COPPER B (BY SIMILARITY).
FT METAL 331 331 COPPER B (BY SIMILARITY).
FT METAL 332 332 COPPER B (BY SIMILARITY).
FT METAL 419 419 IRON (HIGH-SPIN HEME) (BY SIMILARITY).
FT METAL 421 421 IRON (LOW-SPIN HEME) (BY SIMILARITY).
SQ SEQUENCE 551 AA; 61843 MW; 0466F71CD04BFC4D CRC64;

Query Match 80.0%; Score 32; DB 1; Length 551
Best Local Similarity 42.9%; Pred. No. 36;
Matches 3; Conservative 3; Mismatches 1; Indels 6; Gaps 0;
```

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QY 2 QWYVCHI 8
   1 :||:
Db 414 EWGIGHV 420

RESULT 12
GRP_RANRI
ID GRP_RANRI STANDARD; PRT; 10 AA.
AC P23260;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE NEUROMEDIN C.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8406;
   1:]
SEQUENCE.
TX MEDLINE=91315477; PubMed=1859413;
RA Conlon J.M., O'Harte F., Vaudry H.;
RT "Primary structures of the bombesin-like neuropeptides in frog brain
RL Biochem. Biophys. Res. Commun. 178:526-530(1991).
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
   FAMILY.
DR PIR; P00177; P00177.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVCHI 8
   1 :||:
Db 4 WAVGHL 9

RESULT 13
GRP_SCYCA
ID GRP_SCYCA STANDARD; PRT; 25 AA.
AC P09472;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE GASTRIN-RELEASING PEPTIDE (GRP).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
   1:]
SEQUENCE.
RX MEDLINE=88137922; PubMed=3436516;
RA Conlon J.M., Henderson I.W., Thim L.;
RT "Gastrin-releasing peptide from the intestine of the elasmobranch
RT fish, Scyllorhinus canicula (common dogfish).";
RL Gen. Comp. Endocrinol. 68:415-420(1987).
CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER
   GASTROINTESTINAL HORMONES.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
   FAMILY.
DR PIR; S06263; S06263.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 25 25
SQ SEQUENCE 25 AA; 2781 MW; B735F911B89007F8 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVCHI 8
   1 :||:
Db 19 WAVGHL 24

RESULT 14
GRP_CANFA
ID GRP_CANFA STANDARD; PRT; 27 AA.
AC P08989;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP-10),].
GN GRP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
   1:]
SEQUENCE.
RX MEDLINE=83213518; PubMed=6853532;
RA Reeve J.R. Jr., Walsh J.H., Chew P., Clark B., Hawke D.,
RA Shively J.E.;
RT "Amino acid sequences of three bombesin-like peptides from canine
RT intestine extracts."
RL J. Biol. Chem. 258:5582-5588(1983).
CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER
   GASTROINTESTINAL HORMONES.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
   FAMILY.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT PEPTIDE 18 27
FT MOD_RES 27 27
SQ SEQUENCE 27 AA; 2889 MW; 9D9317261B7C7D65 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 27;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WYVCHI 8
   1 :||:
Db 21 WAVGHL 26

RESULT 15
GRP_CHICK
ID GRP_CHICK STANDARD; PRT; 27 AA.
AC P01295;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GASTRIN-RELEASING PEPTIDE (GRP) (PROVENTRICULAR PEPTIDE) [CONTAINS:
   NEUROMEDIN C (GRP-10)].
GN GRP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

```

RN [1]  
 RP MEDLINE=81164953; PubMed=7215543;  
 RX McDonald T.J., Joernvall H., Ghatei M., Bloom S.R., Mutt V.;  
 RA "Characterization of an avian gastric (proventricular) peptide having  
 RT sequence homology with the porcine gastrin-releasing peptide and the  
 RT amphibian peptides bombesin and alcyonin.";  
 RL FEBS Lett. 122:45-48(1980).  
 RN [2]  
 RP MEDLINE=90122926; PubMed=2297533;  
 RX Campbell B.J., Young J., Dimoline R., Dockray G.J.;  
 RA "Isolation, sequence and biosynthetic significance of a novel  
 RT fragment of gastrin-releasing peptide from chicken proventriculus.";  
 RL Biochim. Biophys. Acta 1048:66-71(1990).  
 CC !- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC !- GASTROINTESTINAL HORMONES.  
 CC !- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR; A01563; RHCHA.  
 DR PIR; S08150; S08150.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT PEPTIDE 18 27  
 FT MOD\_RES 27 27  
 FT AMIDATION.  
 SQ SEQUENCE 27 AA; 2842 MW; 3C121D0118D551C7 CRC64;

Query Match 77.5%; Score 31; DB 1; Length 27;  
 Best Local Similarity 66.7%; Pred. No. 3.5;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WYVGH 8  
 DB 21 WAYGHL 26

Search completed: October 25, 2001, 11:28:29  
 Job time: 477 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:21 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-6  
Perfect score: 40  
Sequence: 1 QWXXVGH 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.68:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	90.0	14	1 BSTDY	bombesin - fire-be
2	36	90.0	107	1 BSTDY	bombesin precursor
3	36	90.0	119	2 A39261	bombesin precursor
4	34	85.0	9	2 S07204	litorin I - Austr
5	34	85.0	13	2 A60409	bombesin-like pept
6	34	85.0	82	2 B28945	ranatensin precurs
7	34	85.0	232	2 S32963	hypothetical prote
8	34	85.0	256	2 T48787	hypothetical prote
9	33	82.5	120	2 A47201	bombesinlike pepti
10	33	82.5	308	1 QRECLH	leucine transport
11	33	82.5	308	2 H86012	hypothetical prote
12	32	80.0	406	2 F86576	Nifs-related amino
13	32	80.0	406	2 G72047	nifs-related amino
14	32	80.0	551	1 A55582	cytochrome-c oxida
15	32	80.0	920	2 C96831	hypothetical prote
16	32	80.0	1006	2 T00050	hypothetical prote
17	32	80.0	1147	2 T42627	ADP-ribosylation f
18	31	77.5	9	2 S07205	litorin 2-Glu - Au
19	31	77.5	10	2 P00177	neuromedin C - lau
20	31	77.5	10	2 A60647	neuromedin C - bov
21	31	77.5	25	2 S06263	gastrin-releasing
22	31	77.5	27	1 RHPGA	gastrin-releasing
23	31	77.5	27	1 RHCHA	gastrin-releasing
24	31	77.5	27	1 RHCHA	gastrin-releasing
25	31	77.5	91	2 T19436	hypothetical prote
26	31	77.5	134	2 I47010	gastrin-releasing
27	31	77.5	138	2 A26182	gastrin-releasing
28	31	77.5	147	2 A40922	gastrin-releasing
29	31	77.5	148	1 B26182	gastrin-releasing

30	31	77.5	155	2 A42437	gastrin-releasing
31	31	77.5	276	2 S39702	transc. ion chan
32	31	77.5	279	2 S75087	hypothetical prote
33	31	77.5	350	2 A05212	hypothetical prote
34	31	77.5	372	2 G83074	glutamate 5-kinase
35	31	77.5	375	2 E85035	hypothetical prote
36	31	77.5	423	2 A41204	carboxypeptidase B
37	31	77.5	475	2 D83128	cytochrome-c oxida
38	31	77.5	475	2 C83452	cytochrome-c oxida
39	31	77.5	475	2 E83450	cytochrome-c oxida
40	31	77.5	477	2 F82200	cytochrome-c oxida
41	31	77.5	480	2 G83414	cytochrome-c oxida
42	31	77.5	484	2 G72395	alpha-L glutaminol
43	31	77.5	532	1 S49345	cytochrome-c oxida
44	31	77.5	539	1 S39988	cytochrome-c oxida
45	31	77.5	539	1 S49495	cytochrome-c oxida

## ALIGNMENTS

RESULT 1  
BSTDY  
bombesin - fire-bellied toad  
C:Species: Bombina bombina (fire-bellied toad)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 21 Jul-1998  
C:Accession: A01564  
R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of altytesin and bombesin to  
A:Reference number: A01564; MUID:72163516  
A:Accession: A01564  
A:Molecule type: protein  
A:Residues: 1-14 <ANA>  
C:Superfamily: gastrin-releasing peptide  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neu; pid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experiment  
F:14/Modified site: amidated carboxyl end (Met) #status experimen

Query Match 90.0%; Score 36; DB 1; Length 14;  
Best Local Similarity 71.4%; Pred. No. 0.27;  
Matches 5; Conservative 1; Mismatches 1; Indels

Qy 2 QWXXVGH 8  
|||  
Db 7 QNAVGH 13

RESULT 2  
BSTDY  
bombesin precursor - yellow-bellied toad  
C:Species: Bombina variegata (yellow-bellied toad)  
C:Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S09095; B01564; A01564  
R:Richter, K.; Egger, R.; Kreil, G.  
FEBS Lett. 262, 353-355, 1990  
A:Title: Molecular cloning of a cDNA encoding the bombesin pr in skin  
A:Reference number: S09095; MUID:90242964  
A:Accession: S09095  
A:Molecule type: mRNA  
A:Residues: 1-107 <RIC>  
R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of altytesin and bomba  
A:Reference number: A01564; MUID:72163516  
A:Accession: B01564  
A:Molecule type: protein  
A:Residues: 42-55 <ANA>  
C:Superfamily: ranatensin  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neu.  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-41/Domain: amino-terminal propeptide #status predicted <PK>

F;42-55/Product: bombesin #status experimental <MAT>  
F;56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
F;42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
F;55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 90.0%; Score 36; DB 1; Length 107;  
Best Local Similarity 71.4%; Pred. No. 2.1;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 8  
|| |||  
Db 48 QWAVGHL 54

## RESULT 3

A39261  
bombesin precursor - Bombina orientalis

C;Species: Bombina orientalis  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999

A;Accession: A39261

R;Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990

A;Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet

A;Reference number: A39261; MUID:91088602

A;Accession: A39261

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-119 <SPI>

A;Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017

C;Superfamily: ranatensin

C;Keywords: neuropeptide

Query Match 90.0%; Score 36; DB 2; Length 119;  
Best Local Similarity 71.4%; Pred. No. 2.3;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 8  
|| |||  
Db 51 QWAVGHL 57

## RESULT 4

S07204  
litorin I - Australian tree frog (Litoria aurea)

C;Species: Litoria aurea

C;Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000

A;Accession: S07204

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 510-511, 1975

A;Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide from

A;Reference number: S07204; MUID:75187011

A;Accession: S07204

A;Molecule type: protein

A;Residues: 1-9 <ANA>

C;Superfamily: gastrin-releasing peptide

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 85.0%; Score 34; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 7  
|| |||  
Db 2 QWAVGH 7

## RESULT 5

A60409

bombesin-like peptide L - frog (Pseudophryne guentheri)  
C;Species: Pseudophryne guentheri  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
C;Accession: A60409  
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, P.  
Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of t  
A;Reference number: A60409; MUID:90287814

A;Accession: A60409

A;Molecule type: protein

A;Residues: 1-13 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 85.0%; Score 34; DB 2; Length 13;  
Best Local Similarity 83.3%; Pred. No. 0.63;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 7  
|| |||  
Db 6 QWAVGH 11

## RESULT 6

B28945  
ranatensin precursor - northern leopard frog

C;Species: Rana pipiens (northern leopard frog)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999

C;Accession: B28945

R;Krahe, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.

J. Biol. Chem. 263, 13317-13323, 1988

A;Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide in

A;Reference number: A92667; MUID:88330837

A;Accession: B28945

A;Molecule type: mRNA

A;Residues: 1-82 <KRA>

A;Cross-references: GB:M21552; GB:J03948; NID:g213693; PIDN:AAA49533.1; PID:g213

C;Superfamily: ranatensin

C;Keywords: neuropeptide

Query Match 85.0%; Score 34; DB 2; Length 82;  
Best Local Similarity 83.3%; Pred. No. 4;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXYVGH 7  
|| |||  
Db 51 QWAVGH 56

## RESULT 7

S32963

hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)

N;Alternate names: Hypothetical protein YBR1729

C;Species: Saccharomyces cerevisiae

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000

C;Accession: S32963; S46142

R;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.

Yeast 9, 189-199, 1993

A;Title: The complete sequence of a 19,482 bp segment located on the 100 kb arm

A;Reference number: S29348; MUID:93220397

A;Accession: S32963

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-232 <DOI>

A;Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; PID:g1907246

R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.

submitted to the Protein Sequence Database, August 1994

A;Reference number: S45940

A;Accession: S46142

A:Molecule type: DNA  
A:Residues: 1-232 <AIG>  
A:Cross-references: EMBL:Z36130; NID:g536688; PIDN:CAA85224.1; PID:g536689; MIPS:YBR261  
C:Genetics:  
A:Map position: 2R  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 85.0%; Score 34; DB 2; Length 232;  
Best Local Similarity 71.4%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWYVGHI 8  
|| |||:  
Db 139 QWCVGHL 145

RESULT 8  
T48787  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350 [Imported] - Neurospora crassa  
Species: Neurospora crassa  
Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 28-Jul-2000  
C:Accession: T48787  
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24541  
A:Accession: T48787  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-256 <SCH>  
A:Cross-references: EMBL:AI353820; GSPDB:GN00112; NCSP:13E11.350  
A:Experimental source: cosmid contig 13E11; strain 74  
C:Genetics:  
A:Gene: NCSP:13E11.350  
A:Map position: 2  
A:Introns: 213/2  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 85.0%; Score 34; DB 2; Length 256;  
Best Local Similarity 71.4%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWYVGHI 8  
|| |||:  
Db 162 QWCVGHL 168

RESULT 9  
7201  
C:Superfamily: Bombesinlike peptide - African clawed frog  
C:Species: xenopus laevis (African clawed frog)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998  
C:Accession: A47201  
R:Wechselberger, C.; Kreil, G.; Richter, K.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9819-9822, 1992  
A:Title: Isolation and sequence of a cDNA encoding the precursor of a bombesinlike peptide  
A:Reference number: A47201; MUID:93028554  
A:Accession: A47201  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-120 <NEC>  
A>Note: sequence inconsistent with the nucleotide translation  
A>Note: sequence extracted from NCBI backbone (NCBIN:115857, NCBIIP:115858)  
C:Superfamily: ranatensis

Query Match 82.5%; Score 33; DB 2; Length 120;  
Best Local Similarity 66.7%; Pred. No. 9.5;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWYVGHI 7  
|| |||:

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-308 <STO>  
 A:Cross-references: GB:AE005174; NID:g12518111; PIDN:AAG58564.1; GSPDB:GN00145; UMGp:248  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: livH  
 C:Superfamily: leucine transport protein livH

Query Match 82.5%; Score 33; DB 2; Length 308;  
 Best Local Similarity 83.3%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHI 7  
 : : : : :  
 Db 140 QWVVGHI 145

RESULT 12  
 576  
 Nifs-related aminotransferase [imported] - Chlamydia pneumoniae (strain J138)  
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
 C:Accession: F86576  
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
 A:Reference number: A86491; MUID:20330349  
 A:Accession: F86576  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-406 <STO>  
 A:Cross-references: GB:BA000008; NID:g8979061; PIDN:BAA98896.1; GSPDB:GN00142  
 A:Experimental source: strain J138  
 C:Genetics:  
 A:Gene: yfho\_1  
 C:Superfamily: nifs protein

Query Match 80.0%; Score 32; DB 2; Length 406;  
 Best Local Similarity 57.1%; Pred. No. 52;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHI 8  
 : : : : :  
 Db 370 RWNVGHI 376

RESULT 13  
 G72047  
 nifs-related aminotransferase - Chlamydia pneumoniae (strain CWL029)  
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 05-May-2000  
 C:Accession: G72047  
 R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
 Nature Genet. 21, 385-389, 1999  
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
 A:Reference number: A72000; MUID:99206606  
 A:Accession: G72047  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-406 <ARN>  
 A:Cross-references: GB:AE001651; GB:AE001363; NID:g4376985; PIDN:AAD18828.1; PID:g437699  
 A:Experimental source: strain CWL029  
 C:Genetics:  
 A:Gene: yfho\_1  
 C:Superfamily: nifs protein

Query Match 80.0%; Score 32; DB 2; Length 406;  
 Best Local Similarity 57.1%; Pred. No. 52;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHI 8  
 : : : : :  
 Db 370 RWNVGHI 376

RESULT 14  
 A55582  
 cytochrome-c oxidase (EC 1.9.3.1) fixN chain - Azorhizobium caulinodans  
 N:Alternate names: cb-type cytochrome-c oxidase 45K chain, cytochrome b410, fixN  
 C:Species: Azorhizobium caulinodans  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A55582; S42229  
 R:Mandon, K.; Kaminski, P.A.; Elmerich, C.  
 J. Bacteriol. 176, 2560-2568, 1994  
 A:Title: Functional analysis of the fixNOQP region of Azorhizobium caulinodans  
 A:Reference number: A55582; MUID:94222833  
 A:Accession: A55582  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-551 <MAN1>  
 A:Cross-references: GB:X74410; NID:g456310; PIDN:CAA52429.1; PID:g456411  
 R:Mandon, K.; Kaminski, P.A.; Mougel, C.; Desnoues, N.; Dreyfus R. 1m  
 FEMS Microbiol. Lett. 114, 185-190, 1993  
 A:Title: Role of the fixGHI region of Azorhizobium caulinodans in living an  
 A:Reference number: S42229; MUID:94109675  
 A:Accession: S42229  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-551 <MAN2>  
 A:Cross-references: EMBL:X74410; NID:g456310; PIDN:CAA52429.1; PID:g456411  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 199  
 C:Superfamily: Rhizobium cytochrome-c oxidase fixN chain; cytochrome-c oxidase  
 C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; mem  
 F:73-502/Domain: cytochrome-c oxidase chain 1 homology <COI>  
 F:132,421/Binding site: heme iron (His) (axial ligands) #status predicted  
 F:281,331/Binding site: copper (His) #status predicted  
 F:419/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 80.0%; Score 32; DB 1; Length 551;  
 Best Local Similarity 42.9%; Pred. No. 70;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHI 8  
 : : : : :  
 Db 414 EWGIGHV 420

RESULT 15  
 C96831  
 hypothetical protein F18B13.7 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 2; Mar-2001  
 C:Accession: C96831  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Crilly, T.H.; Dewar,  
 Ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.; Sun, H.; Tallo  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: C96831  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-920 <STO>  
 A:Cross-references: GB:AE005173; NID:g5902363; PIDN:AAD55465.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F18B13.7

A:Map position: 1  
C:Superfamily: coatomer complex beta' chain; WD repeat homology

Query Match 80.0%; Score 32; DB 2; Length 920;  
Best Local Similarity 66.7%; Pred No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXXVGH 8  
I : I I I  
Db 275 WAIGHI 280

Search completed: October 25, 2001, 11:25:21  
Job time: 334 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-6  
Perfect score: 40  
Sequence: 1 XQXVGH 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
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5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	8	1	US-08-168-390-11
2	36	90.0	8	2	US-08-337-127-9
3	36	90.0	8	6	5217955-32
4	36	90.0	8	6	5217955-34
5	36	90.0	9	1	US-07-619-747B-1
6	36	90.0	9	1	US-07-619-747B-2
7	36	90.0	9	1	US-07-619-747B-4
8	36	90.0	9	1	US-07-619-747B-5
9	36	90.0	9	1	US-07-619-747B-9
10	36	90.0	9	1	US-07-619-747B-10
11	36	90.0	9	1	US-07-619-747B-12
12	36	90.0	9	1	US-07-619-747B-14
13	36	90.0	9	1	US-07-619-747B-15
14	36	90.0	9	1	US-07-619-747B-17
15	36	90.0	9	1	US-07-619-747B-18
16	36	90.0	9	1	US-07-619-747B-21
17	36	90.0	9	1	US-07-619-747B-23
18	36	90.0	9	1	US-07-619-747B-24
19	36	90.0	9	1	US-07-619-747B-25
20	36	90.0	9	1	US-07-619-747B-26
21	36	90.0	9	1	US-07-619-747B-27
22	36	90.0	9	1	US-07-619-747B-28
23	36	90.0	9	1	US-07-619-747B-29
24	36	90.0	9	1	US-07-619-747B-30
25	36	90.0	9	1	US-07-619-747B-31
26	36	90.0	9	1	US-07-619-747B-32
27	36	90.0	9	1	US-07-619-747B-33

28	36	90.0	9	1	US-07-619-747B-34	Sequence 34, Appl
29	36	90.0	9	1	US-07-619-747B-35	Sequence 35, Appl
30	36	90.0	9	1	US-07-619-747B-36	Sequence 36, Appl
31	36	90.0	9	1	US-07-619-747B-37	Sequence 37, Appl
32	36	90.0	9	1	US-07-619-747B-38	Sequence 38, Appl
33	36	90.0	9	1	US-07-619-747B-39	Sequence 39, Appl
34	36	90.0	9	1	US-07-619-747B-40	Sequence 40, Appl
35	36	90.0	9	1	US-08-031-325A-37	Sequence 37, Appl
36	36	90.0	9	1	US-08-263-905-4	Sequence 4, Appl
37	36	90.0	9	1	US-08-263-905-5	Sequence 5, Appl
38	36	90.0	9	1	US-08-263-905-6	Sequence 6, Appl
39	36	90.0	9	1	US-08-263-905-7	Sequence 7, Appl
40	36	90.0	9	1	US-08-263-905-10	Sequence 10, Appl
41	36	90.0	9	1	US-08-263-905-11	Sequence 11, Appl
42	36	90.0	9	1	US-07-919-731-3	Sequence 3, Appl
43	36	90.0	9	1	US-08-287-957-116	Sequence 116, Appl
44	36	90.0	9	1	US-08-240-711-6	Sequence 6, Appl
45	36	90.0	9	1	US-08-240-711-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-11

Query Match 90.0%; Score 36; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXGHI 8  
|||  
Db 2 QWAVGHL 8

RESULT 2

US-08-337-127-9  
Sequence 9, Application US/08337127  
Patent No. 5877277

GENERAL INFORMATION:

APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun H.  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
TITLE OF INVENTION: ANALOGS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,127  
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/779,039  
FILING DATE: 10/18/91  
APPLICATION NUMBER: 07/502,438  
FILING DATE: 03/30/90  
APPLICATION NUMBER: 07/397,169  
FILING DATE: 08/21/89  
APPLICATION NUMBER: 07/376,555  
FILING DATE: 07/07/89  
APPLICATION NUMBER: 07/317,941  
FILING DATE: 03/02/89  
APPLICATION NUMBER: 07/282,328  
FILING DATE: 12/09/88  
APPLICATION NUMBER: 07/257,998  
FILING DATE: 10/14/88  
APPLICATION NUMBER: 07/248,771  
FILING DATE: 09/23/88  
APPLICATION NUMBER: 07/207,759  
FILING DATE: 06/16/88  
APPLICATION NUMBER: 07/204,171  
FILING DATE: 06/08/88  
APPLICATION NUMBER: 07/173,311  
FILING DATE: 03/25/88  
APPLICATION NUMBER: 07/100,571  
FILING DATE: 09/24/87

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00537/00900D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The sequence contains at  
OTHER INFORMATION: position 1 a pyroglutamate, rather than  
OTHER INFORMATION: and has an methyl ester C-terminus (i.e.  
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e.  
US-08-337-127-9

Query Match 90.0%; Score 36; DB 2; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXGHI 8  
|||  
Db 2 QWAVGHL 8

RESULT 3

5217955-32  
Patent No. 5217955  
APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:32:  
LENGTH: 8  
5217955-32

Query Match 90.0%; Score 36; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXGHI 8  
|||  
Db 2 QWAVGHL 8

RESULT 4

5217955-34  
Patent No. 5217955  
APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:34:  
LENGTH: 8  
5217955-34

Query Match 90.0%; Score 36; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
|| |||  
Db 2 QWVGH 8

## RESULT 5

US-07-619-747B-1  
; Sequence 1, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATDIN  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-1

Query Match 90.0%; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
|| |||  
Db 2 QWVGH 8

## RESULT 6

US-07-619-747B-2  
; Sequence 2, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi

; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATDIN  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-2

Query Match 90.0%; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 8  
|| |||  
Db 2 QWVGH 8

## RESULT 7

US-07-619-747B-4  
; Sequence 4, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATDIN  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is 5P-D-Trp  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-4

Query Match 90.08; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXVGH1 8  
|||  
DB 2 QWAVGHL 8

RESULT 8  
US-07-619-747B-5  
Sequence 5, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren Zhi  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e

FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATDIN  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Tpi  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-5

Query Match 90.0%; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXVGH1 8  
|||  
DB 2 QWAVGHL 8

RESULT 9  
US-07-619-747B-9  
Sequence 9, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren Zhi  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428

TELEX: 511642 BEPATEDIN  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9  
 TYPE: AMINO  
 STRANDEDNESS: Unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: peptide  
 FEATURE:  
 OTHER INFORMATION: Position 1 is NH2CO-Tip  
 OTHER INFORMATION: Position 8 is a reduced  
 OTHER INFORMATION: isostere of named aminoacid  
 US-07-619-747B-9

Query Match 90.0%; Score 36; DB 1; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0;  
 2 QWAVGHI 8  
 2 QWAVGHL 8

RESULT 10  
 US-07-619-747B-10  
 Sequence 10, Application US/07619747B  
 Patent No. 5244883  
 GENERAL INFORMATION:  
 APPLICANT: Cai, Ren zhi  
 TITLE OF INVENTION: No. 5244883apeptide Bombesin  
 TITLE OF INVENTION: Antagonists  
 NUMBER OF SEQUENCES: 40  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dr. Andrew V. Schally  
 STREET: 5025 Kawanne Avenue  
 CITY: Metairie  
 STATE: Louisiana  
 COUNTRY: USA  
 ZIP: 70002

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 360K Diskette  
 COMPUTER: IBM PC  
 OPERATING SYSTEM: DOS 5.0  
 SOFTWARE: WP 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/619,747B  
 FILING DATE: 19901129  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: No. 5244883e  
 FILING DATE: N/A  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Behr, Omri M.  
 REGISTRATION NUMBER: 22,940  
 REFERENCE/DOCKET NUMBER: SHAL3.0-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908)494-5240  
 TELEFAX: 1-908-494-0428  
 TELEX: 511642 BEPATEDIN  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9  
 TYPE: AMINO  
 STRANDEDNESS: Unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: peptide  
 FEATURE:  
 OTHER INFORMATION: Position 1 is D-Trp  
 OTHER INFORMATION: Position 8 is a reduced

OTHER INFORMATION: isostere of named aminoacid  
 US-07-619-747B-10  
 Query Match 90.0%; Score 36; DB 1; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0;  
 2 QWAVGHI 8  
 2 QWAVGHL 8

RESULT 11  
 US-07-619-747B-12  
 Sequence 12, Application US/07619747B  
 Patent No. 5244883  
 GENERAL INFORMATION:  
 APPLICANT: Cai, Ren zhi  
 TITLE OF INVENTION: No. 5244883apeptide Bombesin  
 TITLE OF INVENTION: Antagonists  
 NUMBER OF SEQUENCES: 40  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dr. Andrew V. Schally  
 STREET: 5025 Kawanne Avenue  
 CITY: Metairie  
 STATE: Louisiana  
 COUNTRY: USA  
 ZIP: 70002

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 360K Diskette  
 COMPUTER: IBM PC  
 OPERATING SYSTEM: DOS 5.0  
 SOFTWARE: WP 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/619,747B  
 FILING DATE: 19901129  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: No. 5244883e  
 FILING DATE: N/A  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Behr, Omri M.  
 REGISTRATION NUMBER: 22,940  
 REFERENCE/DOCKET NUMBER: SHAL3.0-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908)494-5240  
 TELEFAX: 1-908-494-0428  
 TELEX: 511642 BEPATEDIN  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9  
 TYPE: AMINO  
 STRANDEDNESS: Unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: peptide  
 FEATURE:  
 OTHER INFORMATION: Position 1 is D-Tpi  
 OTHER INFORMATION: Position 8 is a reduced  
 OTHER INFORMATION: isostere of named aminoacid  
 US-07-619-747B-12

Query Match 90.0%; Score 36; DB 1; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0;  
 2 QWAVGHI 8  
 2 QWAVGHL 8

RESULT 12  
US-07-619-747B-14  
; Sequence 14, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is Hca  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
; OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-14

Query Match 90.0%; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

Qy 2 QWXYVGH1 8  
|||  
Db 2 QWAVGHL 8

RESULT 13  
US-07-619-747B-15  
; Sequence 15, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin

; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-pGlu  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
; OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-15

Query Match 90.0%; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

Qy 2 QWXYVGH1 8  
|||  
Db 2 QWAVGHL 8

RESULT 14  
US-07-619-747B-17  
; Sequence 17, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:

MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATDIN  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Phe  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-17

Query Match 90.0%; Score 36; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

Qy 2 QWVGHI 8  
Db 2 QWVGHL 8

RESULT 15  
US-07-619-747B-18  
Sequence 18, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren zhi  
APPLICANT: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATDIN  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Trp  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-18  
Query Match 90.0%; Score 36; DB 1; Length 9  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;  
Qy 2 QWVGHI 8  
Db 2 QWVGHL 8

Search completed: October 25, 2001, 11:23:56  
Job time: 269 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-6  
Perfect score: 40  
Sequence: 1 XQXVGH1 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

al number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
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7: /SID88/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
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11: /SID88/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseqp/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	92.5	8	21 AAB08309	Amino acid sequence
2	36	90.0	7	22 AAB48341	Bombesin/gastrin-r
3	36	90.0	8	11 AAR04531	Non-cyclic analogu
4	36	90.0	8	12 AAR11224	Linear litorin ana
5	36	90.0	8	12 AAR11240	Linear litorin ana
6	36	90.0	8	12 AAR14877	Peptide analogue #
7	36	90.0	8	13 AAR28456	Bombesin antagonis
8	36	90.0	8	13 AAR28459	Bombesin antagonis
9	36	90.0	8	16 AAW64910	Bombesin receptor
10	36	90.0	8	19 AAW50941	Bombesin antagonis
11	36	90.0	8	20 AAW92740	Bombesin peptide a

12	36	90.0	8	21 AAB08302	Amino acid sequence
13	36	90.0	8	22 AAB72406	Bombesin/gastrin-r
14	36	90.0	9	11 AAR04526	Non-cyclic analogu
15	36	90.0	9	11 AAR04527	Non-cyclic analogu
16	36	90.0	9	11 AAR04529	Non-cyclic analogu
17	36	90.0	9	11 AAR04528	Non-cyclic analogu
18	36	90.0	9	11 AAR04530	Non-cyclic analogu
19	36	90.0	9	11 AAR08345	Peptide analogue #
20	36	90.0	9	12 AAR11520	Peptide analogue #
21	36	90.0	9	12 AAR11521	Peptide analogue #
22	36	90.0	9	12 AAR11525	Peptide analogue #
23	36	90.0	9	12 AAR11529	Peptide analogue #
24	36	90.0	9	12 AAR12033	Peptide analogue #
25	36	90.0	9	12 AAR14860	Peptide analogue #
26	36	90.0	9	12 AAR14861	Peptide analogue #
27	36	90.0	9	12 AAR14862	Peptide analogue #
28	36	90.0	9	12 AAR14863	Peptide analogue #
29	36	90.0	9	12 AAR14864	Peptide analogue #
30	36	90.0	9	12 AAR14872	Peptide analogue #
31	36	90.0	9	12 AAR14876	Peptide analogue #
32	36	90.0	9	12 AAR14880	Cyclic analogue #1
33	36	90.0	9	12 AAR15038	Cyclic analogue #1
34	36	90.0	9	13 AAR24483	[psi8-9 pseudo] No
35	36	90.0	9	13 AAR24484	[psi8-9 pseudo] No
36	36	90.0	9	13 AAR24486	[psi8-9 pseudo] No
37	36	90.0	9	13 AAR24490	[psi8-9 pseudo] No
38	36	90.0	9	13 AAR24491	[psi8-9 pseudo] No
39	36	90.0	9	13 AAR24492	[psi8-9 pseudo] No
40	36	90.0	9	13 AAR24487	[psi8-9 pseudo] No
41	36	90.0	9	13 AAR24488	[psi8-9 pseudo] No
42	36	90.0	9	13 AAR24489	[psi8-9 pseudo] No
43	36	90.0	9	13 AAR24493	[psi8-9 pseudo] No
44	36	90.0	9	13 AAR28447	[psi8-9 pseudo] No
45	36	90.0	9	13 AAR28448	[psi8-9 pseudo] No

ALIGNMENTS

RESULT	1
AAB08309	
ID	AAB08309 standard; peptide; 8 AA.
XX	
AC	AAB08309;
XX	
DT	04-DEC-2000 (first entry)
XX	
DE	Amino acid sequence of antiangiogenic peptide DT-26.
XX	
KW	Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1-28
KW	VIPI; VIP2; VIP3; BOM1; bombesin; SP1; substance P; MJJ-7; tumour growth
KW	tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
KW	leukaemia; lymphoma.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 1
FT	Location/Qualifiers
FT	/note= "D-form residue"
FT	Modified-site 4
FT	/label= Alb
FT	/note= "alpha-aminoisobutyric acid"
FT	Modified-site 8
FT	/note= "amidated residue"
FT	
FT	WO200047221-A1.
PN	
XX	
PD	17-AUG-2000.
XX	
PF	11-FEB-2000; 2000WO-US03559.
XX	
PR	11-FEB-1999; 99US-0248381.
XX	

PA (NAIN-) NAT INST IMMUNOLOGY.  
PA (DABU-) DABUR RES FOUND.  
PA (CORD/) CORD J I.  
PI Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;  
PI Singh AT;  
XX WPI; 2000-549083/50.  
XX  
XX Novel therapeutically active composition comprising at least 5  
PT peptides, useful for treating angiogenesis especially as a result of  
PT adenocarcinomas -  
XX  
XX Claim 11; Page 31; 42pp; English.  
XX  
XX AAB08304-15 represent peptides which have an antiangiogenic effect. The  
CC specification describes therapeutically active compositions comprising  
CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and  
CC at least four analogues chosen from vasoactive intestinal peptide (VIP)  
CC 1 (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a  
CC VIP receptor antagonist), BOM1 (a bombesin antagonist), and SPI (a  
CC substance P antagonist). The combination of these 7 analogues is known as  
CC MuJ-7. MuJ-7 is used as an anticancer drug to restrict tumour growth and  
CC spread by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits  
CC metastasis through its antiangiogenic activity in all cancers. The  
CC peptides are useful for the treatment and prevention of angiogenesis,  
CC especially as a result of adenocarcinomas of the colon, breast, lung,  
CC prostate, kidney, leukemias or lymphomas.  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 92.5%; Score 37; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 QWXYVGH I 8  
Db 2 qwxvghi 8  
|||||  
  
RESULT 2  
AAB48341  
ID AAB48341 standard; peptide; 7 AA.  
XX AC AAB48341;  
XX  
XX 20-APR-2001 (first entry)  
XX  
XX Bombesin/gastrin-releasing peptide receptor-recognising peptide.  
XX  
XX Cancer; chemotherapy; heparin; thrombospondin; drug resistance;  
KW toxicity; tumour; cytostatic; metalloprotease.  
XX  
XX Synthetic.  
XX  
XX WO200078359-A2.  
XX  
XX 28-DEC-2000.  
XX  
XX 21-JUN-2000; 2000WO-US16955.  
XX  
XX 21-JUN-1999; 99US-0140310.  
XX  
XX (TUSZ/) TUSZYNSKI G.  
XX (WILL/) WILLIAMS T.  
XX (ACTO/) ACTOR P.  
XX  
XX Tuszyński G, Williams T, Actor P;  
XX  
XX WPI; 2001-080760/09.  
XX  
XX Treating cancer involves administering chemotherapy agent conjugated to

a peptide or co-administering chemotherapy agent and the peptide -  
XX  
XX Disclosure; Page 6; 44pp; English.  
XX  
XX The invention relates to a method of treating a patient suffering from  
CC cancer that comprises administering a chemotherapy agent conjugated to a  
CC peptide, or co-administering the agent and the peptide. The peptides can  
CC be selected from heparin binding domains of the thrombospondin protein.  
CC The method and compositions comprising the agent and the peptide are  
CC useful for treating a patient with drug resistant cancer, and for  
CC treating a patient with cancer to prevent drug resistance from occurring.  
CC Toxic chemotherapeutic agent can also be used, as peptide conjugation and  
CC co-administration can considerably reduce the toxicity of the agent and  
CC allow less composition to be administered due to increased efficacy. More  
CC effective treatment at lower doses is achieved by targeting the  
CC chemotherapy agents to the tumour cells. The present sequence represents  
CC bombesin/gastrin-releasing peptide receptor-recognising peptide.  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 90.0%; Score 36; DB 22; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 QWXYVGH I 8  
Db 1 qwavghi 7  
|||  
  
RESULT 3  
AAR04531  
ID AAR04531 standard; protein; 8 AA.  
XX AC AAR04531;  
XX  
XX 24-SEP-1990 (first entry)  
XX  
XX Non-cyclic analogue of amphibian bombesin and mammalian GRP.  
XX  
XX Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
KW therapeutic peptides.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 1 /label= D-phenylalanine  
FT  
XX  
XX WO9003980-A.  
XX  
XX 19-APR-1990.  
XX  
XX 13-OCT-1989; 89WO-US00416.  
XX  
XX 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.  
XX  
XX (TULA ) TULANE E FUND ADMINISTRA.  
XX  
XX Coy DH, Moreau J-P, Taylor JE, Kim SH;  
XX  
XX WPI; 1990-147822/19.  
XX  
XX New non-cyclic analogues of mammalian gastrin releasing peptide  
PT and amphibian bombesin, used for cancer treatment eg small  
PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.  
XX  
XX Claim 21; Page 55; 68pp; English.  
XX  
XX C-terminal = ethylamide or amide.  
CC The peptide has an active site and a binding site for binding to a  
CC target cell receptor, and has one of the following modifications:  
CC (a) a deletion of a residue within the active site and a

CC This peptide is a specifically claimed example of a generic  
CC formula. The C-terminal amino acid (Wet) of the naturally occurring  
CC peptide has been converted to an amide and Phe 8 has been replaced  
CC by Statine.  
CC The peptide is useful for treating benign or malignant tissue  
CC proliferation, atherosclerosis gastrointestinal disorders and

Sequence 8 AA:

Query Match 90.0%; Score 36; DB 12; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHI 8  
 |||||  
 Db 2 qwvghl 8

RESULT 6  
 AAR14877  
 ID AAR14877 standard; Protein; 8 AA.  
 XX  
 AC AAR14877;  
 XX  
 DT 14-FEB-1992 (first entry)  
 XX  
 DE Peptide analogue #18 of litorin, GRP, neuromedin or bombesin.  
 XX  
 KW tissue proliferation; gastrin related peptide; peptide hormone.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= D-Phe  
 FT Modified-site 8  
 FT /label= OTHER  
 FT /note= "Leu-propylamide"  
 XX  
 PN W09117181-A.  
 XX  
 PD 14-NOV-1991.  
 XX  
 PF 09-MAY-1991; 91WO-0003265.  
 XX  
 PR 09-MAY-1990; 90US-0520226.  
 XX  
 PA (TULA ) TULANE E FUND ADMINISTRA.  
 PA (BIOM-) BIOMEASURE INC.  
 XX  
 PI Coy DH, Kim SH, Moreau JP;  
 XX  
 DR WPI; 1991-353721/48.  
 XX

Peptide agonists of litorin, gastrin releasing peptide -  
 neuromedin B or C or bombesin, for treating cancer, preventing  
 smooth muscle proliferation and suppressing appetite and alcohol  
 craving  
 Claim 20; Page 19; 25pp; English.

This peptide is one of 27 specific examples of a highly generic  
 formula. The peptides are all analogues of either litorin; the 10  
 amino acid C-terminal region of mammalian GRP, neuromedin B or  
 neuromedin C; or the 10 amino acid C-terminal region of amphibian  
 bombesin. They act as at least partial agonists of the natural  
 peptides. The peptide analogues are made by standard methods of  
 synthesis and can be cyclised.  
 See AAR14860-R14880 and AAR15035-R15040.

Sequence 8 AA;

Query Match 90.0%; Score 36; DB 12; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHI 8  
 |||||  
 Db 2 qwvghl 8

RESULT 7  
 AAR28456  
 ID AAR28456 standard; Protein; 8 AA.  
 XX  
 AC AAR28456;  
 XX  
 DT 09-DEC-1992 (first entry)  
 XX  
 DE Bombesin antagonist (24).  
 XX  
 KW Bombesin; GRP; gastrin releasing peptide.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Hca-Gln; Hca= hydrocinnamic acid"  
 FT Modified-site 7  
 FT /label= psi  
 FT /note= "residues 7-8 are linked via a pseudo  
 peptide bond"  
 FT Modified-site 8  
 FT /label= psi  
 FT /note= "residues 7-8 are linked via a pseudo  
 peptide bond"  
 XX  
 PN W09209626-A.  
 XX  
 PD 11-JUN-1992.  
 XX  
 PF 15-NOV-1991; 91WO-US08534.  
 XX  
 PR 29-NOV-1990; 90US-0619747.  
 XX  
 PA (TULA ) TULANE EDUCATIONAL FUND.  
 XX  
 PI Cai RZ, Schally AV;  
 XX  
 DR WPI; 1992-217019/26.  
 XX

New nona-peptide bombesin antagonists - used for treating  
 hypergastrinaemic states, such as pernicious anaemia and  
 Zollinger-Ellison syndrome and also used against lung and gastric  
 cancer, etc.

Disclosure; Page 8; 50pp; English.

The C-terminal is amidated. The peptide is an example of a highly  
 generic formula for bombesin antagonists which are [ps18-9 pseudo]  
 nonapeptides contg. D- or L-tryptophan or tryptophan analog  
 2,3,4,9-tetrahydro-1H-pyrido[3,4-b]-indol-3-carboxylic acid (Tpi)  
 at the N- and/or C-terminal.

The peptide is a bombesin/GRP (gastrin releasing peptide) antagonist  
 and is useful for treatment of states of hypergastrinemia, e.g.,  
 pernicious anaemia, chronic atrophic gastritis, Zollinger-Ellison  
 syndrome and vitiligo, associated with diffuse hyperplasia of  
 gastric enterochromaffin-like cells, and with an increased risk of  
 developing multifocal gastric carcinoma tumours. The peptide can  
 also be used to treat lung, colon and gastric cancers. Dosage is  
 1-1000 microg/kg parenterally.

Sequence 8 AA;

Query Match 90.0%; Score 36; DB 13; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHI 8  
 |||||  
 Db 1 qwavghl 7

Db	1	qwavghl 7
RESULT	8	
AAAR28459		
ID	AAAR28459	standard; Protein; 8 AA.
XX	AC	AAAR28459;
XX	09-DEC-1992	(first entry)
DT	XX	Bombesin antagonist (27).
DE	XX	Bombesin; GRP; gastrin releasing peptide.
XX	XX	Bombesin.
OS	XX	Synthetic.
Key	XX	Location/Qualifiers
FT	Modified-site 1	/note= "Mpp-Gln; Mpp= 3-(4-methoxyphenyl) propionic acid"
FT	Modified-site 7	/label= psi
FT	Modified-site 8	/note= "residues 7-8 are linked via a pseudo peptide bond"
FT	Modified-site 8	/label= psi
FT	Modified-site 8	/note= "Trp(For), For= formyl; residues 7-8 are linked via a pseudo peptide bond"
PN	WO9209626-A.	
XX	11-JUN-1992.	
XX	15-NOV-1991;	91WO-US08534.
XX	29-NOV-1990;	90US-0619747.
XX	(TULA )	TULANE EDUCATIONAL FUND.
XX	Cai RZ, Schally AV;	
PI	WPI; 1992-217019/26.	
DR	New nona-peptide bombesin antagonists - used for treating hypergastrinaemic states, such as pernicious anaemia and Zollinger-Ellison syndrome and also used against lung and gastric cancer, etc.	
XX	Disclosure; Page 8; 50pp; English.	
PS	The C-terminal is amidated. The peptide is an example of a highly generic formula for bombesin antagonists which are [psi8-9 pseudo] nonapeptides confg. D- or L-tryptophan or tryptophan analog 2,3,4,9-tetrahydro-1H-pyrido[3,4-b]-indol-3-carboxylic acid (Tpi) at the N- and/or C-terminal.	
CC	The peptide is a bombesin/GRP (gastrin releasing peptide) antagonist and is useful for treatment of states of hypergastrinemia, e.g. pernicious anaemia, chronic atrophic gastritis, Zollinger-Ellison syndrome and vitiligo, associated with diffuse hyperplasia of gastric enterochromaffin-like cells, and with an increased risk of developing multifocal gastric carcinoma tumours. The peptide can also be used to treat lung, colon and gastric cancers. Dosage is 1- 1000 microg/kg parenterally.	
XX	Sequence 8 AA;	
SQ		
Query Match	90.0%;	Score 36; DB 13; Length 8;
Best Local Similarity	71.4%;	Pred. No. 3.4e+05;
Matches	5; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
QY	2 QWVGH1 8	

Db	1	qwavghl 7
RESULT	9	
AAW64910		
ID	AAW64910	standard; peptide; 8 AA.
XX	AC	AAW64910;
XX	06-JUL-1999	(first entry)
DT	XX	Bombesin receptor antagonist.
DE	XX	Bombesin; antagonist; chlorambucil; peptic ulcer; pancreatitis; eating disorder; diabetes; acromegaly; enterocutaneous fistula; psoriasis; growth retardation; gastrointestinal motility disorder; antitumour.
XX	OS	Synthetic.
Key	XX	Location/Qualifiers
FT	Modified-site 1	/note= "The amino terminal is acylated with bromoacetyl, chloroacetyl, [bis(2-chloroethyl), L-phenylalanine or a chlorambucil group"
FT	Modified-site 8	/note= "The carboxy terminal is in the form of an ethyl ester"
PN	WO9500542-A1.	
XX	05-JAN-1995.	
XX	15-JUN-1994;	94WO-US06757.
XX	17-DEC-1993;	93US-0168390.
PR	18-JUN-1993;	93US-0078062.
XX	(PEPT- )	PEPTIDE TECHNOLOGIES CORP.
XX	Chandrasekhar B, Knight M, Takahashi K;	
PI	WPI; 1995-052004/07.	
DR	New bombesin, gastrin releasing peptide or Neuromedin B or C derivs - antagonists for treating conditions such as gastrointestinal disorders, psoriasis and cancers	
XX	Claim 6; Page 34; 45pp; English.	
PS	The patent discloses (1) the peptide sequence of bombesin (Bbn), gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C, the peptide sequence having a chlorambucil group attached to the amino terminal; (2) a BBN receptor antagonist of formula R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3. In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His. The compounds act as potent BBN/GRP-like peptide antagonists. They can be used to inhibit the growth of cells that are sensitive to the growth-promoting effects of BBN, GRP or a related peptide such as pancreatic cells, gastric cells, neurons, hypothalamic cells and cancerous cells or tumours. They can also be used to inhibit the binding of BBN, GRP or a related peptide to cells capable of such binding. They can be used for treating e.g. peptic ulcer, pancreatitis, eating disorders, diabetes, acromegaly, enterocutaneous fistula, psoriasis, growth retardation, gastrointestinal motility disorders or tumours. The terminal structures of the compounds protect them from in vivo proteolysis and provide highly potent antagonist effects that persist for extended periods of time upon administration.	
XX	Sequence 8 AA;	
SQ		

Query Match 90.0%; Score 36; DB 16; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWXXVGH 8  
Db 2 qwavghl 8

RESULT 10  
AAW50941  
ID AAW50941 standard; peptide; 8 AA.  
XX AC AAW50941;  
XX DT 31-JUL-1998 (first entry)  
XX Bombesin antagonist (BOM1).  
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;  
KW Substance P; cancer; inhibition.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 1  
FT Modified-site 8 /note= "D-form residue"  
FT Modified-site 8 /note= "Leu-NHET"  
XX PN EP835662-A2.  
XX PD 15-APR-1998.  
XX PF 11-DEC-1996; 96EP-0309012.  
XX PR 08-OCT-1996; 96US-0727679.  
XX PR 16-AUG-1996; 96IN-0001822.  
XX PA (NAIM-) NAT INST IMMUNOLOGY.  
XX PI Jaggi M, Mukherjee R;  
XX DR WPI; 1998-208959/19.  
XX Composition containing analogues of vasoactive intestinal peptide,  
somatostatin - bombesin and substance P, for treatment of tumours  
and for inhibiting over-expression of these peptide(s)  
XX Claim 1; Page 4; 49pp; English.  
XX The invention relates to a new composition which comprises: (i) the  
somatostatin analogue SOM2 ACKNPFQWKTPTSC (3-14 disulphide bridge),  
and (ii) at least 4 of the peptides: antagonist of vasoactive  
intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP  
receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin  
antagonist (BOM1) and substance P antagonist (SP1). Also claimed are  
more general compositions containing peptide analogues of somatostatin,  
VIP, bombesin and substance P. The compositions are used in human or  
veterinary medicine: (a) to kill (or inhibit multiplication of) tumour  
or cancer cells, particularly for treatment of leukaemia, lymphoma,  
adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,  
breast, kidney or particularly rectum and colon, and (b) to prevent,  
inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer  
cells express receptors for VIP, somatostatin, bombesin and/or substance  
P. The present sequence represents bombesin antagonist (BOM1).  
XX Sequence 8 AA;

Query Match 90.0%; Score 36; DB 19; Length 8;

Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWXXVGH 8  
Db 2 qwavghl 8

RESULT 11  
AAW92740  
ID AAW92740 standard; peptide; 8 AA.  
XX AC AAW92740;  
XX DT 30-APR-1999 (first entry)  
XX Bombesin peptide analogue #6.  
XX Bombesin; gastrin releasing peptide; GRP; GRF; litorin; proliferation;  
KW growth hormone releasing factor; treatment; benign; malignant; tissue;  
KW small-cell lung carcinoma; atherosclerosis; gastrointestinal disorder;  
KW diabetes; diabetes related retinopathy.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Residue is pyroglutamate"  
FT Modified-site 8 /note= "methylester C-terminus"  
XX PN US5877277-A.  
XX PD 02-MAR-1999.  
XX PF 10-NOV-1994; 94US-0337127.  
XX PR 18-OCT-1991; 91US-0779039.  
XX PR 24-SEP-1987; 87US-0100571.  
XX PR 25-MAR-1988; 88US-0173311.  
XX PR 08-JUN-1988; 88US-0204171.  
XX PR 16-JUN-1988; 88US-0207759.  
XX PR 23-SEP-1988; 88US-0248771.  
XX PR 14-OCT-1988; 88US-0257998.  
XX PR 09-DEC-1988; 88US-0282328.  
XX PR 02-MAR-1989; 89US-0317941.  
XX PR 07-JUL-1989; 89US-0376555.  
XX PR 30-MAR-1990; 90US-0502438.  
XX PR 10-NOV-1994; 94US-0337127.  
XX (BIOM-) BIOMEASURE INC.  
XX (TULA ) TULANE EDUCATIONAL FUND.  
XX Coy DH, Kim SH, Moreau J;  
XX WPI; 1999-189718/16.  
XX New peptides - useful for treating benign or malignant tissue  
proliferation, gastrointestinal disorders and diabetes  
XX Disclosure; Column 29-30; 22pp; English.  
XX This invention describes novel peptides which are analogues of litorin  
or the 10 amino acid carboxy-terminal region of mammalian gastrin  
releasing peptide or the 10 amino acid carboxy-terminal region of  
amphibian bombesin of formula (R1)(R2)Al-A2-Trip-A4-A5-A6-A7-W where A1  
D-isomer of p-x-Phe, Trp or beta-Nal; x = F, Cl, Br, NO2, OH, H or Me;  
A2 = Gly, Ala, Val, Gln, Asn, Leu, Ile, Met, p-x-Phe, Trp, Cys,  
beta-Nal, His, 1-methyl-His or 3-methyl-His; A4 = Ala, Val, Gln, Asn,  
Gly, Leu, Ile, Nle, alpha-aminobutyric acid, Met, p-x-Phe, Trp, Cys or  
beta-Nal; A5 = Gln, Asn, Gly, Ala, Leu, Ile, Nle, alpha-aminobutyric  
acid, Met, Val, p-x-Phe, Trp, Thr or beta-Nal; A6 = Sar, Gly or D-isomer  
of Ala, N-methyl-Ala, Val, Gln, Asn, Leu, Ile, Met, p-x-Phe, Trp, Cys or

CC beta-Nal; A7 = His or 1-methyl or 3-methyl-His; W = -N(R3)-CH(21)-R4-  
 CC CH(22)-C(=O)V; R4 = CH2NH; Z1, Z2 = Gly, Ala, Val, Leu, Ile, Ser, Asp,  
 CC Asn, Glu, Gln, p-X-Phe, Trp, Cys, Met, Pro, HypPro or cyclohexylAla; V =  
 CC OR5 or NR6R7; R3, R5, R6, R7 = H, lower alkyl, phenyl(lower alkyl) or  
 CC naphthyl(lower alkyl); R1, R2 = H, 112C alkyl, 7-10C phenylalkyl or  
 CC COE1; where R1 and R2 are bonded to the N-terminal amino acid of the  
 CC peptide; E1 = 1-20C alkyl, 3-20C alkenyl, 3-20C alkynyl, Ph, naphthyl  
 CC or 7-10C phenylalkyl; provided that when 1 of R1 and R2 is COE1, the  
 CC other must be H. The peptides can be used for treating benign or  
 CC malignant proliferation of tissue e.g. small-cell lung carcinoma,  
 CC atherosclerosis, gastrointestinal disorders, and diabetes or diabetes  
 CC related retinopathy. AAW92735-W92742 represent bombesin peptide  
 CC analogues used in the method of the invention.  
 XX  
 XX Sequence 8 AA;

Query Match 90.0%; Score 36; DB 20; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVXVGH I 8  
 Db 11 111:  
 2 qwavghl 8

RESULT 12  
 AAB08302  
 ID AAB08302 standard; peptide; 8 AA.  
 XX  
 AC AAB08302;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Amino acid sequence of bombesin analogue BOM1.  
 XX  
 KW Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;  
 KW VIP1; VIP2; VIP3; BOM1; bombesin; SP1; substance P; MuJ-7; tumour growth;  
 KW tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;  
 KW leukaemia; lymphoma.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Modified-site 8 /note= "residue is Leu-NHET"  
 FT  
 XX WO200047221-A1.

PD 17-AUG-2000.  
 XX  
 XX 11-FEB-2000; 2000WO-US03559.  
 XX  
 XX 11-FEB-1999; 99US-0248381.  
 XX (NAIN-) NAT INST IMMUNOLOGY.  
 XX (DABU-) DABUR RES FOUND.  
 XX (CORD/) CORD J I.  
 XX  
 PI Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;  
 PI Singh AT;  
 XX  
 XX WPI; 2000-549083/50.  
 XX  
 XX Novel therapeutically active composition comprising at least 5  
 PT peptides, useful for treating angiogenesis especially as a result of  
 PT adenocarcinomas -  
 XX  
 XX Disclosure; Page 8; 42pp; English.  
 XX  
 XX The present sequence represents an analogue of bombesin. The

CC specification describes therapeutically active compositions comprising  
 CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and  
 CC at least four analogues chosen from vasoactive intestinal peptide (VIP),  
 CC (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a VIP  
 CC receptor antagonist), BOM1 (a bombesin antagonist), and SP1 (a substance  
 CC P antagonist). The combination of these 7 analogues is known as MuJ-7.  
 CC MuJ-7 is used as an anticancer drug to restrict tumour growth and spread  
 CC by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits the  
 CC metastasis through its antiangiogenic activity in all cancers. The  
 CC peptides are useful for the treatment and prevention of angiogenesis,  
 CC especially as a result of adenocarcinomas of the colon, breast, lung,  
 CC prostate, kidney, leukemias or lymphomas.  
 XX  
 XX Sequence 8 AA;

Query Match 90.0%; Score 36; DB 21; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXVGH I 8  
 Db 11 111:  
 2 qwavghl 8

RESULT 13  
 AAB72406  
 ID AAB72406 standard; peptide; 8 AA.  
 XX  
 AC AAB72406;  
 XX  
 DT 03-MAY-2001 (first entry)  
 XX  
 DE Bombesin analogue.  
 XX  
 KW Gene therapy; gene transfer; gastrin releasing peptide receptor; GRP1;  
 KW bombesin analogue; BBN.  
 XX  
 OS Unidentified.  
 XX WO200112234-A1.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 16-AUG-2000; 2000WO-US22456.  
 XX  
 XX 16-AUG-1999; 99US-0374972.  
 XX  
 XX 01-JUN-2000; 2000US-0585194.  
 XX  
 XX (UABR-) UAB RES FOUND.  
 XX  
 XX Buchsbaum DJ, Curriel DT, Zinn KR, Rogers BE;  
 XX WPI; 2001-218310/22.

XX Monitoring therapeutic gene transfer and expression into a subject, by  
 XX administering vector encoding the gene and gene for membrane expressed  
 XX targeting molecule, and a radiolabeled ligand, and imaging gene  
 XX transfer -  
 XX  
 XX Example 10; Page 33; 107pp; English.  
 XX  
 XX The present invention relates to a method for monitoring therapeutic gene  
 XX transfer and expression into a subject, comprising administering a vector  
 XX encoding a therapeutic gene and a gene for a membrane expressed targeting  
 XX molecule (TM), and a radiolabelled ligand (RL) having high affinity for  
 XX TM, and detecting the binding of RL with TM. The binding is directly  
 XX proportional to the transfer and expression of the therapeutic gene.  
 XX Preferably, the TM is gastrin releasing peptide receptor (GRP1). A  
 XX technique was developed to image GRP1 expression using a 99mTc-labelled  
 XX bombesin (BBN) analogue (the present sequence).  
 XX  
 XX Sequence 8 AA;

Query Match 90.0%; Score 36; DB 22; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXGHI 8  
II III:  
Db 1 qwavghl 7

RESULT 14  
AAR04526  
ID AAR04526 standard; protein; 9 AA.  
XX  
AC AAR04526;  
XX  
DT 24-SEP-1990 (first entry)  
XX  
Non-cyclic analogue of amphibian bombesin and mammalian GRP.  
KW Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
KW therapeutic peptides.  
XX  
OS Synthetic.  
XX

Key Location/Qualifiers  
Modified-site 1  
/label= OTHER  
/note= "D-p-Cl"  
Modified-site 8  
/label-beta-homoleucine

WO9003980-A.  
XX  
PD 19-APR-1990.  
XX  
PF 13-OCT-1989; 89WO-US00416.  
XX  
PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.  
XX  
PA (TULANE ) TULANE E FUND ADMINISTRA.  
XX  
PI Coy DH, Moreau J-P, Taylor JE, Kim SH;  
XX  
WPI; 1990-147822/19.

New non-cyclic analogues of mammalian gastrin releasing peptide -  
and amphibian bombesin, used for cancer treatment eg small  
cell lung carcinoma, atherosclerosis and gastrointestinal disorders.  
PS  
PS Claim 8; Page 49; 68pp; English.

C-terminal = NH2.  
The peptide has an active site and a binding site for binding to a  
target cell receptor, and has one of the following modifications:  
(a) a deletion of a residue within the active site and a  
modification of a residue outside of the active site; and  
(b) a replacement of 1 or 2 residues within the active site with a  
synthetic amino acid.  
On binding to its receptor, the analogue acts as a competitive  
inhibitor of the naturally occurring peptide but due to the  
modifications, fails to exhibit the normal in vivo biological activity.  
The peptides are useful for the treatment of benign or malignant  
proliferation of tissues, eg cancers of the gastrointestinal  
tract, pancreatic cancer, colon cancer, lung cancer or breast  
cancer; for the treatment of atherosclerosis; and disorders of the  
gastrointestinal tissues.  
This peptide is a claimed  
See also AAR04525-R04533.

Sequence 9 AA;

Query Match 90.0%; Score 36; DB 11; Length 9;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVXGHI 8  
II III:  
Db 3 qwavghl 9

RESULT 15  
AAR04527  
ID AAR04527 standard; protein; 9 AA.  
XX  
AC AAR04527;  
XX  
DT 24-SEP-1990 (first entry)  
XX  
Non-cyclic analogue of amphibian bombesin and mammalian GRP.  
KW Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
KW therapeutic peptides.  
XX  
OS Synthetic.  
XX

Key Location/Qualifiers  
Modified-site 1  
/label= D-beta-naphthylalanine  
Modified-site 8  
/label-leucine psi[CH2NH]

WO9003980-A.  
XX  
PD 19-APR-1990.  
XX  
PF 13-OCT-1989; 89WO-US00416.  
XX  
PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.  
XX  
PA (TULANE ) TULANE E FUND ADMINISTRA.  
XX  
PI Coy DH, Moreau J-P, Taylor JE, Kim SH;  
XX  
WPI; 1990-147822/19.

New non-cyclic analogues of mammalian gastrin releasing peptide -  
and amphibian bombesin, used for cancer treatment eg small  
cell lung carcinoma, atherosclerosis and gastrointestinal disorders.  
PS  
PS Claim 12; Page 52; 68pp; English.

C-terminal = NH2.  
The peptide has an active site and a binding site for binding to a  
target cell receptor, and has one of the following modifications:  
(a) a deletion of a residue within the active site and a  
modification of a residue outside of the active site; and  
(b) a replacement of 1 or 2 residues within the active site with a  
synthetic amino acid.  
On binding to its receptor, the analogue acts as a competitive  
inhibitor of the naturally occurring peptide but due to the  
modifications, fails to exhibit the normal in vivo biological activity.  
The peptides are useful for the treatment of benign or malignant  
proliferation of tissues, eg cancers of the gastrointestinal  
tract, pancreatic cancer, colon cancer, lung cancer or breast  
cancer; for the treatment of atherosclerosis; and disorders of the  
gastrointestinal tissues.  
This peptide is a claimed  
See also AAR04525-R04533.

Sequence 9 AA;

Query Match 90.0%; Score 36; DB 11; Length 9;

Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QXXVGH 8  
Db 11 111:  
2 qwavghl 8

Search completed: October 25, 2001, 11:22:46  
Job time: 219 sec

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:44 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-7  
Perfect score: 38  
Sequence: 1 QWAVXHI 8

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

al number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_invertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	34	89.5	806	13 Q9DDL2	Q9ddl2 brachydanio
2	32	84.2	328	2 Q9X5G8	Q9x5g8 streptomyce
3	32	84.2	453	10 Q9M4A9	Q9m4a9 pisum sativ
4	31	81.6	98	14 Q64981	Q64981 artichoke 1
5	31	81.6	119	13 Q90253	Q90253 bombina ori
6	31	81.6	309	5 Q27106	Q27106 trichomonas
7	31	81.6	338	13 Q93576	Q93576 lacerta vir
8	31	81.6	517	14 Q9DSF4	Q9dsp4 saint croix
9	31	81.6	615	13 Q93575	Q93575 emys orbicu
10	31	81.6	696	5 Q9VCU2	Q9vcu2 drosophila
11	31	81.6	1273	4 Q9NU68	Q9nu68 homo sapien
12	31	81.6	1275	4 Q15057	Q15057 homo sapien
13	31	81.6	3209	13 Q93574	Q93574 gallus gall
14	31	81.6	3460	4 P78509	P78509 homo sapien
15	31	81.6	3461	11 Q60841	Q60841 mus musculus
16	30	78.9	100	14 Q9D128	Q9d128 human adeno
17	30	78.9	100	14 Q9D127	Q9d127 human adeno
18	30	78.9	100	14 Q9D126	Q9d126 human adeno
19	30	78.9	100	14 Q9D125	Q9d125 human adeno

20	30	78.9	100	14 Q9D124	Q9d124 human adeno
21	30	78.9	100	14 Q9D123	Q9d123 human adeno
22	30	78.9	100	14 Q9D122	Q9d122 human adeno
23	30	78.9	100	14 Q9D121	Q9d121 human adeno
24	30	78.9	100	14 Q9D120	Q9d120 human adeno
25	30	78.9	100	14 Q9D119	Q9d119 human adeno
26	30	78.9	100	14 Q9D118	Q9d118 human adeno
27	30	78.9	100	14 Q9D117	Q9d117 human adeno
28	30	78.9	100	14 Q9D116	Q9d116 human adeno
29	30	78.9	119	5 Q9NH76	Q9nh76 naegleria
30	30	78.9	174	10 Q9M2H1	Q9m2h1 arabidopsis
31	30	78.9	230	2 Q9L911	Q9l911 salmonella
32	30	78.9	289	2 Q9HT14	Q9ht14 pseudomonas
33	30	78.9	291	14 Q72694	Q72694 barley malv
34	30	78.9	353	5 Q21051	Q21051 anorthodid
35	30	78.9	520	10 Q65815	Q65815 helianth
36	30	78.9	574	2 P96591	P96591 bacillus s
37	30	78.9	574	2 Q82894	Q82894 escherichia
38	30	78.9	611	8 Q9G6S7	Q9g6s7 sardinops m
39	30	78.9	719	14 P87541	P87541 barley mill
40	30	78.9	934	14 Q91858	Q91858 human adeno
41	30	78.9	934	14 Q9YIE0	Q9yie0 human adeno
42	30	78.9	934	14 Q9YVE1	Q9yve1 human adeno
43	30	78.9	934	14 Q9YVE0	Q9yve0 human adeno
44	30	78.9	934	14 Q9YVD9	Q9yvd9 human adeno
45	30	78.9	936	14 Q67814	Q67814 human adeno

## ALIGNMENTS

RESULT 1  
Q9DDL2 PRELIMINARY;  
AC Q9DDL2: 806 AA.  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE PARACASPASE.

OS Brachydanio rerio (Zebrafish) (zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID:7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed:11090634;  
RA Uren A.G., O'Rourke K., Aravind L., Pisabarro M.T., Seshagiri S.,  
Koonin E.V., Dixit V.M.;  
RT "Identification of Paracaspases and Metacaspases. Two Ancient Families  
of Caspase-like Proteins, One of which Plays a Key Role in MAIT  
Lymphoma".  
RL Mol. Cell 6:961-967(2000).  
DR EMBL; AF316598; AAG38590.1; ... 589A8BC2013B0A51 CRC64;  
SQ SEQUENCE 806 AA; 90754 MW; 589A8BC2013B0A51 CRC64;

Query Match 89.5%; Score 34; DB 13; Length 806  
Best Local Similarity 57.18; Pred. No. 48;  
Matches 4; Conservative 2; Mismatches 1; Indels

QY 2 QWAVXHI 8  
Db 559 QWAVXHI 565

RESULT 2  
Q9X5G8 PRELIMINARY;  
ID Q9X5G8: 328 AA.  
AC Q9X5G8;  
DT 01-NOV-1999 (TRENBLrel. 12, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

DE PUTATIVE DEACETYLCEPHALOSPORIN C ACETYLTRANSFERASE.  
 GN CVM4.  
 OS Streptomyces clavuligerus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.  
 ON NCBI\_TaxID=1901;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL 3585;  
 RX MEDLINE=99240369; PubMed=10223939;  
 RA Mosher R.H., Paraskar A.S., Anders C., Barton B., Jensen S.E.;  
 RT "Genes specific for the biosynthesis of clavam metabolites antipodal  
 RT to clavulanic acid are clustered with the gene for clavaminase  
 RT synthase 1 in Streptomyces clavuligerus."  
 RL Antimicrob. Agents Chemother. 43:1215-1224(1999).  
 CC -!- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.  
 DR EMBL; AF124929; AAD30471.1; -.  
 DR InterPro; IPR000073; -.  
 DR Pfam; PF00561; abhydrolase; 1.  
 DR Transferase; Porin.  
 SEQUENCE 328 AA; 34642 MW; 4C8C78DAD5215034 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 328;  
 Best Local Similarity 83.3%; Pred. No. 48;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXH 7  
 Db 133 QWAVSH 138

RESULT 3  
 Q9M4A9 PRELIMINARY; PRT; 453 AA.  
 ID Q9M4A9;  
 AC Q9M4A9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE BETA-1,3 GLUCANASE PRECURSOR (EC 3.2.1.39).  
 GN GNS2.  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 OC Fabales; Fabaceae; Papilionoideae; Pisum.  
 ON NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SEED COAT;  
 RA Buchner P., Wuilleme S., Boutin J.P., Rochat C.;  
 RT "Characterization of a new isolated tissue specific and developmental  
 RT regulated 1,3-b-glucanase gene in pea (Pisum sativum).";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ251646; CAB85903.1; -.  
 DR InterPro; IPR000490; -.  
 DR InterPro; IPR002815; -.  
 DR Pfam; PF00332; Glyco\_hydro\_17; 1.  
 DR ProDom; PD008669; -; 1.  
 DR Signal; Hydrolase; Glycosidase.  
 KW SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 453 BETA-1,3 GLUCANASE.  
 SQ SEQUENCE 453 AA; 49278 MW; BA150E1F8807A888 CRC64;

Query Match 84.2%; Score 32; DB 10; Length 453;  
 Best Local Similarity 71.4%; Pred. No. 68;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 Db 97 QWVTHI 103

RESULT 4  
 Q64981 PRELIMINARY; PRT; 98 AA.  
 ID Q64981;  
 AC Q64981;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)  
 DE MRNA UNKNOWN FUNCTION (523BP) (FRAGMENT).  
 OS Artichoke latent potyvirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 ON NCBI\_TaxID=46076;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Grieco F.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X87255; CAA60708.1; -.  
 DR NON\_TER 1  
 SQ SEQUENCE 98 AA; 11570 MW; C4A6316685E31078 CRC64;

Query Match 81.6%; Score 31; DB 14; Length 98;  
 Best Local Similarity 83.3%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXH 7  
 Db 89 QWAVEH 94

RESULT 5  
 Q90253 PRELIMINARY; PRT; 119 AA.  
 ID Q90253;  
 AC Q90253;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE PHE-13 BOMBESIN PREPROHORMONE.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 ON NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96205965; PubMed=8631814;  
 RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,  
 RA Dong J.Z., Spindel E.R.;  
 RT "There are three distinct forms of bombesin. Identification of  
 RT [leu13]bombesin, [phe13]bombesin, and [ser3,Arg10,Phe13]bombesin in  
 RT the frog Bombina orientalis.";  
 RL J. Biol. Chem. 271:7731-7737(1996).  
 DR EMBL; U49450; AAC59784.1; -.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR ProSITE; PS00257; BOMBESIN; 1.  
 FT CHAIN 45 59 PHE-13 BOMBESIN.  
 SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 81.6%; Score 31; DB 13; Length 119;  
 Best Local Similarity 83.3%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXH 7  
 Db 51 QWAVGH 56

RESULT 6  
 Q27106 PRELIMINARY; PRT; 309 AA.  
 ID Q27106;  
 AC Q27106;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE CYSTEINE PROTEINASE, PUTATIVE.  
 GN CPI.  
 OS Trichomonas vaginalis.  
 OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonas.  
 OX NCBI\_TaxID=5722;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G3;  
 RX MEDLINE=95093621; PubMed=8000542;  
 RA Mallinson D.J., Lockwood B.C., Coombs G.H., North M.J.;  
 RT "Identification and molecular cloning of four cysteine proteinase  
 genes from the pathogenic protozoan Trichomonas vaginalis.";  
 RL Microbiology 140:2725-2735(1994).  
 DR EMBL; X77218; CAA54435.1; -;  
 DR HSP; P07711; ICJL;  
 DR MEROPS; C01.082; -;  
 DR InterPro; IPR000169; -;  
 DR InterPro; IPR000668; -;  
 DR Pfam; PF00112; Peptidase\_C1; 1.  
 PRINTS; PR00705; PAPAIN.  
 DR PROSITE; PS00640; THIOI\_PROTEASE\_ASN; 1.  
 DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; 1.  
 KW Hydrolase; Thiol protease.  
 FT CHAIN 90 309  
 CYSSTEINE PROTEINASE, PUTATIVE.  
 SQ SEQUENCE 309 AA; 34408 MW; B03D5BC6077F69E5 CRC64;  
  
 Query Match 81.6%; Score 31; DB 5; Length 309;  
 Best Local Similarity 83.3%; Pred. No. 73;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 2 QWAVXH 7  
 |||||  
 DB 126 QWAVKH 131  
  
 RESULT 7  
 O93576 PRELIMINARY; PRT; 338 AA.  
 ID O93576  
 AC O93576  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE REELIN (FRAGMENT).  
 GN RELN.  
 OS Lacerta viridis.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Lacertoidea;  
 OC Lacertidae; Lacerta.  
 OX NCBI\_TaxID=65476;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bernier B., Goffinet A.M.;  
 RT "Comparative study of reelin expression in vertebrates.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF090951; AAC36362.1; -;  
 DR EMBL; AF090951; AAC36362.1; -;  
 DR InterPro; IPR000561; -;  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR SMART; SM00181; EGF; 1.  
 KW EGF-like domain; Glycoprotein.  
 FT NON\_TER 1  
 SQ SEQUENCE 338 AA; 38175 MW; C9D2142E115A388B CRC64;  
  
 Query Match 81.6%; Score 31; DB 13; Length 338;  
 Best Local Similarity 57.1%; Pred. No. 81;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 2 QWAVXH 8  
 |||||  
 DB 126 QWAVKH 131

DB 295 QWALDHV 301  
  
 RESULT 8  
 Q9DSP4 PRELIMINARY; PRT; 517 AA.  
 ID O9DSP4  
 AC O9DSP4  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE NS1.  
 OS Saint Croix river virus.  
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.  
 OX NCBI\_TaxID=104581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Attoui H., De Micco P., de Lamballerie X.;  
 RT "Complete nucleotide sequence of Saint Croix river virus.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF145403; AAG34262.1; -;  
 SQ SEQUENCE 517 AA; 58030 MW; 0104A543FB2A1B1A CRC64;  
  
 Query Match 81.6%; Score 31; DB 14; Length 517;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0;  
  
 QY 2 QWAVXH 8  
 |||||  
 DB 500 QWALAHV 506  
  
 RESULT 9  
 O93575 PRELIMINARY; PRT; 615 AA.  
 ID O93575  
 AC O93575  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE REELIN (FRAGMENT).  
 OS Ems orbicularis.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidea; Emydidae; Emys.  
 OX NCBI\_TaxID=82168;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bernier B., Goffinet A.M.;  
 RT "Comparative study of reelin expression in vertebrates.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF090843; AAC35993.1; -;  
 DR InterPro; IPR000561; -;  
 DR InterPro; IPR002860; -;  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF02012; BNR; 2.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR SMART; SM00181; EGF; 1.  
 KW EGF-like domain; Glycoprotein.  
 FT NON\_TER 1  
 SQ SEQUENCE 615 AA; 69837 MW; A074D7AD9979C9DB CRC64;  
  
 Query Match 81.6%; Score 31; DB 13; Length 615  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0;  
  
 QY 2 QWAVXH 8  
 |||||  
 DB 572 QWALDHV 578  
  
 RESULT 10  
 Q9VCU2

ID Q9VCU2 PRELIMINARY; PRT; 696 AA.  
 AC Q9VCU2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE CG4723 PROTEIN.  
 GN CG4723  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Geibart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 FT "the genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003740; AAF56063.1;  
 DR FlyBase; FBgn0039023; CG4723.  
 DR InterPro; IPR000718;  
 DR InterPro; IPR001230;  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR PROSITE; PS00294; PRENYLATION; 1.  
 SQ SEQUENCE 696 AA; 80128 MW; C1997E6B1C9CAD11 CRC64;

Query Match 81.6%; Score 31; DB 5; Length 696;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 Db 150 QWAVXH 155  
 |||||

RESULT 11

Q9NU68  
 ID Q9NU68 PRELIMINARY; PRT; 1273 AA.  
 AC Q9NU68;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE DJ392M17.3 (KIAA0349 PROTEIN) (FRAGMENT).  
 GN DJ392M17.3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Collier R.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL049843; CAB75421.1;  
 DR InterPro; IPR000408;  
 DR PROSITE; PS00626; RCC1\_2; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 1273 AA; 145060 MW; A43DCE0EF4C72B39 CRC64;  
 Query Match 81.6%; Score 31; DB 4; Length 1273;  
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXH 7  
 Db 424 QWAVXH 429  
 |||||

RESULT 12  
 O15057  
 ID O15057 PRELIMINARY; PRT; 1275 AA.  
 AC O15057;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE KIAA0349 (FRAGMENT).  
 GN KIAA0349.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE=97349984; PubMed=9205841;  
 RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,  
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VII.  
 RT The complete sequences of 100 new cDNA clones from human which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 4:141-150(1997).  
 DR EMBL; AB002347; BAA20806.1;  
 DR InterPro; IPR000408;  
 DR InterPro; IPR001841;  
 DR PROSITE; PS00626; RCC1\_2; UNKNOWN\_1.  
 DR SMART; SM00184; RING; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 1275 AA; 145331 MW; 101FF1F66E056066 CRC64;

Query Match 81.6%; Score 31; DB 4; Length 1275;  
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 Db 426 QWAVXH 431  
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RESULT 13
O93574
ID O93574 PRELIMINARY; PRT; 3209 AA.
AC O93574;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE EXTRACELLULAR REELIN (FRAGMENT).
GN RELN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bernier B., Goffinet A.M.;
RT "Comparative study of reelin in vertebrates.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090441; AAC35559.1; -.
InterPro; IPR000561; -.
DR InterPro; IPR002860; -.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF02012; BNR; 15.
DR PROSITE; PS00022; EGF_1; UNKNOWN_7.
DR PROSITE; PS01186; EGF_2; 7.
DR SMART; SM00181; EGF; 1.
KW EGF-like domain; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 3209 AA; 361291 MW; 81A7B6676BCAA3D1 CRC64;

Query Match 81.6%; Score 31; DB 13; Length 3209;
Best Local Similarity 57.1%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNAVXHII 8
DB 3166 QWALDHV 3172
III: I:

RESULT 14
P78509
ID P78509 PRELIMINARY; PRT; 3460 AA.
AC P78509;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE REELIN.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Desilva U., D'Arcangelo G., Braden V.V., Chen J., Miao G.G.,
Curran T., Green E.D.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 194-430 FROM N.A.
RA Lamar B., Wamsley P., Gibson A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79716; AAC51105.1; -.
DR EMBL; AC000121; BAB46357.1; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR002860; -.
DR InterPro; IPR002861; -.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF02012; BNR; 15.
DR Pfam; PF02014; Reeler; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_7.
DR PROSITE; PS01186; EGF_2; 6.
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DR SMART; SM00181; EGF; 1.
KW EGF-like domain; Glycoprotein.
SQ SEQUENCE 3460 AA; 388399 MW; BB2COBA415AB93C1 CRC64;

Query Match 81.6%; Score 31; DB 4; Length 3460.
Best Local Similarity 57.1%; Pred. No. 9.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels

QY 2 QNAVXHII 8
DB 3417 QWALDHV 3423
III: I:

RESULT 15
Q60841
ID Q60841 PRELIMINARY; PRT; 3461 AA.
AC Q60841;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE REELIN (REELER PROTEIN).
GN RELN OR RL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=95231649; PubMed=7715726;
RA D'Arcangelo G., Miao G.G., Chen S.C., Soares H.D., Morgan J.,
Curran T.;
RT "A protein related to extracellular matrix proteins deleted in the
mouse mutant reeler."
RL Nature 374:719-723(1995).
RN [2]
RP SEQUENCE OF 2581-3461 FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE=95375789; PubMed=7647795;
RA Hirotsune S., Takahara T., Sasaki N., Hirose K., Yoshiki A.,
Ohashi T., Kusakabe M., Murakami Y., Muramatsu M., Watanabe J.,
Nakao K., Katsuki M., Hayashizaki Y.;
RA "The reeler gene encodes a protein with an EGF-like motif ex-
posed in pioneer neurons."
RL Nat. Genet. 10:77-83(1995).
RN [3]
RP SEQUENCE OF 2581-3461 FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE=96021025; PubMed=7550305;
RA Curran T., D'Arcangelo G., Goffinet A., Hayashizaki Y.;
RT "Reeler gene discrepancies."
RL Nat. Genet. 11:112-113(1995).
DR EMBL; U24703; AAB91599.1; -.
DR EMBL; D63520; BAA09788.1; -.
DR MGD; MGI:103022; Reln.
DR InterPro; IPR000561; -.
DR InterPro; IPR002860; -.
DR InterPro; IPR002861; -.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF02012; BNR; 15.
DR Pfam; PF02014; Reeler; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_7.
DR PROSITE; PS01186; EGF_2; 6.
DR SMART; SM00181; EGF; 1.
KW EGF-like domain; Glycoprotein.
SQ SEQUENCE 3461 AA; 387510 MW; 4131F3E84A9D4AE2 CRC64;

Query Match 81.6%; Score 31; DB 11; Length 3461.
Best Local Similarity 57.1%; Pred. No. 9.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels
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Qy 2 QWAVXHI 8  
| | | : | :  
Db 3418 QWALDHW 3424

Search completed: October 25, 2001, 11:27:45  
Job time: 448 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:28:29 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-7

Perfect score: 38

Sequence: 1 QWAVXHI 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

1 number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	86.8	14	1 ALYT_ALYOB	P08944 alytes obst
2	33	86.8	107	1 BOMB_BOMVA	P01296 bombina var
3	33	86.8	119	1 BOMB_BOMOR	P21591 bombina ori
4	31	81.6	9	1 LITO_LITAU	P08945 litoria aur
5	31	81.6	13	1 BOML_PSEGU	P42991 pseudophryn
6	31	81.6	82	1 RANA_RANPI	P08950 rana pipien
7	30	78.9	120	1 NEUB_XENLA	P43443 xenopus lae
8	30	78.9	406	1 UL43_VZVD	P02273 varicella-z
9	30	78.9	458	1 GYP6_YEAST	P32806 saccharomyc
10	30	78.9	909	1 HEX_ADEM1	P48308 mouse adeno
11	30	78.9	937	1 HEX_ADE07	P36851 human adeno
12	30	78.9	940	1 HEX_ADE16	P36854 human adeno
13	30	78.9	944	1 HEX_ADE03	P36849 human adeno
14	29	76.3	122	1 YHDM_ECOLI	P36677 escherichia
15	29	76.3	232	1 YB9H_YEAST	P38340 saccharomyc
16	29	76.3	262	1 ATP6_HAETN	P43719 haemophilus
17	29	76.3	263	1 IML2_DROME	Q09024 drosophila
18	29	76.3	265	1 IHA_SHEEP	P38440 ovis aries
19	29	76.3	270	1 ATP6_VIBAL	P12984 vibrio algi
20	29	76.3	271	1 ATP6_ECOLI	P00855 escherichia
21	29	76.3	272	1 ATP6_BUCAP	O51878 buchnera ap
22	29	76.3	274	1 ATP6_BUCAI	P57118 buchnera ap
23	29	76.3	360	1 IHA_BOVIN	P07994 bos taurus
24	29	76.3	364	1 IHA_PIG	P04087 sus scrofa
25	29	76.3	366	1 IHA_MOUSE	Q04997 mus muscula
26	29	76.3	366	1 IHA_RAT	P17490 rattus norv
27	29	76.3	395	1 ZAAA_PEA	P36875 pisum sativ
28	29	76.3	427	1 CG23_YEAST	P24870 saccharomyc
29	29	76.3	769	1 SWI6_KLULA	P40418 kluyveromyc
30	28	73.7	10	1 GRP_RANRI	P23260 rana ridibu
31	28	73.7	25	1 GRP_SCYCA	P09472 scyllorhinu
32	28	73.7	27	1 GRP_CANFA	P08989 canis famil
33	28	73.7	27	1 GRP_CHICK	P01295 gallus gall

34 28 73.7 27 1 GRP\_PIG P01294  
35 28 73.7 28 1 GRP\_ALIMI P3188  
36 28 73.7 131 1 RS11\_AERPE Q9VBF  
37 28 73.7 134 1 GRP\_SHEEP P47851  
38 28 73.7 147 1 GRP\_RAT P24393  
39 28 73.7 148 1 GRP\_HUMAN P07492  
40 28 73.7 155 1 GRP\_BOMOR P29007  
41 28 73.7 197 1 YCB7\_PSEDE P2994  
42 28 73.7 250 1 AGI8\_SOLCO Q22321  
43 28 73.7 276 1 SACT\_BACSU P26212  
44 28 73.7 308 1 ACPI\_ENTHI P36184  
45 28 73.7 361 1 IHA\_TRIVU O77755

#### ALIGNMENTS

RESULT 1  
ALYT\_ALYOB  
ID ALYT\_ALYOB STANDARD; PRT; 14 AA.  
AC P08944:  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE ALYTESIN.

OS Alytes obstetricans (Midwife toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.  
OX NCBI\_TaxID=8443;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=84131098; PubMed=6141890;  
RA Ersamer V., Ersamer G.F., Mazzanti G., Endean R.;  
RT "Active peptides in the skins of one hundred amphibian species from  
RT Australia and Papua New Guinea";  
RL Comp. Biochem. Physiol. 77C:99-108(1984).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.

DR InterPro; IPR000874;  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 14 14 AMIDATION.  
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 86.8%; Score 33; DB 1; Length 14;  
Best Local Similarity 71.4%; Pred. No. 0.42;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 7 QWAVGHL 13

RESULT 2  
BOMB\_BOMVA  
ID BOMB\_BOMVA STANDARD; PRT; 107 AA.  
ID P01296:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE BOMBESIN PRECURSOR.  
OS Bombina variegata (Yellow-bellied toad), and  
OS Bombina bombina (fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina  
OX NCBI\_TaxID=8348, 8345;  
RN [1]

RP SEQUENCE FROM N.A.  
RC SPECIES=B.variegata; TISSUE=Skin;  
RX MEDLINE=90242964; PubMed=2335218;

RA Richter K., Egger R., Kreil G.;  
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
 of Bombina variegata.";  
 RL FEBS Lett. 262:353-355(1990).  
 RN [2]  
 RP SEQUENCE OF 42-55.  
 RC SPECIES=B.variegata, and B.bombina;  
 RX MEDLINE=72163516; PubMed=4537042;  
 RA Anastasi A., Erspamer V., Buccì M.;  
 RT "Isolation and amino acid sequences of altytesin and bombesin, two  
 analogous active tetradecapeptides from the skin of European  
 discolloid frogs.";  
 RL Arch. Biochem. Biophys. 148:443-446(1972).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
 GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
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 CC -----  
 DR EMBL; X52447; CAA36686.1; -;  
 DR PIR; A01564; BSTD.  
 DR PIR; B01564; BSTDY.  
 DR PIR; S09095; S09095.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT PEPTIDE 42 55 BOMBESIN.  
 FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;  
 Query Match 86.88; Score 33; DB 1; Length 107;  
 Best Local Similarity 71.4%; Pred. No. 2.9;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 DQ 48 QWAVGHL 54  
 |||||  
 2 QWAVXHI 8  
 48 QWAVGHL 54

RESULT 3  
 BOMB\_BOMBOR STANDARD; PRT; 119 AA.  
 AC P21591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE BOMBESIN PRECURSOR.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088602; PubMed=2263631;  
 RA Spindel E.R., Gibson B.W., Reeve J.R., Kelly M.;  
 RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
 relationship between bombesin and gastrin-releasing peptide.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
 CC -!- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN  
 THE SKIN AND THE BRAIN.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
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 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; M55255; AAA48551.1; -;  
 DR PIR; A39261; A39261.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 58 BOMBESIN.  
 FT PEPTIDE 45 58  
 FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2A45A44A CRC64;  
 Query Match 86.88; Score 33; DB 1; Length 119;  
 Best Local Similarity 71.4%; Pred. No. 3.2;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps  
 QY 2 QWAVXHI 8  
 DQ 51 QWAVGHL 57  
 |||||  
 RESULT 4  
 LITO\_LITAU STANDARD; PRT; 9 AA.  
 AC P08945;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LITORIN.  
 OS Litoria aurea (Australian frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75187011; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Eudean R.;  
 RT "Amino acid composition and sequence of litorin, a bombesin-like  
 nonapeptide from the skin of the Australian leptodactylid frog  
 Litoria aurea.";  
 RL Experientia 31:510-511(1975).  
 RN [2]  
 RP SEQUENCE (METHYLATED VARIANT).  
 RX MEDLINE=78003546; PubMed=908397;  
 RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Eudean R.;  
 RT "Glu(Ome)3-litorin, the second bombesin-like peptide occurring in  
 methanol extracts of the skin of the Australian frog Litoria aurea.";  
 RL Experientia 33:1289-1289(1977).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
 CC PIR; S07204; S07204.  
 DR PIR; S07205; S07205.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Methylation.  
 FT MOD\_RES 1  
 OF PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 2 2 METHYLATION (IN A VARIANT).  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1103 MW; D7CCCE1E862CDC366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 9;  
Best Local Similarity 83.3%; Pred. No. 9.3e+04;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
Db 2 QWAVGH 7

RESULT 5  
BOML\_PSEGU STANDARD; PRT; 13 AA.  
AC P42991.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
OS BOMBESIN-LIKE PEPTIDE L (PG-L).  
OC Pseudophryne guentheri (Frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.",  
RL Peptides 11:299-304(1990).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.

DR PIR; A60409.  
DR InterPro; IPR000874; .  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT MOD\_RES 1 1  
FT MOD\_RES 13 13  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 13;  
Best Local Similarity 83.3%; Pred. No. 1;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
Db 6 QWAVGH 11

RESULT 6  
RANA\_RANPI STANDARD; PRT; 82 AA.  
AC P08950;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE RANATENSIN PRECURSOR.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88330837; PubMed=2458345;  
RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;

RT "Molecular cloning of cDNAs encoding the human bombesin-like peptide  
RT neuromedin B. Chromosomal localization and comparison to cDNA;  
RT encoding its amphibian homolog ranatensin.",  
RL J. Biol. Chem. 263:13317-13323(1988).  
RN [2]  
RP SEQUENCE OF 48-58.  
RA Nakajima T., Tanimura T., Pisano J.J.;  
RT "Isolation and structure of a new vasoactive polypeptide.",  
RL Fed. Proc. 29:282-282(1970).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.

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CC  
DR EMBL; M21552; AAA49533.1; .  
DR PIR; B28945; B28945  
DR InterPro; IPR000874; .  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 27 POTENTIAL.  
FT PROPEP 28 47  
FT PEPTIDE 48 58  
FT MOD\_RES 58 58  
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 81.6%; Score 31; DB 1; Length 82;  
Best Local Similarity 83.3%; Pred. No. 5.8;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
Db 51 QWAVGH 56

RESULT 7  
NEUB\_XENLA STANDARD; PRT; 120 AA.  
AC P43443.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE NEUROMEDIN B PRECURSOR.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93028554; PubMed=1409705;  
RA Wechsberger C., Kreil G., Richter K.;  
RT "Isolation and sequence of a cDNA encoding the precursor of a  
RT bombesin-like peptide from brain and early embryos of Xenopus  
RT laevis.",  
RL Proc. Natl. Acad. Sci. U.S.A. 89:9819-9822(1992).  
CC -!- FUNCTION: MAY BE A GROWTH FACTOR REQUIRED FOR THE HIGH RATE OF  
CC CELL DIVISION ENSUING AFTER FERTILIZATION, OR MAY HAVE A ROLE IN  
CC SECRETAGOGUE THAT TRIGGERS THE RELEASE OF STORED COMPONENTS.  
CC -!- TISSUE SPECIFICITY: BRAIN, INTESTINE, AND OVARIES AND EARLY  
CC EMBRYOS (STAGES 2 AND 10).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.

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CC -----

DR EMBL; L01530; AAA49912.1; -;  
DR InterPro; IPR000874; -;  
DR Pfam; PF02044; Bombesin; 1;  
DR PROSITE; PS00257; BOMBESIN; 1;  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW SIGNAL.  
FT SIGNAL 1 29 POTENTIAL.  
FT PROPEP 30 44  
FT PEPTIDE 45 54 NEUROMEDIN B.  
FT MOD\_RES 54 54 AMIDATION (G-55 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 120 AA; 14384 MW; 2CB146BA082A2442 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 120;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXH 7  
|||: |  
Db 47 QWAIHG 52

## RESULT 8

UL43\_VZVD  
ID UL43\_VZVD STANDARD; PRT; 406 AA.  
AC P09273;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE GENE 15 MEMBRANE PROTEIN.  
GN 15.  
OS Varicella-zoster virus (strain Dumas) (VZV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_TaxID=10338;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86306657; PubMed=3018124;  
RA Davison A.J., Scott J.E.;  
RA "The complete DNA sequence of varicella-zoster virus.";  
J. Gen. Virol. 67:1759-1816(1986).  
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED OR TRANSMEMBRANE  
CC PROTEIN (POTENTIAL).  
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL43,  
CC EHV-1 17, AND VZV 15.  
CC -----

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CC -----

DR EMBL; X04370; CAA27898.1; -;  
DR PIR; F27342; WZBE15.  
KW Membrane.  
SQ SEQUENCE 406 AA; 44524 MW; 726DF7D084DE5387 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 406;  
Best Local Similarity 66.7%; Pred. No. 42;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WAVXHI 8

Db 280 WAISHI 285  
||: ||

## RESULT 9

GYP6\_YEAST  
ID GYP6\_YEAST STANDARD; PRT; 458 AA.  
AC P32806;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE GYPASE-ACTIVATING PROTEIN OF YPT6.  
GN GYP6 OR YJL044C OR J1202.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93180913; PubMed=8441469;  
RA Strom M., Vollmer P., Tan T.J., Gallwitz D.;  
RA "A yeast GTPase-activating protein that interacts specifically with a  
RT member of the Ypt/Rab family.";  
RL Nature 361:736-739(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Pohl T.M., Aljinovic G.;  
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: STIMULATES SPECIFICALLY THE GTPASE ACTIVITY OF YPT6.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).  
CC -----

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CC -----

DR EMBL; X68506; CAA48518.1; -;  
DR EMBL; Z49319; CAA89335.1; -;  
DR PIR; S30061; S30061.  
DR SWISS-2DPAGE; P32806; YEAST.  
DR YEPD; 5590; -;  
DR SGD; S0003580; GYP6.  
DR InterPro; IPR000195; -;  
DR Pfam; PF00566; TBC; 1.  
KW GTPase activation.  
FT CONFLICT 413 F -> L (JN REF. 1).  
SQ SEQUENCE 458 AA; 53814 MW; DDC21820E00EE06C CRC64;

Query Match 78.9%; Score 30; DB 1; Length 458;  
Best Local Similarity 66.7%; Pred. No. 47;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXH 7  
|||: |  
Db 6 QWAIHG 11

## RESULT 10

HEX\_ADEM1  
ID HEX\_ADEM1 STANDARD; PRT; 909 AA.  
AC P48308; O11839;

DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HEXON PROTEIN (LATE PROTEIN 2).  
GN PII.

OS Mouse adenovirus type 1 (MAV-1).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10530;

```

RN SEQUENCE FROM N.A.
RC STRAIN=FL;
RX MEDLINE=94157453; PubMed=7509368;
RA Weber J.M., Cai F., Murali R., Burnett R.M.;
RT "Sequence and structural analysis of murine adenovirus type 1 hexon.";
RL J. Gen. Virol. 75:141-147(1994).
RN [2]
RP REVISIONS TO 443.
RA Weber J.M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE
CC VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
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CC -----
DR EMBL; M81889; AAB48187.1; -.
DR HSSP; P03277; 1DHX.
DR InterPro; IPR000736; -.
DR Pfam; PF01065; Adeno_hexon; 1.
DR Coat protein; Hexon protein; Late protein.
DR SEQUENCE 909 AA; 102368 MW; 7E1C17DF7F0E95A0 CRC64;
SQ
Query Match 78.9%; Score 30; DB 1; Length 909;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 QWAVXHI 8
DB 9 QWAFMHI 15
RESULT 11
HEX_ADE07
ID HEX_ADE07 STANDARD; PRT; 937 AA.
AC P36851;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEXON PROTEIN (LATE PROTEIN 2).
PII.
Human adenovirus type 7.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10519;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=GMEN;
RX MEDLINE=96431672; PubMed=8834754;
RA Pring-Akerblom P., Trijssenaar F.E.J., Adrian T.;
RT "Hexon sequence of adenovirus type 7 and comparison with other
RT serotypes of subgenus B.";
RL Res. Virol. 146:383-388(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE
CC VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
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CC -----
DR EMBL; X76551; CAA54053.1; -.

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DR PIR; S39301; S39301.
DR HSSP; P03277; 1DHX.
DR InterPro; IPR000736; -.
DR Pfam; PF01065; Adeno_hexon; 1.
DR Coat protein; Hexon protein; Late protein.
DR SEQUENCE 937 AA; 105839 MW; 7C6348A51BF5C42D CRC64;
SQ
Query Match 78.9%; Score 30; DB 1; Length 937;
Best Local Similarity 71.4%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 QWAVXHI 8
DB 9 QWAYMHI 15
RESULT 12
HEX_ADE16
ID HEX_ADE16 STANDARD; PRT; 940 AA.
AC P36854;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEXON PROTEIN (LATE PROTEIN 2).
PII.
Human adenovirus type 16.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31544;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ISOLATE CH.79;
RX MEDLINE=95407102; PubMed=7676636;
RA Pring-Akerblom P., Trijssenaar J., Adrian T.;
RT "Sequence characterization and comparison of human adenovirus
RT subgenus B and E hexons.";
RL Virology 212:232-236(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE
CC VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
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CC -----
DR EMBL; X74662; CAA52726.1; -.
DR PIR; S37216; S37216.
DR HSSP; P03277; 1DHX.
DR InterPro; IPR000736; -.
DR Pfam; PF01065; Adeno_hexon; 1.
DR Coat protein; Hexon protein; Late protein.
DR SEQUENCE 940 AA; 105501 MW; E5A3493E68236D15 CRC64;
SQ
Query Match 78.9%; Score 30; DB 1; Length 940;
Best Local Similarity 71.4%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 QWAVXHI 8
DB 9 QWAYMHI 15
RESULT 13
HEX_ADE03
ID HEX_ADE03 STANDARD; PRT; 944 AA.
AC P36849;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

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DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE HEXON PROTEIN (LATE PROTEIN 2).  
 GN P1.  
 OS Human adenovirus type 3.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=45659;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ISOLATE GB;  
 RX MEDLINE=95407102; PubMed=7676636;  
 RA Pring-Akerblom P., Trijsenaar J., Adrian T.;  
 RT "Sequence characterization and comparison of human adenovirus  
 RT subgenus B and E hexons.";  
 RL Virology 212:232-236(1995).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN=ISOLATE GB;  
 RC Pring-Akerblom P.;  
 RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RA -!- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE  
 RA VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.  
 CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
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 CC -----  
 DR EMBL; X76549; CAA54051.1; -;  
 DR PIR; S39298; S39298.  
 DR HSSP; P03277; LDHX.  
 DR InterPro; IPR000736; -;  
 DR Pfam; PF01065; Adeno\_hexon.1.  
 KW Coat protein; Hexon protein; Late protein.  
 SQ SEQUENCE 944 AA; 16088 MW; E779C679417F49D9 CRC64;  
 Query Match 78.9%; Score 30; DB 1; Length 944;  
 Best Local Similarity 71.4%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 Db ||| ||  
 9 QWAYMHI 15  
 RESULT 14  
 YHDI\_ECOLI  
 ID YHDI\_ECOLI STANDARD; PRT; 122 AA.  
 AC P36677;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HYPOTHETICAL 13.9 KDA PROTEIN IN MSLC-RPLQ INTERGENIC REGION.  
 GN YHDI.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94341562; PubMed=8063098;  
 RA Christie G.E., White T.J., Goodwin T.S.;  
 RT "A merR homologue at 74 minutes on the Escherichia coli genome.";  
 RL Gene 146:131-132(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
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 CC -----  
 DR EMBL; L29458; AAA24774.1; -;  
 DR EMBL; U18997; AAA58090.1; -;  
 DR EMBL; AE000407; AAC76318.1; -;  
 DR EcoGene; EG11970; yhdN.  
 KW Hypothetical protein.  
 SQ SEQUENCE 122 AA; 13945 MW; F404919BA6590DF3 CRC64;  
 Query Match 76.3%; Score 29; DB 1; Length 122;  
 Best Local Similarity 71.4%; Pred. No. 21;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 Db ||| ||  
 6 QWAERHI 12  
 RESULT 15  
 YB9H\_YEAST  
 ID YB9H\_YEAST STANDARD; PRT; 232 AA.  
 AC P38340;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE HYPOTHETICAL 26.1 KDA PROTEIN IN POP4-SHMI INTERGENIC REGION.  
 GN YBR261C OR YBR1729.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=93220397; PubMed=8465606;  
 RA Daignon F., Biteau N., Crouzet M., Aigle M.;  
 RT "The complete sequence of a 19,482 bp segment located on the right  
 RT arm of chromosome II from Saccharomyces cerevisiae.";  
 RL Yeast 9:189-199(1993).  
 CC -!- SIMILARITY: TO S.POMBE SPAC16E8.14C.  
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 CC -----  
 DR EMBL; X70529; CAA49926.1; -;  
 DR EMBL; Z36130; CAA85224.1; -;  
 DR PIR; S32963; S32963.  
 DR SGD; S0000465; YBR261C.  
 KW Hypothetical protein.  
 SQ SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;  
 Query Match 76.3%; Score 29; DB 1; Length 232;  
 Best Local Similarity 57.1%; Pred. No. 39;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0;

Oy 2 QWAVXHI 8  
| | | |  
Db 139 QMCVGH 145

Search completed: October 25, 2001, 11:28:29  
Job time: 477 sec

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	33	86.8	14	1	BSTD	bombesin - fire-be
2	33	86.8	107	1	BSTDY	bombesin precursor
3	33	86.8	119	2	A3261	bombesin precursor
4	32	84.2	453	2	T50645	glucan endo-1,3-be
5	31	81.6	9	2	S07204	litorin I - Austr
6	31	81.6	13	2	A60409	bombesin-like pept
7	31	81.6	82	2	B28945	ranatensin precurs
8	31	81.6	309	2	S41427	cysteine proteinas
9	31	81.6	3461	2	S58870	reelin precursor -
10	30	78.9	120	2	A47201	bombesinlike pepti
11	30	78.9	174	2	A45665	hypothetical prote
12	30	78.9	289	2	A82953	ATP synthase A cha
13	30	78.9	353	2	T34312	hypothetical prote
14	30	78.9	406	1	W2BE15	gene 15 protein -
15	30	78.9	458	2	S56816	GFPase-activating
16	30	78.9	505	2	T10896	cytochrome P450 (E
17	30	78.9	574	2	G63769	pyruvate oxidase h
18	30	78.9	574	2	T00245	reverse transcript
19	30	78.9	936	2	S57637	hexon protein - hu
20	30	78.9	937	2	S39301	hexon protein - hu
21	30	78.9	937	2	S35504	hexon protein - hu
22	30	78.9	940	2	T37216	hexon protein - hu
23	30	78.9	942	2	S39298	hexon protein - hu
24	30	78.9	1041	2	PQ0442	polyprotein - barl
25	30	78.9	1213	2	T37959	hypothetical prote
26	30	78.9	13055	2	T16580	hypothetical prote
27	29	76.3	95	2	H83378	hypothetical prote
28	29	76.3	122	2	I67893	hypothetical prote
29	29	76.3	122	2	B85994	hypothetical prote

F;42-55/Product: bombesin #status experimental <MAT>  
 F;56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
 F;42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F;55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 86.8%; Score 33; DB 1; Length 107;  
 Best Local Similarity 71.4%; Pred. No. 6.2;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
 |||||  
 Db 48 QWAVGHL 54

RESULT 3

A39261 bombesin precursor - Bombina orientalis

C;Species: Bombina orientalis  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999  
 C;Accession: A39261

R;Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990

A;Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet  
 A;Reference number: A39261; MUID:91088602

A;Accession: A39261

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-119 <SPI>

A;Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017

A;Superfamily: ranatensin

C;Keywords: neuropeptide

Query Match 86.8%; Score 33; DB 2; Length 119;  
 Best Local Similarity 71.4%; Pred. No. 6.9;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
 |||||  
 Db 51 QWAVGHL 57

RESULT 4

T50645 glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) [imported] - garden pea

C;Species: Pisum sativum (garden pea)

C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 02-Sep-2000

C;Accession: T50645

R;Buchner, P.; Willeme, S.; Boutin, J.P.; Rochat, C.

submitted to the EMBL Data Library, November 1999

A;Description: Characterization of a new isolated tissue specific and developmental regu

A;Reference number: Z25152

A;Accession: T50645

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-453 <BUC>

A;Cross-references: EMBL:AJ251646; PIDN:CAB85903.1

C;Genetics:

A;Gene: gns2

C;Superfamily: beta-1,3-glucanase

C;Keywords: glycosidase; hydrolase

Query Match 84.2%; Score 32; DB 2; Length 453;  
 Best Local Similarity 71.4%; Pred. No. 41;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
 |||||  
 Db 97 QWVTHI 103

RESULT 5

S07204 litorin I - Australian tree frog (Litoria aurea)

C;Species: Litoria aurea

C;Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000

C;Accession: S07204

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 510-511, 1975

A;Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide f

A;Reference number: S07204; MUID:75187011

A;Accession: S07204

A;Molecule type: protein

A;Residues: 1-9 <ANA>

C;Superfamily: gastrin-releasing peptide

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 9;

Best Local Similarity 83.3%; Pred. No. 2.2e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7

|||||

Db 2 QWAVGH 7

RESULT 6

A60409

bombesin-like peptide L - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C;Accession: A60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.P.; H

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the

A;Reference number: A60409; MUID:90287814

A;Accession: A60409

A;Molecule type: protein

A;Residues: 1-13 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 13;

Best Local Similarity 83.3%; Pred. No. 2;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7

|||||

Db 6 QWAVGH 11

RESULT 7

B28945

ranatensin precursor - northern leopard frog

C;Species: Rana pipiens (northern leopard frog)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999

C;Accession: B28945

R;Krane, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.

J. Biol. Chem. 263, 13317-13323, 1988

A;Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromod

A;Reference number: A92667; MUID:88330837

A;Accession: B28945

A;Molecule type: mRNA

A;Residues: 1-82 <KRA>

A;Cross-references: GB:M21552; GB:J03948; NID:g213693; PIDN:AAAA495 .1; PID:g213693

C;Superfamily: ranatensin

C;Keywords: neuropeptide

Query Match 81.6%; Score 31; DB 2; Length 82;  
Best Local Similarity 83.3%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
Db 51 QWAVGH 56

RESULT 8  
S41427  
cysteine proteinase (EC 3.4.22.-) CPl precursor - Trichomonas vaginalis  
C:Species: Trichomonas vaginalis  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 04-Feb-2000  
C:Accession: S41427  
R:Malinson, D.J.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41425  
A:Accession: S41427  
A:Molecule type: mRNA  
A:Residues: 1-309 <MAL>  
A:Cross-references: EMBL:X77218; NID:g452291; PIDN:CAA54435.1; PID:g452292  
A:Experimental source: G3  
C:Genetics:  
A:Gene: CPl  
A:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase  
F:1-89/Domain: signal sequence #status predicted <SIG>  
F:90-309/Product: cysteine proteinase CPl #status predicted <MAT>  
F:114,254,274/Active site: Cys, His, Asn #status predicted

Query Match 81.6%; Score 31; DB 2; Length 309;  
Best Local Similarity 83.3%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
Db 126 QWAVKH 131

RESULT 9  
S58870  
reelin precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 11-Jan-2000  
C:Accession: S58870; S71844; I49297  
R:Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.  
Fire 374, 719-723, 1995  
A:Title: A protein related to extracellular matrix proteins deleted in the mouse mutant  
A:Reference number: I49297; MUID:95231649  
A:Accession: S58870  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-3461 <DAR>  
A:Cross-references: EMBL:U24703; NID:g902486; PID:g902487  
R:D'Arcangelo, G.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: S71844  
A:Accession: S71844  
A:Molecule type: mRNA  
A:Residues: 1-215, 'T', 217-1905, 'S', 1907-3355, 'V', 3357-3391, 'N', 3393-3461 <DA2>  
A:Cross-references: EMBL:U24703; NID:g902486; PID:g902487  
C:Superfamily: unassigned EGF-related proteins; EGF homology  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-3461/Product: reelin #status predicted <MAT>  
F:1769-1795/Domain: EGF homology <EGF>

Query Match 81.6%; Score 31; DB 2; Length 3461;  
Best Local Similarity 57.1%; Pred. No. 4.9e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
|||||  
Db 3418 QWALDHV 3424

RESULT 10  
A47201  
bombesinlike peptide - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Feb-1998  
C:Accession: A47201  
R:Wechselberger, C.; Kreil, G.; Richter, K.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9819-9822, 1992  
A:Title: Isolation and sequence of a cDNA encoding the precursor of a bombesin-like peptide  
A:Reference number: A47201; MUID:93028554  
A:Accession: A47201  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-120 <WEC>  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:115857, NCBIN:115858)  
C:Superfamily: ranatensin

Query Match 78.9%; Score 30; DB 2; Length 120;  
Best Local Similarity 66.7%; Pred. No. 29;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
Db 47 QWAIGH 52

RESULT 11  
T45665  
hypothetical protein F14P22.40 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T45665  
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; et al.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z23011  
A:Accession: T45665  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-174 <DAN>  
A:Cross-references: EMBL:AL137082  
A:Experimental source: cultivar Columbia; BAC clone F14P22  
C:Genetics:  
A:Map position: 3  
A:Introns: 90/1; 126/3; 166/2  
A:Note: F14P22.40

Query Match 78.9%; Score 30; DB 2; Length 174;  
Best Local Similarity 57.1%; Pred. No. 41;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
|||||  
Db 47 EWAVDHL 53

RESULT 12  
AB2953  
ATP synthase A chain PA5560 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Feb-2000  
C:Accession: AB2953  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrington, J.; Beckwith, J.; Adams, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kjos, M.; Laribak, L.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: A82953  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-289 <STO>  
A:Cross-references: GB:AE004967; GB:AE004091; NID:g9951884; PIDN:AAG08945.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: atpB; PA5560

Query Match 78.9%; Score 30; DB 2; Length 289;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHI 8  
||| |  
258 WAVFHI 263

RESULT 13  
T34312  
hypothetical protein F59G1.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T34312  
R:Latreille, P.  
submitted to the EMBL Data Library, April 1996  
A:Description: The sequence of C. elegans cosmid F59G1.  
A:Reference number: Z21504  
A:Accession: T34312  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-353 <LAT>  
A:Cross-references: EMBL:U53332; PIDN:AAC71158.1; GSPDB:GN000020; CESP:F59G1.4  
A:Experimental source: strain Bristol N2; clone F59G1  
C:Genetics:  
A:Gene: CESP:F59G1.4  
A:Map position: 2  
A:Introns: 23/1; 47/2; 83/3; 114/3; 151/1; 187/2; 229/3; 257/3; 316/1  
C:Superfamily: Caenorhabditis elegans hypothetical protein F59G1.4

Query Match 78.9%; Score 30; DB 2; Length 353;  
Best Local Similarity 57.1%; Pred. No. 83;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
||| |  
201 EWAVNHL 207

RESULT 14  
WZBE15  
gene 15 protein - human herpesvirus 3  
C:Species: human herpesvirus 3, varicella-zoster virus  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 16-Jul-1999  
C:Accession: F27342  
R:Davidson, A.J.; Scott, J.E.  
J. Gen. Virol. 67, 1759-1816, 1986  
A:Title: The complete DNA sequence of varicella-zoster virus.  
A:Reference number: A27345; MUID:86306657  
A:Accession: F27342  
A:Molecule type: DNA  
A:Residues: 1-406 <DAV>  
A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27898.1; PID:g60004  
C:Genetics:  
A:Gene: 15  
C:Superfamily: varicella-zoster virus gene 15 protein

Query Match 78.9%; Score 30; DB 1; Length 406;  
Best Local Similarity 66.7%; Pred. No. 95;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHI 8  
||| |  
280 WAISHI 285

RESULT 15  
S56816  
GTPase-activating protein GYP6 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein J1202; protein YJL044c  
C:Species: Saccharomyces cerevisiae  
C:Date: 08-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 0; MUID:2000  
C:Accession: S56816; S30061  
R:Pohl, T.M.; Aljinovic, G.  
submitted to the Protein Sequence Database, September 1995  
A:Reference number: S56793  
A:Accession: S56816  
A:Molecule type: DNA  
A:Residues: 1-458 <TOV>  
A:Cross-references: EMBL:Z49319; NID:gl008172; PIDN:CAA89335.1; MUID:1008172; MUID:1008172  
R:Strom, M.; Vollmer, P.; Tan, T.J.; Gallwitz, D.  
Nature 361, 736-739, 1993  
A:Title: A yeast GTPase-activating protein that interacts specifically with a membrane protein  
A:Reference number: S30061; MUID:93180913  
A:Accession: S30061  
A:Molecule type: DNA  
A:Residues: 1-412, 414-458 <STR>  
A:Cross-references: EMBL:X68506; NID:g441264; PIDN:CAA48518.1; MUID:10521  
C:Genetics:  
A:Gene: SGD:GYP6  
A:Cross-references: SGD:S0003580; MIPS:YJL044c  
A:Map position: 10L  
C:Superfamily: Saccharomyces cerevisiae GTPase-activating protein GYP6

Query Match 78.9%; Score 30; DB 2; Length 458;  
Best Local Similarity 66.7%; Pred. No. 11e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
||| |  
6 QWAI DH 11

Search completed: October 25, 2001, 11:25:21  
Job time: 334 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-7

Perfect score: 38

Sequence: 1 XQWAVXHI 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

1 number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/6C\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/6D\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	89.5	8	1	US-08-168-390-12
2	34	89.5	8	6	Sequence 12, Appl Patent No. 5217955
3	34	89.5	8	6	Patent No. 5217955
4	34	89.5	9	6	Sequence 1, Appl Patent No. 5217955
5	34	89.5	9	6	Patent No. 5217955
6	34	89.5	9	6	Sequence 2, Appl Patent No. 5217955
7	34	89.5	9	6	Patent No. 5217955
8	34	89.5	9	6	Sequence 3, Appl Patent No. 5217955
9	33	86.8	8	2	US-08-337-127-9
10	33	86.8	8	6	Sequence 9, Appl Patent No. 5217955
11	33	86.8	8	6	Patent No. 5217955
12	33	86.8	9	1	US-07-619-747B-1
13	33	86.8	9	1	Sequence 1, Appl Patent No. 5217955
14	33	86.8	9	1	US-07-619-747B-2
15	33	86.8	9	1	Sequence 2, Appl Patent No. 5217955
16	33	86.8	9	1	US-07-619-747B-4
17	33	86.8	9	1	Sequence 4, Appl Patent No. 5217955
18	33	86.8	9	1	US-07-619-747B-5
19	33	86.8	9	1	Sequence 5, Appl Patent No. 5217955
20	33	86.8	9	1	US-07-619-747B-9
21	33	86.8	9	1	Sequence 9, Appl Patent No. 5217955
22	33	86.8	9	1	US-07-619-747B-10
23	33	86.8	9	1	Sequence 10, Appl Patent No. 5217955
24	33	86.8	9	1	US-07-619-747B-12
25	33	86.8	9	1	Sequence 12, Appl Patent No. 5217955
26	33	86.8	9	1	US-07-619-747B-14
27	33	86.8	9	1	Sequence 14, Appl Patent No. 5217955
28	33	86.8	9	1	US-07-619-747B-15
29	33	86.8	9	1	Sequence 15, Appl Patent No. 5217955
30	33	86.8	9	1	US-07-619-747B-17
31	33	86.8	9	1	Sequence 17, Appl Patent No. 5217955
32	33	86.8	9	1	US-07-619-747B-18
33	33	86.8	9	1	Sequence 18, Appl Patent No. 5217955
34	33	86.8	9	1	US-07-619-747B-22
35	33	86.8	9	1	Sequence 22, Appl Patent No. 5217955
36	33	86.8	9	1	US-07-619-747B-23
37	33	86.8	9	1	Sequence 23, Appl Patent No. 5217955
38	33	86.8	9	1	US-07-619-747B-24
39	33	86.8	9	1	Sequence 24, Appl Patent No. 5217955
40	33	86.8	9	1	US-07-619-747B-25
41	33	86.8	9	1	Sequence 25, Appl Patent No. 5217955
42	33	86.8	9	1	US-07-619-747B-26
43	33	86.8	9	1	Sequence 26, Appl Patent No. 5217955

28	33	86.8	9	1	US-07-619-747B-27	Sequence 27, Appl Patent No. 5217955
29	33	86.8	9	1	US-07-619-747B-28	Sequence 28, Appl Patent No. 5217955
30	33	86.8	9	1	US-07-619-747B-29	Sequence 29, Appl Patent No. 5217955
31	33	86.8	9	1	US-07-619-747B-30	Sequence 30, Appl Patent No. 5217955
32	33	86.8	9	1	US-07-619-747B-31	Sequence 31, Appl Patent No. 5217955
33	33	86.8	9	1	US-07-619-747B-32	Sequence 32, Appl Patent No. 5217955
34	33	86.8	9	1	US-07-619-747B-33	Sequence 33, Appl Patent No. 5217955
35	33	86.8	9	1	US-07-619-747B-34	Sequence 34, Appl Patent No. 5217955
36	33	86.8	9	1	US-07-619-747B-35	Sequence 35, Appl Patent No. 5217955
37	33	86.8	9	1	US-07-619-747B-36	Sequence 36, Appl Patent No. 5217955
38	33	86.8	9	1	US-07-619-747B-37	Sequence 37, Appl Patent No. 5217955
39	33	86.8	9	1	US-07-619-747B-38	Sequence 38, Appl Patent No. 5217955
40	33	86.8	9	1	US-07-619-747B-39	Sequence 39, Appl Patent No. 5217955
41	33	86.8	9	1	US-07-619-747B-40	Sequence 40, Appl Patent No. 5217955
42	33	86.8	9	1	US-08-031-325A-37	Sequence 37, Appl Patent No. 5217955
43	33	86.8	9	1	US-08-263-905-4	Sequence 4, Appl Patent No. 5217955
44	33	86.8	9	1	US-08-263-905-5	Sequence 5, Appl Patent No. 5217955
45	33	86.8	9	1	US-08-263-905-6	Sequence 6, Appl Patent No. 5217955

## ALIGNMENTS

RESULT 1  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELEPHONE: (202) 371-2540  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."

FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "The alanine at position 6  
; OTHER INFORMATION: is dextrorotatory alanine."  
; FEATURE:

; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-12

Query Match 89.5%; Score 34; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAV AHL 8

RESULT 2  
5217955-35  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:35:  
; LENGTH: 8  
5217955-35

Query Match 89.5%; Score 34; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAV AHL 8

RESULT 3  
5217955-36  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:36:  
; LENGTH: 8  
5217955-36

Query Match 89.5%; Score 34; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAV AHL 8

RESULT 4  
5217955-13  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:13:  
; LENGTH: 9  
5217955-13

Query Match 89.5%; Score 34; DB 6; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAV AHL 8

RESULT 5  
5217955-14  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:14:  
; LENGTH: 9  
5217955-14

Query Match 89.5%; Score 34; DB 6; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAV AHL 8

RESULT 6  
5217955-15  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989  
; SEQ ID NO:15:  
; LENGTH: 9  
5217955-15

Query Match 89.5%; Score 34; DB 6; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHI 8  
||||| 1;  
Db 2 QWAVLHL 8

## RESULT 7

5217955-22  
; Patent No. 5217955  
; APPLICANT: aBODGEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989

; SEQ ID NO:22:  
; LENGTH: 9  
5217955-22

Query Match 89.5%; Score 34; DB 6; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHI 8  
||||| 1;  
Db 2 QWAVLHL 8

## RESULT 8

US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK

; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-11

Query Match 86.8%; Score 33; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

Qy 2 QWAVXHI 8  
||||| 1;  
Db 2 QWAVLHL 8

## RESULT 9

US-08-337-127-9  
; Sequence 9, Application US/08337127  
; Patent No. 5877277  
; GENERAL INFORMATION:  
; APPLICANT: Coy, David H.  
; APPLICANT: Moreau, Jacques-Pierre  
; APPLICANT: Kim, Sun H.  
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
; TITLE OF INVENTION: ANALOGS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,127  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/779,039  
; FILING DATE: 10/18/91  
; APPLICATION NUMBER: 07/502,438  
; FILING DATE: 03/30/90  
; APPLICATION NUMBER: 07/397,169  
; FILING DATE: 08/21/89  
; APPLICATION NUMBER: 07/376,555  
; FILING DATE: 07/07/89  
; APPLICATION NUMBER: 07/317,941  
; FILING DATE: 03/02/89  
; APPLICATION NUMBER: 07/282,328  
; FILING DATE: 12/09/88  
; APPLICATION NUMBER: 07/257,998

; FILING DATE: 10/14/88  
; APPLICATION NUMBER: 07/248,771  
; FILING DATE: 09/23/88  
; APPLICATION NUMBER: 07/207,759  
; FILING DATE: 06/16/88  
; APPLICATION NUMBER: 07/204,171  
; FILING DATE: 06/08/88  
; APPLICATION NUMBER: 07/173,311  
; FILING DATE: 03/25/88  
; APPLICATION NUMBER: 07/100,571  
; FILING DATE: 09/24/87  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00537/00900D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The sequence contains at  
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,  
; OTHER INFORMATION: and has an methylester C-terminus (i.e., COOCH3),  
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).  
US-08-337-127-9

Query Match 86.8%; Score 33; DB 2; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAVGHL 8

RESULT 10  
5217955-32  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:32:  
; LENGTH: 8  
5217955-32

Query Match 86.8%; Score 33; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAVGHL 8

RESULT 11  
5217955-34

; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:34:  
; LENGTH: 8  
5217955-34

Query Match 86.8%; Score 33; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
Db 2 QWAVGHL 8

RESULT 12  
US-07-619-747B-1  
; Sequence 1, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanee Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide

;  
;  
;  
; FEATURE:  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-1

Query Match 86.8%; Score 33; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

QY 2 QWAVXHI 8  
DB 2 QWAVGHL 8

RESULT 13  
US-07-619-747B-2  
; Sequence 2, Application US/07619747B  
; Patent No. 5244883

GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-2

Query Match 86.8%; Score 33; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

QY 2 QWAVXHI 8

DB 2 QWAVGHL 8  
RESULT 14

US-07-619-747B-4  
; Sequence 4, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is 5F-D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-4

Query Match 86.8%; Score 33; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;

QY 2 QWAVXHI 8  
DB 2 QWAVGHL 8

RESULT 15  
US-07-619-747B-5  
; Sequence 5, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,

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; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION: Position 1 is D-Tpi
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: isostere of named aminoacid
;
US-07-619-747B-5

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; Query Match 86.8%; Score 33; DB 1; Length 9;
; St Local Similarity 71.4%; Pred. No. 1.5e+05;
; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
Qy 2 QWAVXHI 8
Db 2 QWAVGHL 8

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Search completed: October 25, 2001, 11:23:56  
Job time: 269 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-7  
Perfect score: 38  
Sequence: 1 XQWAVXHI 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

1 number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT:\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
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13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	8	21 AAB08310	Amino acid sequenc
2	35	92.1	245	19 AAW64220	Human secreted pro
3	35	92.1	336	21 AAY44245	Human cell signall
4	34	89.5	7	10 AAP91147	Sequence of new ne
5	34	89.5	7	13 AAR20585	Antagonist of bomb
6	34	89.5	7	13 AAR32998	[D-Ala11]-bombesin
7	34	89.5	7	20 AAW94610	Bombesin/gastrin r
8	34	89.5	8	3 AAP20294	Bombesin analog pe
9	34	89.5	8	12 AAR11241	Linear litorin ana
10	34	89.5	8	12 AAR11242	Linear litorin ana
11	34	89.5	8	13 AAR29155	Bombesin analogue

12	34	89.5	8	13 AAR29157	Bombesin analogue
13	34	89.5	8	16 AAW64911	Bombesin receptor
14	34	89.5	9	11 AAR09335	Sequence of Bombes
15	34	89.5	9	12 AAR11522	Example of peptide
16	34	89.5	9	12 AAR14865	Peptide analogue #
17	34	89.5	9	12 AAR14866	Peptide analogue #
18	34	89.5	9	12 AAR14867	Peptide analogue #
19	34	89.5	9	12 AAR14873	Peptide analogue #
20	34	89.5	9	14 AAR40903	Bombesin analogue
21	34	89.5	9	19 AAW51195	Peptide derived fr
22	34	89.5	9	19 AAW51201	Peptide derived fr
23	34	89.5	10	10 AAP96113	Sequence of new ne
24	33	86.8	7	22 AAB48341	Bombesin/gastrin-r
25	33	86.8	8	11 AAR04531	Non-cyclic analogu
26	33	86.8	8	12 AAR11224	Linear litorin ana
27	33	86.8	8	12 AAR11240	Linear litorin ana
28	33	86.8	8	12 AAR14877	Peptide analogue #
29	33	86.8	8	13 AAR28456	Bombesin antagonis
30	33	86.8	8	13 AAR28459	Bombesin antagonis
31	33	86.8	8	16 AAW64910	Bombesin receptor
32	33	86.8	8	19 AAW50941	Bombesin antagonis
33	33	86.8	8	20 AAW92740	Bombesin peptide a
34	33	86.8	8	21 AAB08302	Amino acid sequenc
35	33	86.8	8	21 AAB08308	Amino acid sequenc
36	33	86.8	8	22 AAB72406	Bombesin analogue
37	33	86.8	9	11 AAR04526	Non-cyclic analogu
38	33	86.8	9	11 AAR04527	Non-cyclic analogu
39	33	86.8	9	11 AAR04529	Non-cyclic analogu
40	33	86.8	9	11 AAR04528	Non-cyclic analogu
41	33	86.8	9	11 AAR04530	Non-cyclic analogu
42	33	86.8	9	11 AAR08345	Peptide bombesin
43	33	86.8	9	12 AAR11520	Example of peptide
44	33	86.8	9	12 AAR11521	Example of peptide
45	33	86.8	9	12 AAR11525	Example of peptide

#### ALIGNMENTS

RESULT 1  
AAB08310  
ID AAB08310 standard; peptide; 8 AA.  
XX  
AC AAB08310;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE Amino acid sequence of antiangiogenic peptide DT-27.  
XX  
KW Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2.  
KW VIP1; VIP2; VIP3; BOM1; bombesin; SPL; substance P; Mm. 7; tumour growth;  
KW tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;  
KW leukaemia; lymphoma.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "D-form residue"  
FT Modified-site 6 /label= Aib  
FT Modified-site 8 /note= "alpha-aminoisobutyric acid"  
FT Modified-site 8 /note= "amidated residue"  
FT WO200047221-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US03559.  
XX  
PR 11-FEB-1999; 99US-0248381.  
XX

PA (NAIM-) NAT INST IMMUNOLOGY.  
 PA (DABU-) DABUR RES FOUND.  
 PA (CORD/) CORD J I.  
 XX  
 XX Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;  
 PI Singh AT;  
 XX  
 XX WPI; 2000-549083/50.  
 XX  
 XX Novel therapeutically active composition comprising at least 5  
 PT peptides, useful for treating angiogenesis especially as a result of  
 PT adenocarcinomas -  
 XX  
 XX Claim 11; Page 31; 42pp; English.  
 PS  
 CC AAB08304-15 represent peptides which have an antiangiogenic effect. The  
 CC specification describes therapeutically active compositions comprising  
 CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and  
 CC at least four analogues chosen from vasoactive intestinal peptide (VIP)  
 CC 1 (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a  
 CC VIP receptor antagonist), BOM1 (a bombesin antagonist), and SP1 (a  
 CC substance P antagonist). The combination of these 7 analogues is known as  
 CC MuJ-7. MuJ-7 is used as an anticancer drug to restrict tumour growth and  
 CC spread by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits  
 CC metastasis through its antiangiogenic activity in all cancers. The  
 CC peptides are useful for the treatment and prevention of angiogenesis,  
 CC especially as a result of adenocarcinomas of the colon, breast, lung,  
 CC prostate, kidney, leukemias or lymphomas.  
 XX  
 XX Sequence 8 AA;  
 SQ

Query Match 92.1%; Score 35; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 Db 2 qwavxhi 8  
 DE  
 DE 06-OCT-1998 (first entry)  
 XX  
 XX Human secreted protein from clone CG300\_3.  
 XX  
 XX Secreted protein; human adult testes; nutrition; cytokine; stimulant;  
 KW cell proliferation; differentiation; immune system; suppressor; ligand;  
 KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;  
 KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;  
 KW anti-inflammatory.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9827205-A2.  
 PN  
 XX 25-JUN-1998.  
 PD  
 XX 17-DEC-1997; 97WO-US23330.  
 XX  
 XX 16-DEC-1997; 97US-0991872.  
 PR  
 PR 18-DEC-1996; 96US-0769192.  
 PR  
 PR 13-JAN-1997; 97US-0783401.  
 XX  
 XX (GEMY ) GENETICS INST INC.  
 PA  
 XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
 PI Racie LA, Spaulding V, Treacy M;  
 PF

XX WPI; 1998-362774/31.  
 DR N-PSDB; AAV44294.  
 XX  
 PT New polynucleotides and secreted proteins - obtained from human  
 PT foetal brain, human adult testes, human adult brain and human adult  
 PT salivary gland cDNA libraries  
 XX  
 XX Claim 14j; Page 68; 110pp; English.  
 PS  
 CC This sequence represents a novel secreted protein from clone CG300\_3  
 CC isolated from a human adult testes cDNA library. This protein has  
 CC applications for nutritional use, cytokine and cell  
 CC proliferation/differentiation activity, immune stimulating activity  
 CC suppressing activity, hematopoiesis regulating activity, tissue growth  
 CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,  
 CC haemostatic and thrombotic activity, receptor/ligand activity,  
 CC anti-inflammatory activity, cadherin/tumour invasion suppressor activity,  
 CC tumour inhibition activity and other activities.  
 XX  
 XX Sequence 245 AA;  
 SQ

Query Match 92.1%; Score 35; DB 19; Length 245;  
 Best Local Similarity 85.7%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 Db 128 qwavxhi 134  
 DE  
 DE 28-FEB-2000 (first entry)  
 XX  
 XX Human cell signalling protein-8.  
 DE  
 XX Cell signalling protein-8; CSIGP-8; cell proliferation; arterio-sclerosis;  
 KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;  
 KW Addison's disease; multiple sclerosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 34 /note= "Potential phosphorylation site"  
 FT Modified-site 110 /note= "Potential phosphorylation site"  
 FT Modified-site 148 /note= "Potential phosphorylation site"  
 FT Modified-site 311 /note= "Potential phosphorylation site"  
 FT Modified-site 137 /note= "Potential phosphorylation site"  
 FT Modified-site 144 /note= "Potential glycosylation site"  
 FT Modified-site 169 /note= "Potential glycosylation site"  
 FT Region 175..195 /label= Signature\_sequence  
 FT Region 236..254 /label= Signature\_sequence  
 XX  
 XX WO958558-A2.  
 PN  
 XX 18-NOV-1999.  
 PD  
 XX 13-MAY-1999; 99WO-US10567.  
 PF

XX 13-MAY-1998; 98US-0085343.  
 PR 26-AUG-1998; 98US-0098010.  
 XX (INCY-) INCYTE PHARM INC.  
 XX Bandnan O, Hillman JL, Lal P, Yue H, Tang YT, Patterson C;  
 PI Baughn MR, Yang J;  
 XX WPI; 2000-086432/07.  
 DR N-PSDB; AA229229.  
 XX Human cell signaling proteins useful for, e.g. diagnosing cell  
 PT proliferative and inflammatory disorders -  
 XX Claim 1; Page 72-73; 90pp; English.  
 PS The present sequence is cell signalling protein-8 (CSIGP-8) encoded  
 CC by cDNA obtained from incyte clone 054191 of FIBROT01 library. It is  
 CC expressed in cardiovascular, gastrointestinal and nervous  
 CC tissues and is found to be homologous to putative G-protein-coupled  
 CC receptor. Fragments of CSIGP encoding nucleic acid can be used as  
 CC hybridisation probe for detecting CSIGP related sequences or allelic  
 CC variants. Recombinant CSIGP can be produced in host cells by transforming  
 CC them with genetically engineered vectors. Agonists or antagonists can be  
 CC used in the treatment of cell proliferative and inflammatory disorders  
 CC associated with decreased or increased CSIGP expression. CSIGP is used in  
 CC the diagnosis, prevention and treatment of cell proliferative disorders  
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory  
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.  
 XX Sequence 336 AA;  
 SQ

Query Match 92.1%; Score 35; DB 21; Length 336;  
 Best Local Similarity 85.7%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHI 8  
 Db 220 qwavihi 226

RESULT 4  
 ID AAP91147  
 AC AAP91147 standard; protein; 7 AA.  
 XX  
 XX 13-MAY-1990 (first entry)  
 DT 22-DEC-1990 (corrected)  
 DE Sequence of new neuromedin C deriv.  
 KW Bombesin antagonist; malignant disease; therapy; gastric acid secretion.  
 XX  
 FT Key Location/Qualifiers  
 FT Misc-difference 1 /label=OTHER  
 FT /note="Ac-D-Gln"  
 FT Misc-difference 5 /label=OTHER  
 FT /note="D-Ala"  
 FT Misc-difference 7 /label=OTHER  
 FT /note="Leu-Ome"  
 XX EP315367-A.  
 PN 10-MAY-1989.  
 XX  
 XX 27-OCT-1988; 88EP-0310094.  
 XX

PR 06-JUN-1988; 88GB-0013355.  
 XX (ICIL ) IMPERIAL CHEM INDS PLC.  
 XX Camble R, Cotton R, Dutta AS, Hayward CF;  
 PI WPI; 1989-139341/19.  
 DR New Neuromedin C polypeptide derivs.  
 XX are potent bombesin antagonist used for treating malignant  
 PT disease and conditions associated with gastrin or gastric acid  
 PT secretion  
 XX Disclosure; Page 929; 49pp; English.  
 PS It is a potent bombesin antagonist. It may be used for the treatment of  
 CC e.g. malignant disease, conditions associated with the over-prod. of  
 CC bombesin and conditions associated with failure of normal physiological  
 CC control of the regulation of gastric acid secretion.  
 XX Sequence 7 AA;  
 SQ

Query Match 89.5%; Score 34; DB 10; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps  
 QY 2 QWAVXHI 8  
 Db 1 qwavahi 7

RESULT 5  
 ID AAR20585  
 XX AAR20585 standard; Peptide; 7 AA.  
 AC AAR20585;  
 XX 07-MAY-1992 (first entry)  
 DT Antagonist of bombesin/GRP.  
 DE Antitumour agent; leukaemia.  
 KW Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 5 /note="D-Ala"  
 FT EP468497-A.  
 XX 29-JAN-1992.  
 PD 25-JUL-1991; 91EP-0112504.  
 XX 26-JUL-1990; 90US-0558031.  
 PR (RICH ) MERRELL DOW PHARM INC.  
 XX Krstenansky JL;  
 PI WPI; 1992-034251/05.  
 DR New peptide bombesin-CRP antagonists - used as antitumour agents  
 PT to treat e.g. leukaemia, small cell lung and prostatic carcinoma  
 PT and to inhibit gastric acid secretion.  
 XX Claim 7; Page 12; 14pp; English.  
 PS The peptide is modified at the N-terminal with a lauryl, palmitoyl  
 CC or esp. an octanoyl gp. The Leu at position 7 may be absent from  
 CC C-terminal (Leu or His) is amidated. The peptides and deri

CC salts can be used to treat small cell lung carcinoma, prostatic  
 CC carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-  
 CC ciated conditions, and to effect antagonism of bombesin/gastrin  
 CC releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at  
 CC 5-200 mg/dose.

XX SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 13; Length 7;  
 Best Local Similarity 71.4%; Pred. NO. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
 Db 1 qwavahl 7

RESULT 6

AAW94610  
 AAR32998 standard; peptide; 7 AA.

AC AAR32998;

XX 13-APR-1993 (first entry)

DE [D-Ala11]-bombesin(7-13)amide derivs.

XX Intracellular signal; inhibition; gastrointestinal tract;  
 KW Iltorin; Gastrin Releasing Peptide; GRP.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER  
 FT /note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,  
 FT N-alpha-lauryl-Gln or N-alpha-palmityl-Gln"

FT Misc-difference 5

FT /note= "D-Ala"

FT Modified-site 7  
 FT /note= "amidated"

XX WO9220707-A.

XX 26-NOV-1992.

XX 21-APR-1992; 92WO-US03287.

XX 23-MAY-1991; 91US-0704863.

XX (RICH ) MERRELL DOW PHARM INC.

XX Edwards JV, Fanger BO;

XX WPI; 1992-415707/50.

XX New bombesin peptide agonists and antagonists - stimulate or  
 PT inhibit digestion, increase susceptibility of tumours to  
 PT chemotherapeutic agents, treat gastric ulcers and tumours etc.

XX Example; Page 40; 64pp; English.

XX The peptides in this example are bombesin analogues. The peptides  
 CC were tested in a competitive binding assay and a Phosphatidyl Inositol  
 CC (PI)-turnover assay in mouse pancreas. None of the peptides  
 CC demonstrated agonist activity but all inhibited PI-turnover (c.f.  
 CC stimulation produced by 100nM GRP). Analogues of bombesin are  
 CC potentially useful for growth therapy and the treatment of digestive  
 CC disorders, e.g. for stimulating digestion, stimulating growth of  
 CC tissue in the lung, pancreas and intestine, stimulating NK cell  
 CC activity against tumour cells and stimulating growth of tumours to  
 CC increase susceptibility to chemotherapeutic agents.

XX SQ Sequence 7 AA;

Query Match 89.5%; Score 34; DB 13; Length 7;  
 Best Local Similarity 71.4%; Pred. NO. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
 Db 1 qwavahl 7

RESULT 7

AAW94610  
 ID AAW94610 standard; peptide; 7 AA.

XX AC AAW94610;

XX 27-APR-1999 (first entry)

DE Bombesin/gastrin releasing peptide type inhibitor peptide #2.

XX Bombesin; gastrin releasing peptide; GRP; inhibitor; antagonist;  
 KW small cell lung carcinoma; tumour; frog; antimitotic; antiseccretory;  
 KW peptic ulcer.

XX Synthetic.

OS Bombina bombina.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "optionally modified by octanoyl, lauroyl or  
 FT palmitoyl"

FT Modified-site 7  
 FT /note= "amidated"

XX US5834433-A.

XX 10-NOV-1998.

XX 23-FEB-1996; 96US-0960130.

XX 24-JUL-1991; 91US-0735402.

XX 26-JUL-1990; 90US-058031.

XX 21-JUL-1994; 94US-0278692.

XX 23-MAY-1995; 95US-0447528.

XX 23-FEB-1996; 96US-0960130.

XX (RICH ) MERRELL PHARM INC.

XX Krstenansky JL;

XX WPI; 1999-141255/12.

XX New peptide antagonists of bombesin or gastrin releasing peptide -  
 PT are useful as antimitotic and antiseccretory agents in treating,  
 PT e.g., small cell lung carcinoma or peptic ulcers

XX Claim 5; Column 14; 9pp; English.

XX The present sequence represents a bombesin/gastrin releasing peptide  
 CC type inhibitor peptide. The peptide may be used as an antimitotic and  
 CC antiseccretory peptide. It can control growth of small cell lung and  
 CC prostatic carcinomas, and it can also inhibit gastric secretions which  
 CC are causative and symptomatic of peptic ulcers. Administration may be  
 CC oral but is preferably subcutaneous, intravenous, intramuscular or  
 CC intraperitoneal, by depot injection, by implant preparation or by  
 CC application to the mucous membranes (e.g. of the nose or bronchial  
 CC tubes) by aerosol.

XX SQ Sequence 7 AA;

```

Query Match      89.5%; Score 34; DB 20; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8
DB 1 qwavahl 7

RESULT 8
AAP20294
ID AAP20294 standard; peptide; 8 AA.
XX
AC AAP20294;
XX
DT 09-DEC-1992 (first entry)
XX
DE Bombesin analog peptide.
XX
Bombesin; hypothermic; analgesic.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= D-Glu
FT FT
FT Misc-difference 5 /label= D-Ala
XX
XX US4331661-A.
XX
XX 25-MAY-1982.
XX
XX 03-OCT-1980; 80US-0193621.
XX
XX 03-OCT-1980; 80US-0193621.
XX
XX (SALK-) SALK INST BIOLOGICA.
XX
XX Marki WE, Brown MR, Rivier JEF;
XX
XX WPI; 1982-48049E/23 (48049E).
XX
XX Octa:peptide bombesin analogues - having hypothermic and
XX analgesic props.
XX
XX Claim 8; Column 8; 5pp; English.
XX
The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl
or benzoyl group at its C-terminal. The peptide may be used for
reducing the body temp. of a mammal, as well as for inducing
analgesia. It produces hypothermia when injected i.c., but not
when given i.v. or s.c. See also AAP20291-3.
XX
SQ Sequence 8 AA;

Query Match      89.5%; Score 34; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8
DB 1 qwavahl 7

RESULT 9
AAR11241
ID AAR11241 standard; Protein; 8 AA.
XX
AC AAR11241;
XX
Bombesin; litorin analogue; linear; receptor affinity; cancer;

```

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DT 17-MAY-1991 (first entry)
XX
XX Linear litorin analogue (III).
XX
KW Bombesin; litorin analogue; linear; receptor affinity; cancer;
XX diabetes.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1..1
FT /label= D-p-chloro-phenylalanine
XX
XX WO9102746-A.
XX
XX 07-MAR-1991.
XX
XX 17-AUG-1990; 90WO-US04646.
XX
XX 21-AUG-1989; 89US-0397169.
XX
XX 30-MAR-1990; 90US-0502438.
XX
XX (TULA ) ADMIN TULANE EDUCATIONAL.
XX (BIOM-) BIOMEASURE INC.
XX
XX Coy DH, Moreau JP, Kim SH;
XX WPI; 1991-087241/12.
XX
XX New linear peptide analogues of bombesin - modified to eliminate
XX biological activity while retaining receptor affinity, for treating
XX cancer, diabetes, etc.
XX
XX Claim 18; Page 54; 58pp; English.
XX
XX This peptide is a specifically claimed example of a generic
XX formula. The C-terminal amino acid (Met) of the naturally occurring
XX peptide has been converted to an amide and Phe 8 has been replaced
XX by beta-Leu. Gly 6 has also been replaced by D-Ala.
XX
XX The peptide is useful for treating benign or malignant tissue
XX proliferation, atherosclerosis, gastrointestinal disorders and
XX diabetes. They act as competitive inhibitors of natural peptides,
XX since they bind to the cell receptors but have no biological
XX activity.
XX
XX The analogue may also be of a naturally occurring peptide
XX terminating at the C-terminus with a Met residue, such as the
XX 10 amino acid C-terminal region of mammalian GRP or amphibian
XX bombesin.
XX
XX See also AAR11239-242.
XX
XX Sequence 8 AA;

Query Match      89.5%; Score 34; DB 12; Length 8;
Best Local Similarity 71.4%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8
DB 2 qwavahl 8

RESULT 10
AAR11242
ID AAR11242 standard; Protein; 8 AA.
XX
XX AAR11242;
XX
XX 17-MAY-1991 (first entry)
XX
XX Linear litorin analogue (IV).
XX
XX Bombesin; litorin analogue; linear; receptor affinity; cancer;

```

KW diabetes.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
XX Modified-site 1..1  
FT /label=D-Phe, pentafluoro-Phe  
FT Modified-site 6..6  
FT /label= N-methyl-D-Ala  
XX  
XX W09102746-A.  
XX  
XX 07-MAR-1991.  
XX  
XX 17-AUG-1990; 90WO-US04646.  
XX  
XX 21-AUG-1989; 89US-0397169.  
XX 30-MAR-1990; 90US-0502438.  
XX  
XX (TULA ) ADMIN TULANE EDUCATIONAL.  
XX (BIOM-) BIOMEASURE INC.  
XX  
XX Coy DH, Moreau JP, Kim SH;  
XX WPI; 1991-087241/12.  
XX  
XX New linear peptide analogues of bombesin - modified to eliminate  
XX biological activity while retaining receptor affinity, for treating  
XX cancer, diabetes, etc.  
XX  
XX Claim 20+21; Page 54; 58pp; English.  
XX  
XX These peptides are specifically claimed examples of a generic  
XX formula. The C-terminal amino acid (Met) of the naturally occurring  
XX peptide has been converted to a methylester.  
XX The peptide is useful for treating benign or malignant tissue  
XX proliferation, arteriosclerosis, gastrointestinal disorders and  
XX diabetes. They act as competitive inhibitors of natural peptides,  
XX since they bind to the cell receptors but have no biological  
XX activity.  
XX The analogue may also be of a naturally occurring peptide  
XX terminating at the C-terminus with a Met residue, such as the  
XX 10 amino acid C-terminal region of mammalian GRP or amphibian  
XX bombesin.  
XX See also AAR11239-242.  
XX  
XX Sequence 8 AA;  
XX  
XX Query Match 89.5%; Score 34; DB 12; Length 8;  
XX Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 2 QWAVXHI 8  
XX | | | | |  
XX 2 qwavahl 8  
XX  
XX  
XX RESULT 11  
XX AAR29155  
XX ID AAR29155 standard; peptide; 8 AA.  
XX  
XX AC AAR29155;  
XX  
XX 16-APR-1993 (first entry)  
XX Bombesin analogue (5).  
XX  
XX Hepatoma; liver cancer; antagonist.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 1  
XX /note= "D-F5-Phe"  
XX  
XX Misc-difference 6  
XX /note= "D-form residue"  
XX  
XX Modified-site 8  
XX /note= "Leu-OMe"  
XX  
XX W09220363-A.  
XX  
XX 26-NOV-1992.  
XX  
XX 11-MAY-1992; 92WO-US03916.  
XX  
XX 10-MAY-1991; 91US-0698681.  
XX (BIOM-) BIOMEASURE INC.  
XX (TULA ) TULANE EDUCATIONAL FUND.  
XX  
XX Bodgen AE, Coy DH, Kim SH, Moreau J;  
XX WPI; 1992-415466/50.  
XX  
XX Treatment of hepatoma - by admin. of admixed bombesin analogue  
XX with carrier  
XX  
XX Claim 14; Page 48; 54pp; English.  
XX  
XX The peptide is an example of a highly generic formula. It is used  
XX in a medicament for treating hepatoma. The epd. acts as antagonist  
XX to bombesin, which has been detected in a number of human cancer  
XX lines.  
XX  
XX Sequence 8 AA;  
XX  
XX Query Match 89.5%; Score 34; DB 13; Length 8;  
XX Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 2 QWAVXHI 8  
XX | | | | |  
XX 2 qwavahl 8  
XX  
XX  
XX RESULT 12  
XX AAR29157  
XX ID AAR29157 standard; peptide; 8 AA.  
XX  
XX AC AAR29157;  
XX  
XX 16-APR-1993 (first entry)  
XX Bombesin analogue (6).  
XX  
XX Hepatoma; liver cancer; antagonist.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 1  
XX /note= "D-F5-Phe"  
XX  
XX Misc-difference 6  
XX /note= "D-form residue"  
XX  
XX Modified-site 8  
XX /note= "Leu-OMe"  
XX  
XX W09220363-A.  
XX  
XX 26-NOV-1992.  
XX  
XX 11-MAY-1992; 92WO-US03916.  
XX  
XX 10-MAY-1991; 91US-0698681.  
XX

disorders, psoriasis and cancers

Claim 6; Page 34; 45pp; English.

The patent discloses (1) the peptide sequence of bombesin (BBN), gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C, the peptide sequence having a chlorambucil group attached to the amino terminal; (2) a BBN receptor antagonist of formula R4-His-Trip-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor antagonist of formula R4-Asp-R5-Trip-Ala-Val-R2-His-Leu-CO-CH2CH3. In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-amino]-L-phenylalanine or a chlorambucil group; and R5 = Gin or His. The compounds act as potent BBN/GRP-like peptide antagonists. They can be used to inhibit the growth of cells that are sensitive to the growth-promoting effects of BBN, GRP or a related peptide such as pancreatic cells, gastric cells, neurons, hypothalamic cells and cancerous cells or tumours. They can also be used to inhibit binding of BBN, GRP or a related peptide to cells capable of such binding. They can be used for treating e.g. peptic ulcer, pancreatitis, eating disorders, diabetes, acromegaly, enterocutaneous fistula, psoriasis, growth retardation, gastrointestinal motility disorders or tumours. The terminal structures of the compounds protect them from *in vivo* proteolysis and provide highly potent antagonist effects that persist for extended periods of time upon administration.

Sequence 8 AA;

Query Match 89.5%; Score 34; DB 16; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHI 8  
| | | | |  
Db 2 qwavahl 8

RESULT 14

AAR09335  
ID AAR09335 standard; peptide; 9 AA.  
XX  
XX AAR09335;  
XX  
DT 30-MAR-1992 (first entry)  
XX  
DE Sequence of Bombesin receptor peptide ligand with irreversible effects.  
DE  
XX Bombesin receptor; agonist; antagonist.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= H-pMel  
FT /note= "pMel= p-bis (2-chloroethyl)  
FT amino-L-phenylalanine"  
FT Modified-site 9  
FT /label= Met-NH2  
XX  
PN W09001037-A.  
XX  
XX 08-FEB-1990.  
XX  
XX 19-JUL-1989; 89WO-EP00842.  
XX  
XX 28-MAR-1989; 89GB-0006900.  
XX 21-JUL-1988; 88GB-001379.  
XX  
XX (FARM ) FARMITALIA C ERBA SPA.  
XX  
XX de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciommi I;  
XX Molinari I;  
XX

DR WPI; 1990-067161/09.  
 XX Bombesin receptor peptide ligands with irreversible effects - as  
 PT agonists and antagonists both weak and strong  
 XX  
 XX Claim 2; Page 26; 32pp; English.  
 XX  
 CC The inventors claim 36 peptides. Also claimed are:  
 CC (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.  
 CC of the peptides.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 89.5%; Score 34; DB 11; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Caps 0;  
 QY 2 QWAVXHI 8  
 DB 2 qwavahl 8

Search completed: October 25, 2001, 11:22:46  
 Job time: 219 sec

RESULT 15  
 AAR11522  
 ID AAR11522 standard; Protein; 9 AA.  
 XX  
 XX AC AAR11522;  
 XX  
 XX 13-JUN-1991 (first entry)  
 XX  
 DE Example of peptide agonist of GRP, neuromedin, bombesin and litorin.  
 XX  
 KW Non-malignant proliferative disease; cancer.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1..1  
 FT /label= OTHER  
 FT /note= "D-p-chlorophenylalanine"  
 XX  
 XX WO9104040-A.  
 XX  
 XX 04-APR-1991.  
 XX  
 XX 17-SEP-1990; 90WO-US05271.  
 XX  
 XX 05-MAY-1990; 90US-0520225.  
 XX 15-SEP-1989; 89US-0408125.  
 XX 21-NOV-1989; 89US-0440039.  
 XX  
 XX (BIOM-) BIOMEASURE INC.  
 XX  
 XX Bogden AE, Moreau J-P;  
 XX  
 XX WPI; 1991-117320/16.  
 XX  
 PT Treatment of non malignant proliferative disease and cancer - by  
 PT administration of natural peptide or fragment selected from  
 PT gastrin-releasing peptide, neuromedin, amphibian bombesin or  
 PT litorin  
 XX  
 XX Claim 22; page 54; 73pp; English.  
 XX  
 CC This is a peptide analogue of mammalian gastrin releasing peptide  
 CC (GRP), neuromedin-B or -C, amphibian bombesin and litorin.  
 CC It is an agonist of these cpds. and is used to treat smooth muscle  
 CC proliferation and cancer of the prostate, breast or lung.  
 CC Residue 6 (Ala) is D-alanine.  
 CC See also AAR11519-21 and AAR11523-30.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 89.5%; Score 34; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Caps 0;  
 QY 2 QWAVXHI 8  
 DB 2 qwavahl 8

Search completed: October 25, 2001, 11:22:46  
 Job time: 219 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-8  
Perfect score: 28  
Sequence: 1 QXAVXHL 8

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Maximum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*

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5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
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15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
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19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	85.7	9	14	AAAR0907
2	23	82.1	7	10	AAAP91147
3	23	82.1	7	13	AAAR20585
4	23	82.1	7	13	AAAR32998
5	23	82.1	7	20	AAAW94610
6	23	82.1	8	3	AAAP20294
7	23	82.1	8	12	AAAR11241
8	23	82.1	8	12	AAAR11242
9	23	82.1	8	13	AAAR29155
10	23	82.1	8	13	AAAR29157
11	23	82.1	8	16	AAAW64911

12	23	82.1	9	11	AAAR09335	Sequence of Bombesin
13	23	82.1	9	12	AAAR11522	Example of peptide
14	23	82.1	9	12	AAAR14865	Peptide analogue
15	23	82.1	9	12	AAAR14866	Peptide analogue
16	23	82.1	9	12	AAAR14867	Peptide analogue
17	23	82.1	9	12	AAAR14873	Peptide analogue
18	23	82.1	9	14	AAAR40903	Bombesin analogue
19	23	82.1	9	19	AAAW51195	Peptide derived from
20	23	82.1	9	19	AAAW51201	Peptide derived from
21	23	82.1	10	10	AAAP96113	Sequence of new
22	23	82.1	24	19	AAAW75003	Human secreted
23	23	82.1	180	20	AAAY37918	Amino acid sequen
24	23	82.1	218	21	AAAB58984	Breast and ovaria
25	23	82.1	396	21	AAAY52829	Neisseria gonorrh
26	23	82.1	500	20	AAAY00207	Enterococcus faec
27	23	82.1	531	21	AAAY59404	Human RICK prote
28	23	82.1	540	20	AAAY31140	Human CARD-3 pro
29	23	82.1	540	20	AAAW2795	Human B1 protein
30	23	82.1	540	21	AAAY68774	Amino acid sequen
31	23	82.1	540	22	AAAB20079	Human CARD-3 pro
32	23	82.1	544	21	AAAB43570	Human cancer ass
33	23	82.1	768	20	AAAW98108	Caenorhabditis el
34	23	82.1	935	21	AAAB07570	Protein encoded
35	23	82.1	1074	20	AAAY00206	Enterococcus faec
36	23	82.1	1074	20	AAAY00188	Enterococcus faec
37	22	78.6	7	22	AAAB48341	Bombesin/gastrin
38	22	78.6	8	11	AAAR04531	Non-cyclic anal
39	22	78.6	8	12	AAAR11224	Linear litorin
40	22	78.6	8	12	AAAR11240	Linear litorin
41	22	78.6	8	12	AAAR14877	Peptide analogue
42	22	78.6	8	13	AAAR28456	Bombesin antagonis
43	22	78.6	8	13	AAAR28459	Bombesin antagonis
44	22	78.6	8	16	AAAW64910	Bombesin receptor
45	22	78.6	8	22	AAAB72406	Bombesin analogue

#### ALIGNMENTS

RESULT 1  
AAAR40907  
ID AAAR40907 standard; peptide; 9 AA.

XX AC AAAR40907;

XX DT 10-FEB-1994 (first entry)

XX Bombesin analogue #9.

DE Bombesin analogue.

DE Bombesin; antagonist; agonist; antimitotic; anti-secretory  
activity; digestion; food intake; tissue growth; lung; pancrea

KW intestine; ulcer; cancer.

OS Synthetic.

XX Key

XX Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "Gip"

XX W09316105-A.

XX 19-AUG-1993.

XX 07-JAN-1993; 93WO-US00183.

XX [D-Ala11]-bombesin

XX Bombesin/gastrin r

XX Bombesin analog pe

XX (RICH ) MERRELL DOW PHARM INC.

XX Edwards JV, Fanger BO;

XX Bombesin analogue

XX Bombesin analogue

XX WPI; 1993-272830/34.

XX Bombesin analogues contg. modified phenylalanine derivs. - used  
 PT for stimulating digestion, decreasing food intake and stimulating  
 PT growth of organ tissues  
 XX  
 PS Example 1; Page 43; 54pp; English.  
 XX  
 CC The sequences given in AAR40899-908 are bombesin analogues. These  
 CC peptides were prepared by solid phase sequential or block  
 CC synthesis. These peptides act as bombesin antagonists or agonists  
 CC and have antimitotic and/or anti-secretory activity. They may be  
 CC used for stimulating digestion in patients, decreasing food intake  
 CC in patients or stimulating growth of organ tissue of lung, pancreatic  
 CC or intestinal origin in patients. They can be used for the treatment  
 CC of gastrointestinal and pancreatic ulcers and for the treatment of  
 CC cancers.  
 XX  
 SQ Sequence 9 AA;

Query Match 85.7%; Score 24; DB 14; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 3 qtavghl 9

RESULT 2  
 AAP91147  
 ID AAP91147 standard; protein; 7 AA.  
 XX  
 AC AAP91147;  
 XX  
 DT 13-MAY-1990 (first entry)  
 DT 22-DEC-1990 (corrected)  
 XX  
 DE Sequence of new neuromedin C deriv.  
 XX  
 KW Bombesin antagonist; malignant disease; therapy; gastric acid secretion.  
 XX

Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /label=OTHER  
 FT /note="Ac-D-Gln"  
 FT Misc-difference 5  
 FT /label=OTHER  
 FT /note="D-Ala"  
 FT Misc-difference 7  
 FT /label=OTHER  
 FT /note="Leu-OME"

EP315367-A.  
 XX  
 PD 10-MAY-1989.  
 XX  
 XX 27-OCT-1988; 88EP-0310094.  
 XX  
 XX 06-JUN-1988; 88GB-0013355.  
 XX  
 XX (ICIL ) IMPERIAL CHEM INDS PLC.  
 XX  
 XX Camble R, Cotton R, Dutta AS, Hayward CF;  
 XX WPI; 1989-139341/19.  
 DR

XX New Neuromedin C polypeptide derivs. -  
 PT are potent bombesin antagonist used for treating malignant  
 PT disease and conditions associated with gastrin or gastric acid  
 PT secretion  
 XX  
 PS Disclosure; Page 929; 49pp; English.

XX  
 CC It is a potent bombesin antagonist. It may be used for the treatment of  
 CC e.g. malignant disease, conditions associated with the over-prodn. of  
 CC bombesin and conditions associated with failure of normal physiological  
 CC control of the regulation of gastric acid secretion.  
 XX  
 SQ Sequence 7 AA;

Query Match 82.1%; Score 23; DB 10; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 1 qwavahl 7

RESULT 3  
 AAR20585  
 ID AAR20585 standard; Peptide; 7 AA.  
 XX  
 AC AAR20585;

DT 07-MAY-1992 (first entry)  
 DE Antagonist of bombesin/GRP.  
 XX  
 KW Antitumour agent; leukaemia.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 5  
 FT /note="D-Ala"

EP468497-A.  
 XX  
 PD 29-JAN-1992.  
 XX  
 PF 25-JUL-1991; 91EP-0112504.  
 XX  
 PR 26-JUL-1990; 90US-0558031.  
 XX  
 PA (RICH ) MERRELL DOW PHARM INC.  
 XX  
 PI Krstenansky JL;  
 XX  
 DR WPI; 1992-034251/05.

XX New peptide bombesin-GRP antagonists - used as antitumour agent.  
 PT to treat e.g. leukaemia, small cell lung and prostatic carcinoma  
 PT and to inhibit gastric acid secretion.

PS Claim 7; Page 12; 14pp; English.

XX The peptide is modified at the N-terminal with a lauryl, palmitoyl  
 CC or esp. an octanoyl gp. The Leu at position 7 may be absent. The  
 CC C-terminal (Leu or His) is amidated. The peptides and derived  
 CC salts can be used to treat small cell lung carcinoma, prostatic  
 CC carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-  
 CC ciated conditions, and to effect antagonism of bombesin/gastrin  
 CC releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at  
 CC 5-200 mg/dose.  
 XX

SQ Sequence 7 AA;

Query Match 82.1%; Score 23; DB 13; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8

Db | | | | |  
1 qwavahl 7

## RESULT 4

AAR32998  
ID AAR32998 standard; peptide; 7 AA.

AC AAR32998;

DT 13-APR-1993 (first entry)

DE [D-Ala11]-bombesin(7-13)amide derivs.

KW Intracellular signal; inhibition; gastrointestinal tract;

KW litotin; Gastrin Releasing Peptide; GRP.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,

FT N-alpha-lauryl-Gln or N-alpha-palmityl-Gln"

FT Misc-difference 5

FT /note= "D-Ala"

FT Modified-site 7

FT /note= "amidated"

FT W09220707-A.

PN 26-NOV-1992.

PD 21-APR-1992; 92WO-US03287.

XX 23-MAY-1991; 91US-0704863.

XX (RICH ) MERRELL DOW PHARM INC.

XX Edwards JV, Fanger BO;

XX WPI; 1992-415707/50.

XX New bombesin peptide agonists and antagonists - stimulate or

XX inhibit digestion, increase susceptibility of tumours to

XX chemotherapeutic agents, treat gastric ulcers and tumours etc.

XX Example; Page 40; 64pp; English.

XX The peptides in this example are bombesin analogues. The peptides

XX were tested in a competitive binding assay and a Phosphatidyl Inositol

XX (PI)-turnover assay in mouse pancreas. None of the peptides

XX demonstrated agonist activity but all inhibited PI-turnover (c.f.

XX stimulation produced by 100nM GRP). Analogues of bombesin are

XX potentially useful for growth therapy and the treatment of digestive

XX disorders, e.g. for stimulating digestion, stimulating growth of

XX tissue in the lung, pancreas and intestine, stimulating NK cell

XX activity against tumour cells and stimulating growth of tumours to

XX increase susceptibility to chemotherapeutic agents.

XX Sequence 7 AA;

XX Query Match 82.1%; Score 23; DB 13; Length 7;

XX Best Local Similarity 71.4%; Pred. No. 3.4e+05;

XX Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 2 QXAVXHL 8

XX | | | | |

XX 1 qwavahl 7

XX RESULT 5

XX ID AAR32998 standard; peptide; 7 AA.

XX

AAW94610

ID AAW94610 standard; peptide; 7 AA.

XX

AC AAW94610;

XX

DT 27-APR-1999 (first entry)

XX

DE Bombesin/gastrin releasing peptide type inhibitor peptide #2

XX

KW Bombesin; gastrin releasing peptide; GRP; inhibitor; antagonists

KW small cell lung carcinoma; tumour; frog; antimitotic; antiserum; frog;

KW peptic ulcer.

XX Synthetic.

OS Bombina bombina.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "optionally modified by octanoyl, lauroyl or

FT palmitoyl"

FT Modified-site 7

FT /note= "amidated"

FT US5834433-A.

XX 10-NOV-1998.

XX 23-FEB-1996; 96US-0960130.

XX 24-JUL-1991; 91US-0735402.

XX 26-JUL-1990; 90US-0558031.

XX 21-JUL-1994; 94US-0278692.

XX 23-MAY-1995; 95US-047528.

XX 23-FEB-1996; 96US-0960130.

XX (RICH ) MERRELL PHARM INC.

XX Krstenansky JL;

XX WPI; 1999-141255/12.

XX New peptide antagonists of bombesin or gastrin releasing peptide -

XX are useful as antimitotic and antisecretory agents in treating,

XX e.g., small cell lung carcinoma or peptic ulcers

XX Claim 5; Column 14; 9pp; English.

XX The present sequence represents a bombesin/gastrin releasing peptide

XX type inhibitor peptide. The peptide may be used as an antimitotic,

XX antisecretory peptide. It can control growth of small cell lung,

XX prostatic carcinomas, and it can also inhibit gastric secretion.

XX are causative and symptomatic of peptic ulcers. Administration of

XX oral but is preferably subcutaneous, intravenous, intramuscular, or

XX intraperitoneal, by depot injection, by implant preparation or by

XX application to the mucous membranes (e.g. of the nose or bronchial

XX tubes) by aerosol.

XX Sequence 7 AA;

XX Query Match 82.1%; Score 23; DB 20; Length 7;

XX Best Local Similarity 71.4%; Pred. No. 3.4e+05;

XX Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 2 QXAVXHL 8

XX | | | | |

XX 1 qwavahl 7

XX RESULT 6

XX ID AAR32998 standard; peptide; 8 AA.

XX

AC AAP20294;  
 XX 09-DEC-1992 (first entry)  
 DT Bombsesin analog peptide.  
 DE Bombsesin; hypothermic; analgesic.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1 /label= D-Glu  
 FT Misc-difference 5 /label= D-Ala  
 FT  
 XX US4331661-A.  
 PN 25-MAY-1982.  
 XX 03-OCT-1980; 80US-0193621.  
 PF 03-OCT-1980; 80US-0193621.  
 PR (SALK-) SALK INST BIOLOGICA.  
 XX Marki WE, Brown MR, Rivier JEF;  
 PI WPI; 1982-48049E/23 (48049E).  
 DR Octa;peptide bombsesin analogues - having hypothermic and  
 XX analgesic props.  
 PT Claim 8; Column 8; 5pp; English.  
 PS The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl  
 XX or benzoyl group at its C-terminal. The peptide may be used for  
 CC reducing the body temp. of a mammal, as well as for inducing  
 CC analgesia. It produces hypothermia when injected i.c., but not  
 CC when given i.v. or s.c. See also AAP20291-3.  
 XX Sequence 8 AA;  
 SQ  
 Query Match 82.1%; Score 23; DB 3; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 Db 1 qvavahl 7  
 RESULT 7  
 AAR11241  
 ID AAR11241 standard; Protein; 8 AA.  
 XX AAR11241;  
 AC 17-MAY-1991 (first entry)  
 DT Linear litorin analogue (III).  
 DE Bombsesin; litorin analogue; linear; receptor affinity; cancer;  
 XX diabetes.  
 KW Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 1.1  
 FT /label= D-p-chloro-phenylalanine  
 FT WO9102746-A.  
 PN

XX 07-MAR-1991.  
 PD 17-AUG-1990; 90WO-US04646.  
 PF 21-AUG-1989; 89US-0397169.  
 PR 30-MAR-1990; 90US-0502438.  
 XX (TULA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.  
 XX Coy DH, Moreau JP, Kim SH;  
 PI WPI; 1991-087241/12.  
 DR New linear peptide analogues of bombsesin - modified to eliminate  
 XX biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.  
 PT Claim 18; Page 54; 58pp; English.  
 PS This peptide is a specifically claimed example of a generic  
 XX formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to an amide and Phe 8 has been replaced  
 CC by beta-leu. Gly 6 has also been replaced by D-Ala.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, arteriosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological  
 CC activity.  
 CC The analogue may also be of a naturally occurring peptide  
 CC terminating at the C-terminus with a Met residue, such as the  
 CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
 CC bombsesin.  
 CC See also AAR11239-242.  
 XX Sequence 8 AA;  
 SQ  
 Query Match 82.1%; Score 23; DB 12; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 Db 2 qvavahl 8  
 RESULT 8  
 AAR11242  
 ID AAR11242 standard; Protein; 8 AA.  
 XX AAR11242;  
 AC 17-MAY-1991 (first entry)  
 DT Linear litorin analogue (IV).  
 DE Bombsesin; litorin analogue; linear; receptor affinity; cancer;  
 XX diabetes.  
 KW Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 1.1  
 FT /label= D-Phe, pentafluoro-Phe  
 FT Modified-site 6.6  
 FT /label= N-methyl-D-Ala  
 FT WO9102746-A.  
 PN 07-MAR-1991.  
 PD

PF 17-AUG-1990; 90WO-US04646.  
XX  
PR 21-AUG-1989; 89US-0397169.  
PR 30-MAR-1990; 90US-0502438.  
XX  
XX  
PA (TULA ) ADMIN TULANE EDUCATIONAL.  
PA (BIOM-) BIOMEASURE INC.  
XX  
PI Coy DH, Moreau JP, Kim SH;  
XX WPI; 1991-087241/12.  
XX  
XX New linear peptide analogues of bombesin - modified to eliminate  
PT biological activity while retaining receptor affinity, for treating  
PT cancer, diabetes, etc.  
XX  
PS Claim 20+21; Page 54; 58pp; English.  
XX  
XX These peptides are specifically claimed examples of a generic  
CC formula. The C-terminal amino acid (Met) of the naturally occurring  
CC peptide has been converted to a methylester.  
CC The peptide is useful for treating benign or malignant tissue  
CC proliferation, arteriosclerosis, gastrointestinal disorders and  
CC diabetes. They act as competitive inhibitors of natural peptides,  
CC since they bind to the cell receptors but have no biological  
CC activity.  
CC The analogue may also be of a naturally occurring peptide  
CC terminating at the C-terminus with a Met residue, such as the  
CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
CC bombesin.  
CC See also AAR11239-242.  
XX  
XX Sequence 8 AA;  
SQ

Query Match 82.1%; Score 23; DB 12; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 2 qwavahl 8  
| | | | |  
| | | | |

RESULT 9  
AAR29155  
ID AAR29155 standard; peptide; 8 AA.  
XX  
AC AAR29155;  
XX  
DT 16-APR-1993 (first entry)  
XX  
DE Bombesin analogue (5).  
XX  
KW Hepatoma; liver cancer; antagonist.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "D-P5-Phe"  
FT Misc-difference 6 /note= "D-form residue"  
FT Modified-site 8 /note= "Leu-OMe"  
XX  
PN WO9220363-A.  
XX  
PD 26-NOV-1992.  
XX  
PF 11-MAY-1992; 92WO-US03916.  
XX  
PR 10-MAY-1991; 91US-0698681.  
XX  
PA (BIOM-) BIOMEASURE INC.  
PA (TULA ) TULANE EDUCATIONAL FUND.  
XX  
PI Bodgen AE, Coy DH, Kim SH, Moreau J;  
XX WPI; 1992-415466/50.  
DR  
XX Treatment of hepatoma - by admin. of admixed bombesin analo  
PT with carrier  
XX  
PS Claim 15; Page 48; 54pp; English.  
XX  
XX The peptide is an example of a highly generic formula. It is

XX  
PA (BIOM-) BIOMEASURE INC.  
PA (TULA ) TULANE EDUCATIONAL FUND.  
XX  
PI Bodgen AE, Coy DH, Kim SH, Moreau J;  
XX WPI; 1992-415466/50.  
XX  
PT Treatment of hepatoma - by admin. of admixed bombesin analo  
PT with carrier  
XX  
PS Claim 14; Page 48; 54pp; English.  
XX  
CC The peptide is an example of a highly generic formula. It is used  
CC in a medicament for treating hepatoma. The cpd. acts as antagonist  
CC to bombesin, which has been detected in a number of human can  
CC lines.  
XX  
SQ Sequence 8 AA;  
Query Match 82.1%; Score 23; DB 13; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels  
QY 2 QXAVXHL 8  
Db 2 qwavahl 8  
| | | | |  
| | | | |

RESULT 10  
AAR29157  
ID AAR29157 standard; peptide; 8 AA.  
XX  
AC AAR29157;  
XX  
DT 16-APR-1993 (first entry)  
XX  
DE Bombesin analogue (6).  
XX  
KW Hepatoma; liver cancer; antagonist.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "D-P5-Phe"  
FT Misc-difference 6 /note= "D-form residue"  
FT Modified-site 8 /note= "Leu-OMe"  
XX  
PN WO9220363-A.  
XX  
PD 26-NOV-1992.  
XX  
PF 11-MAY-1992; 92WO-US03916.  
XX  
PR 10-MAY-1991; 91US-0698681.  
XX  
PA (BIOM-) BIOMEASURE INC.  
PA (TULA ) TULANE EDUCATIONAL FUND.  
XX  
PI Bodgen AE, Coy DH, Kim SH, Moreau J;  
XX WPI; 1992-415466/50.  
DR  
XX Treatment of hepatoma - by admin. of admixed bombesin analo  
PT with carrier  
XX  
PS Claim 15; Page 48; 54pp; English.  
XX  
XX The peptide is an example of a highly generic formula. It is

CC In a medicament for treating hepatoma. The cpd. acts as antagonist  
CC to bombesin, which has been detected in a number of human cancer  
CC lines.

XX Sequence 8 AA;

Query Match 82.1%; Score 23; DB 13; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
I I I I I  
Db 2 qwavahl 8

RESULT 11  
AAW64911  
ID AAW64911 standard; peptide; 8 AA.

XX AAW64911;

DT 06-JUL-1999 (first entry)

DE Bombesin receptor antagonist.

KW Bombesin; antagonist; chlorambucil; peptic ulcer; pancreatitis;  
KW eating disorder; diabetes; acromegaly; enterocutaneous fistula;  
KW psoriasis; growth retardation; gastrointestinal motility disorder;  
KW antitumour.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1  
/note= "The amino terminal is acylated with acetyl,  
FT bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-amino]-  
FT L-phenylalanine or a chlorambucil group"

FT Modified-site 8  
/note= "The carboxy terminal is in the form of an  
FT ethyl ester"

XX WO9500542-A1.

XX 05-JAN-1995.

XX 15-JUN-1994; 94WO-US06757.

XX 17-DEC-1993; 93US-0168390.

XX 18-JUN-1993; 93US-0078062.

XX (PEPT-) PEPTIDE TECHNOLOGIES CORP.

XX Chandrasekhar B, Knight M, Takahashi K;

XX WPI; 1995-052004/07.

XX New bombesin, gastrin releasing peptide or Neuromedin B or C derivs.  
XX - antagonists for treating conditions such as gastrointestinal  
XX disorders, psoriasis and cancers

XX Claim 6; Page 34; 45pp; English.

XX The patent discloses (1) the peptide sequence of bombesin (BBN),  
XX gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C,  
XX the peptide sequence having a chlorambucil group attached to the  
XX amino terminal; (2) a BBN receptor antagonist of formula  
XX R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
XX antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
XX In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
XX Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
XX amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His.  
XX The compounds act as potent BBN/GRP-like peptide antagonists. They

CC can be used to inhibit the growth of cells that are sensitive to the  
CC growth-promoting effects of BBN, GRP or a related peptide such as  
CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
CC cancerous cells or tumours. They can also be used to inhibit the  
CC binding of BBN, GRP or a related peptide to cells capable of such  
CC binding. They can be used for treating e.g. peptic ulcer, pancreatitis,  
CC eating disorders, diabetes, acromegaly, enterocutaneous fistula,  
CC psoriasis, growth retardation, gastrointestinal motility disorders or  
CC tumours. The terminal structures of the compounds protect them from  
CC in vivo proteolysis and provide highly potent antagonist effects that  
CC persist for extended periods of time upon administration.

XX Sequence 8 AA;

Query Match 82.1%; Score 23; DB 16; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
I I I I I  
Db 2 qwavahl 8

RESULT 12

AAW09335

ID AAW09335 standard; peptide; 9 AA.

XX AAW09335;

XX 30-MAR-1992 (first entry)

DE Sequence of Bombesin receptor peptide ligand with irreversible  
DE effects.

XX Bombesin receptor; agonist; antagonist.

XX Key Location/Qualifiers

FT Modified-site 1  
/label= H-pMel  
/note= "pMel= p-bis (2-chloroethyl)  
FT amino-L-phenylalanine"

FT Modified-site 9  
/label= Met-NH2

XX WO9001037-A.

XX 08-FEB-1990.

XX 19-JUL-1989; 89WO-EF00842.

XX 28-MAR-1989; 89GB-0006900.

XX 21-JUL-1988; 88GB-0017379.

XX (FARM ) FARMITALIA C ERBA SPA.

XX de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciom...

XX Molinari I;

XX WPI; 1990-067161/09.

XX Bombesin receptor peptide ligands with irreversible effects - ...  
XX agonists and antagonists both weak and strong

XX Claim 2; Page 26; 32pp; English.

XX The inventors claim 36 peptides. Also claimed are:

XX (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.  
XX of the peptides.

XX Sequence 9 AA;

Query Match 82.1%; Score 23; DB 11; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qwavahl 8

## RESULT 13

AAR11522  
 ID AAR11522 standard; Protein; 9 AA.

XX AC AAR11522;  
 XX

DT 13-JUN-1991 (first entry)

DE Example of peptide agonist of GRP, neuromedin, bombesin and litorin.

XX KW Non-malignant proliferative disease; cancer.

XX FH Key Location/Qualifiers  
 FT Modified-site 1.1  
 FT /label= OTHER  
 FT /note= "D-p-chlorophenylalanine"

XX PN W09104040-A.

XX PD 04-APR-1991.

XX PF 17-SEP-1990; 90WO-US05271.

XX PR 05-MAY-1990; 90US-0520225.

XX PR 15-SEP-1989; 89US-0408125.

XX PR 21-NOV-1989; 89US-0440039.

XX PA (BIOM-) BIOMEASURE INC.

XX PI Bogden AE, Moreau J-P;

XX WPI; 1991-117320/16.

XX Treatment of non malignant proliferative disease and cancer - by  
 administration of natural peptide or fragment selected from  
 gastrin-releasing peptide, neuromedin, bombesin or  
 litorin

XX PS Claim 22; page 54; 73pp; English.

XX This is a peptide analogue of mammalian gastrin releasing peptide  
 (GRP), neuromedin-B or -C, amphibian bombesin and litorin.  
 CC It is an agonist of these cpds. and is used to treat smooth muscle  
 CC proliferation and cancer of the prostate, breast or lung.  
 CC Residue 6 (Ala) is D-alanine  
 CC See also AAR11519-21 and AAR11523-30.

XX SQ Sequence 9 AA;

Query Match 82.1%; Score 23; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qwavahl 8

## RESULT 14

AAR14865  
 ID AAR14865 standard; Protein; 9 AA.

XX AC AAR14865;

XX 14-FEB-1992 (first entry)

XX Peptide analogue #6 of litorin, GRP, neuromedin or bombesin.

XX KW tissue proliferation; gastrin related peptide; peptide hormone.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= D-Phe  
 FT Modified-site 6  
 FT /label= D-Ala

XX PN W09117181-A.

XX PD 14-NOV-1991.

XX PF 09-MAY-1991; 91WO-0003265.

XX PR 09-MAY-1990; 90US-0520226.

XX PA (TULA) TULANE E FUND ADMINISTRA.

XX PI (BIOM-) BIOMEASURE INC.

XX PI Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

XX Peptide agonists of litorin, gastrin releasing peptide -  
 neuromedin B or C or bombesin, for treating cancer, preventing  
 smooth muscle proliferation and suppressing appetite and alcohol  
 craving

XX PS Claim 8; Page 18; 25pp; English.

XX The C-terminal residue is amidated. This peptide is one of 27  
 CC specific examples of a highly generic formula. The peptides are all  
 CC analogues of either litorin; the 10 amino acid C-terminal region of  
 CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 CC C-terminal region of amphibian bombesin. They act as at least partial  
 CC agonists of the natural peptides. The peptide analogues are made by  
 CC standard methods of synthesis and can be cyclised.  
 CC See AAR14860-R14880 and AAR15035-R15040.

XX SQ Sequence 9 AA;

Query Match 82.1%; Score 23; DB 12; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+05;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | |  
 Db 2 qwavahl 8

## RESULT 15

AAR14866  
 ID AAR14866 standard; Protein; 9 AA.

XX AC AAR14866;

XX DT 14-FEB-1992 (first entry)

XX Peptide analogue #7 of litorin, GRP, neuromedin or bombesin.

XX KW tissue proliferation; gastrin related peptide; peptide hormone.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= D-Phe  
FT Modified-site 6 /label= D-Ala  
FT  
XX WO9117181-A.  
XX  
XX 14-NOV-1991.  
XX  
XX 09-MAY-1991; 91WO-0003265.  
XX  
XX 09-MAY-1990; 90US-0520226.  
XX  
XX (TULA ) TULANE E FUND ADMINISTRA.  
XX (BIOM-) BIOMEASURE INC.  
XX  
XX Coy DH, Kim SH, Moreau JP;  
XX WPI; 1991-353721/48.  
XX  
XX Peptide agonists of litorin, gastrin releasing peptide -  
PT neuromedin B or C or bombesin, for treating cancer, preventing  
PT smooth muscle proliferation and suppressing appetite and alcohol  
PT craving  
XX  
XX Claim 9; Page 18; 25pp; English.  
XX  
XX The C-terminal residue is amidated. This peptide is one of 27  
XX specific examples of a highly generic formula. The peptides are all  
XX analogues of either litorin; the 10 amino acid C-terminal region of  
XX mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
XX C-terminal region of amphibian bombesin. They act as at least partial  
XX agonists of the natural peptides. The peptide analogues are made by  
XX standard methods of synthesis and can be cyclised.  
XX See AAR14860-R14880 and AAR15035-R15040.  
XX  
SQ Sequence 9 AA;  
  
Query Match 82.1%; Score 23; DB 12; Length 9;  
Best Local Similarity 71.4%; Pred. NO. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 QXAVXHL 8  
| | | | |  
Db 2 qwavahl 8  
  
Search completed: October 25, 2001, 11:22:46  
Job time: 219 sec

Result No.	Score	Query %			ID	Description
		Match	Length	DB		
1	24	85.7	1510	1	MUKB_HAEIN	P45187 haemophilus
2	23	82.1	85	1	PTHP_ECOLI	P07006 escherichia
3	23	82.1	85	1	PTHP_HAEIN	P43921 haemophilus
4	23	82.1	85	1	PTHP_KLEPN	P16481 klebsiella
5	23	82.1	276	1	END8_STRCO	O86820 streptomyces
6	23	82.1	320	1	VS10_TRYBB	P06013 trypanosoma
7	23	82.1	420	1	PHR_THETH	P37250 thermus aqu
8	23	82.1	432	1	HEMI_CYAPA	P48077 cyanophora
9	23	82.1	434	1	HEMI_PASMU	P95525 pasteurella
10	23	82.1	472	1	IFT2_MOUSE	O64112 mus musculus
11	23	82.1	495	1	THDF_TREPA	O83561 treponema p
12	23	82.1	496	1	RECQ_BACSU	P05729 bacillus su
13	23	82.1	546	1	TCPE_SCHPO	Q9utm4 schizosacch
14	23	82.1	768	1	EF2K_CAEEL	O01991 caenorhabdi
15	23	82.1	910	1	PERT_BOPEE	P14283 borderella
16	23	82.1	936	1	MSH4_HUMAN	O15457 homo sapien
17	23	82.1	1206	1	FM14_MOUSE	Q05859 mus musculus
18	23	82.1	1213	1	FMN_CHICK	Q05858 gallus gall
19	23	82.1	1468	1	FMN1_MOUSE	Q05860 mus musculu
20	23	82.1	1741	1	RPC1_GIALA	P25202 giardia lam
21	23	82.1	2347	1	KROS_HUMAN	P08922 homo sapien
22	23	82.1	4447	1	PKSK_BACSU	P40803 bacillus su
23	22	78.6	14	1	ALYT_ALYOB	P08944 alytes obst
24	22	78.6	101	1	SMD3_YEAST	P43321 saccharomyc
25	22	78.6	107	1	BOMB_BOMVA	P01296 bombina var
26	22	78.6	119	1	BOMB_BOMOR	P21591 bombina ori
27	22	78.6	246	1	PS61_ARATH	O81146 arabidopsis
28	22	78.6	246	1	PS62_ARATH	O81147 arabidopsis
29	22	78.6	246	1	PSA6_TOBAC	Q9Xg77 nicotiana t
30	22	78.6	261	1	YP9A_CAEEL	Q93247 caenorhabdi
31	22	78.6	310	1	PURU_MYCTU	O50453 mycobacteri
32	22	78.6	358	1	MTG2_HAEGA	P25283 haemophilus
33	22	78.6	261	1	RUVB_STN3	Q57396 synecocyst

Query Match 85.7%; Score 24; DB 1; Length 1510;  
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXVYXHL 8  
 I I I I I  
 Db 371 QSAVDHL 377

RESULT 2  
 PTHP\_ECOLI STANDARD; PRT; 85 AA.  
 AC P07006; P05525;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN).  
 GN PTHP OR HPR.  
 OS Escherichia coli, and Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562, 602;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12;  
 RX MEDLINE=88314869; PubMed=2457575;  
 RA de Reuse H., Danchin A.;  
 RT "The ptsH, ptsI, and crr genes of the Escherichia coli  
 RT phosphoenolpyruvate-dependent phosphotransferase system: a complex  
 RT operon with several modes of transcription.";  
 RL J. Bacteriol. 170:3827-3837(1988).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12;  
 RX MEDLINE=85286351; PubMed=2411636;  
 RA de Reuse H., Roy A., Danchin A.;  
 RT "Analysis of the ptsH-ptsI-crr region in Escherichia coli K-12:  
 RT nucleotide sequence of the ptsH gene.";  
 RL Gene 35:199-207(1985).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RC SPECIES=E.coli;  
 RX MEDLINE=88058992; PubMed=2960675;  
 RA Saffen D.W., Presper K.A., Doering T.L., Roseman S.;  
 RT "Sugar transport by the bacterial phosphotransferase system.  
 RT Molecular cloning and structural analysis of the Escherichia coli  
 RT ptsH, ptsI, and crr genes.";  
 RL J. Biol. Chem. 262:16241-16253(1987).  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=E.coli, and S.typhimurium; STRAIN=K12, AND LT2;  
 RX MEDLINE=88257033; PubMed=3290198;  
 RA Byrne C.R., Monroe R.S., Ward K.A., Kredich N.M.;  
 RT "DNA sequences of the cysK regions of Salmonella typhimurium and  
 RT Escherichia coli and linkage of the cysK regions to ptsH.";  
 RL J. Bacteriol. 170:3150-3157(1988).  
 RN [5]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA May B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [6]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12;  
 RX MEDLINE=97349980; PubMed=9205837;  
 RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,

RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
 RA Mizobuchi K., Mori H., Nakade S., Makamura Y., Nashimoto H.,  
 RA Oshima T., Oyama S., Saito N., Sampei G., Sato Y., Sivasubramanian S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada K.,  
 RA Yamagata S., Horiuchi T.;  
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
 RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and  
 RT analysis of its sequence features.";  
 RL DNA Res. 4:91-113(1997).  
 RN [7]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium; STRAIN=LT2;  
 RX MEDLINE=89237892; PubMed=2497295;  
 RA Schnierow B.J., Yamada M., Saler M.H. Jr.;  
 RT "Partial nucleotide sequence of the pts operon in Salmonella  
 RT typhimurium: comparative analyses in five bacterial genera.";  
 RL Mol. Microbiol. 3:113-118(1989).  
 RN [8]  
 RC SPECIES=S.typhimurium;  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=83056997; PubMed=6754732;  
 RA Weigel N., Powers D.A., Roseman S.;  
 RT "Sugar transport by the bacterial phosphotransferase system. Primary  
 RT structure and active site of a general phosphocarrier protein (HPR)  
 RT from Salmonella typhimurium.";  
 RL J. Biol. Chem. 257:14499-14509(1982).  
 RN [9]  
 RC REVISIONS.  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=85080006; PubMed=6392295;  
 RA Powers D.A., Roseman S.;  
 RT "The primary structure of Salmonella typhimurium HPR, a  
 RT phosphocarrier protein of the phosphoenolpyruvate:glycose  
 RT phosphotransferase system. A correction.";  
 RL J. Biol. Chem. 259:15212-15214(1984).  
 RN [10]  
 RC SEQUENCE OF 1-12.  
 RC SPECIES=E.coli; STRAIN=K12 / EMG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 RT in the genome of Escherichia coli K-12.";  
 RL Electrophoresis 18:1259-1313(1997).  
 RN [11]  
 RC SEQUENCE OF 1-12.  
 RC STRAIN=K12 / W3110;  
 RA Frutiger S., Hughes G.J., Pasquali C., Hochstrasser D.F.;  
 RL Submitted (FEB-1996) to the SWISS-PROT data bank.  
 RN [12]  
 RC X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=94043003; PubMed=8226757;  
 RA Jia Z., Quail J.W., Waygood E.B., Delbaere L.T.J.;  
 RT "The 2.0-A resolution structure of Escherichia coli  
 RT histidine-containing phosphocarrier protein HPR. A redetermination.";  
 RL J. Biol. Chem. 268:22490-22501(1993).  
 RN [13]  
 RC X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RX MEDLINE=96378616; PubMed=8784179;  
 RA Napper S., Anderson J.W., Georges F., Quail J.W., Delbaere L.T.J.,  
 RA Waygood E.B.;  
 RT "Mutation of serine-46 to aspartate in the histidine-containing  
 RT protein of Escherichia coli mimics the inactivation by  
 RT phosphorylation of serine-46 in HPRs from gram-positive bacteria.";  
 RL Biochemistry 35:11260-11267(1996).  
 RN [14]  
 RC STRUCTURE BY NMR.  
 RX MEDLINE=87101066; PubMed=3542036;  
 RA Klevit R.E., Waygood E.B.;  
 RT "Two-dimensional 1H NMR studies of histidine-containing protein from  
 RT Escherichia coli. 3. Secondary and tertiary structure as determined  
 RT by NMR.";  
 RL Biochemistry 25:7774-7781(1986).  
 RN [15]

RP STRUCTURE BY NMR.  
RX MEDLINE-92089095; PubMed-1751501;  
RA Hammen P.K., Waygood E.B., Klevit R.E.;  
RT "Reexamination of the secondary and tertiary structure of histidine-  
RT containing protein from Escherichia coli by homonuclear and  
RT heteronuclear NMR spectroscopy.";  
RL Biochemistry 30:11842-11850(1991).  
RN [16]  
RP STRUCTURE BY NMR.  
RX MEDLINE-93130914; PubMed-1483471;  
RA van Nuland N.A.J., Groetzing J., Dijkstra K., Scheek R.M.,  
RA Robillard G.T.;  
RT "Determination of the three-dimensional solution structure of the  
RT histidine-containing phosphocarrier protein HPr from Escherichia coli  
RT using multidimensional NMR spectroscopy.";  
RL Eur. J. Biochem. 210:881-891(1992).  
RN [17]  
RP STRUCTURE BY NMR.  
RX MEDLINE-94210480; PubMed-8158637;  
RA van Nuland N.A.J., Hangyi I.W., van Schaik R.C., Berendsen H.J.,  
RA van Gunsteren W.F., Scheek R.M., Robillard G.T.;  
RT "The high-resolution structure of the histidine-containing  
RT phosphocarrier protein HPr from Escherichia coli determined by  
RT restrained molecular dynamics from nuclear magnetic resonance nuclear  
RT Overhauser effect data.";  
RL J. Mol. Biol. 237:544-559(1994).  
RN [18]  
RP STRUCTURE BY NMR.  
RX MEDLINE-95156481; PubMed-7853396;  
RA van Nuland N.A.J., Boelens R., Scheek R.M., Robillard G.T.;  
RA "High-resolution structure of the phosphorylated form of the  
RT histidine-containing phosphocarrier protein HPr from Escherichia  
RT coli determined by restrained molecular dynamics from NMR-NOE data.";  
RL J. Mol. Biol. 246:180-193(1995).  
RN [19]  
RP STRUCTURE BY NMR.  
RX MEDLINE-97022120; PubMed-8868480;  
RA van Nuland N.A.J., Wiersma J.A., van der Spoel D., de Groot B.L.,  
RA Scheek R.M., Robillard G.T.;  
RT "Phosphorylation-induced torsion-angle strain in the active center of  
RT HPr, detected by NMR and restrained molecular dynamics refinement.";  
RL Protein Sci. 5:442-446(1996).  
RN [20]  
RP STRUCTURE BY NMR.  
RX MEDLINE-99140298; PubMed-10048929;  
RA Garrett D.S., Seok Y.-J., Peterkofsky A., Gronenborn A.M., Clore G.M.;  
RT "Solution structure of the 40,000 Mr phosphoryl transfer complex  
RT between the N-terminal domain of enzyme I and HPr.";  
RL Nat. Struct. Biol. 6:166-173(1999).  
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT  
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE  
CC -TRANSPORT SYSTEM. THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE  
CC (PEP) IS TRANSFERRED TO THE PHOSPHORYL CARRIER PROTEIN HPR BY  
CC ENZYME I. PHOSPHO-HPR THEN TRANSFERS IT TO THE PERMEASE (ENZYMES  
CC I/II/III). HPR IS COMMON TO ALL PTS.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- SIMILARITY: TO ALL OTHER HPR OR HPR DOMAINS.  
CC  
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CC  
CC EMBL; U32844; AAC23358.1; -  
CC HSSP; P07006; 1PPH.  
CC TIGR; H11713; -  
CC InterPro; IPR001020; -  
CC Pfam; PF00381; PTS-HPR; 1.  
CC PRINTS; PR00107; PHOSPHOPHPR.  
CC PROSITE; PS00369; PTS\_HPR\_HIS; 1.  
CC PROSITE; PS00589; PTS\_HPR\_SER; 1.  
KW Phosphotransferase system; Sugar transport; Phosphorylation.  
FT MOD\_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 85 AA; 9004 MW; 3D8D599742311830 CRC64;  
Query Match 82.1%; Score 23; DB 1; Length 85;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
DR EMBL; M10425; AAA24438.1; -

QY 2 QXAVXHL 8

Db 71 OKAVEHL 77  
RESULT 3  
PTHP\_HAEIN  
ID PTHP\_HAEIN STANDARD; PRT; 85 AA.  
AC P43921;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN).  
GN PTHP OR H11713.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE-95350630; PubMed-7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kertavagis A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Utterback T.R., Hanna M.C., Nguyen D.T., Stauder D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
RT influenzae Rd.";  
RL Science 269:496-512(1995).  
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT  
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE  
CC -TRANSPORT SYSTEM. THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE  
CC (PEP) IS TRANSFERRED TO THE PHOSPHORYL CARRIER PROTEIN HPR BY  
CC ENZYME I. PHOSPHO-HPR THEN TRANSFERS IT TO THE PERMEASE (ENZYMES  
CC I/II/III). HPR IS COMMON TO ALL PTS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
CC -!- SIMILARITY: TO ALL OTHER HPR OR HPR DOMAINS.  
CC  
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CC  
CC EMBL; U32844; AAC23358.1; -  
CC HSSP; P07006; 1PPH.  
CC TIGR; H11713; -  
CC InterPro; IPR001020; -  
CC Pfam; PF00381; PTS-HPR; 1.  
CC PRINTS; PR00107; PHOSPHOPHPR.  
CC PROSITE; PS00369; PTS\_HPR\_HIS; 1.  
CC PROSITE; PS00589; PTS\_HPR\_SER; 1.  
KW Phosphotransferase system; Sugar transport; Phosphorylation.  
FT MOD\_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 85 AA; 9004 MW; 3D8D599742311830 CRC64;  
Query Match 82.1%; Score 23; DB 1; Length 85;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
Db 71 QXAVEHL 77  
RESULT 4

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PTHF_KLEPN      STANDARD;          PRT;          85 AA.
AC P16481;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN).
GN PTHS.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-5P14 / KAY2026;
RX MEDLINE=90245592; PubMed=2186369;
RA Titgemeyer F., Eiserich R., Lengstenberg W., Lengel J.W.;
RT "The nucleotide sequence of pth gene from Klebsiella pneumoniae.";
RL Nucleic Acids Res. 18:1898-1898(1990).
CC -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
CC -TRANSPORT SYSTEM. THE PHOSPHORYL GROUP FROM PHOSPHOENOLPYRUVATE
CC (PEP) IS TRANSFERRED TO THE PHOSPHORYL CARRIER PROTEIN HPR BY
CC ENZYME I. PHOSPHO-HPR THEN TRANSFERS IT TO THE PERMEASE (ENZYMES
CC II/III). HPR IS COMMON TO ALL PTS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL031031; CAA19861.1; -
CC InterPro; IPR000191; -
CC Pfam; PF01149; Fapy_DNA_glyco; 1.
CC PROSITE; PS01242; FPG; 1.
KW DNA repair; Hydrolyase; Glycosidase; Endonuclease; Zinc.
FT ZN_FING 231 258 POTENTIAL.
SQ SEQUENCE 276 AA; 30408 MW; 01106CD65EF94DE9 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 276;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 QXAVXHL 8
DB 118 QRAVGHL 124

RESULT 6
VS10_TRYBB STANDARD; PRT; 320 AA.
AC P06013; 1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE VARIANT SURFACE GLYCOPROTEIN ILTAT 1.2 (VSG) (FRAGMENT).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rice-Ficht A.C., Chen K.K., Donelson J.E.;
RT "Sequence homologues near the C-termini of the variable surface
RT glycoproteins of Trypanosoma brucei.";
RL Nature 294:53-57(1981).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
CC TYRANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
CC VSG GENES.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A
CC PI-PLC.
CC
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CC
CC EMBL; J01220; AAA30286.1; -
CC PIR; S09639; S09639.
CC Pfam; PF00913; Trypan_glycop; 1.
KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane.
FT NON_TER 1
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 82.1%; Score 23; DB 1; Length 85;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8
DB 71 QKAVEHL 77

RESULT 5
END8_STRCO STANDARD; PRT; 276 AA.
AC O86920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).
GN NEI OR SC7C7.15C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);

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FT NON\_TER 320 320  
SQ SEQUENCE 320 AA: 33871 MW; D6F18DA8208063C8 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 320;  
Best Local Similarity 57.1%; Pred. No. 57;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
DB 157 QTAIMHL 163

RESULT 7  
PHR\_THETH  
ID PHR\_THETH STANDARD; PRT; 420 AA.  
AC P37250;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE DEOXYRIBODIPYRIMIDINE PHOTOLYASE (EC 4.1.99.3) (DNA PHOTOLYASE)  
DE (PHOTOREACTIVATING ENZYME).  
GN PHR  
OS Thermus aquaticus (subsp. thermophilus).  
OC Bacteria; Thermus/Delnococcus group; Thermus group; Thermus.  
OX NCBI\_TaxID=274;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.  
RC STRAIN-HB27;  
RX MEDLINE-97474278; PubMed=9335302;  
RA Kato R., Hasegawa K., Hidaka Y., Kuramitsu S., Hoshino T.;  
RT "Characterization of a thermostable DNA photolyase from an extremely  
thermophilic bacterium, thermus thermophilus HB27.";  
RL J. Bacteriol. 179:6499-6503(1997).  
RN [2]  
RP SEQUENCE OF 1-194 FROM N.A.  
RC STRAIN-HB27;  
RX MEDLINE-94028944; PubMed=8215386;  
RA Hoshino T., Fujii R., Nakahara T.;  
RT "Molecular cloning and sequence analysis of the crtB gene of Thermus  
thermophilus HB27, an extreme thermophile producing carotenoid  
pigments.";  
RL Appl. Environ. Microbiol. 59:3150-3153(1993).  
CC -!- FUNCTION: THIS ENZYME CATALYZES THE LIGHT-DEPENDENT MONOMERIZATION  
(300-600 NM) OF CYCLOBUTYL PYRIMIDINE DIMERS (IN CIS-SYN  
CONFIGURATION), WHICH ARE FORMED BETWEEN ADJACENT BASES ON THE  
SAME DNA STRAND, UPON EXPOSURE TO ULTRAVIOLET RADIATION.  
CC -!- CATALYTIC ACTIVITY: CYCLOBUTADIPYRIMIDINE (IN DNA) = 2 PYRIMIDINE  
RESIDUES (IN DNA).  
CC -!- COFACTOR: CONTAINS ONE REDUCED FLAVIN (FADH2) CHROMOPHORE THAT IS  
BOUND BY NON-COVALENT INTERACTIONS.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SIMILARITY: BELONGS TO THE DNA PHOTOLYASE CLASS-1 FAMILY.  
CC -----  
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CC -----  
CC EMBL; AB001637; BAA22943.1; -;  
CC InterPro; IPR000474; -;  
CC PRINTS; PR00147; DNAPHOTLYASE.  
CC PROSITE; PS00394; DNA\_PHOTOLYASES.1.1; 1.  
CC PROSITE; PS00691; DNA\_PHOTOLYASES.1.2; FALSE NEG.  
KW Lyase; Chromophore; Flavoprotein; FAD; DNA repair; DNA-binding.  
SQ SEQUENCE 420 AA: 47823 MW; BEA2170963672B97 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 420;

Best Local Similarity 71.4%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
DB 318 QFAVKHL 324

RESULT 8  
HEMI\_CYAPA  
ID HEMI\_CYAPA STANDARD; PRT; 432 AA.  
AC P48077;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR).  
GN HEMA.  
OS Cyanophora paradoxa.  
OG Cyanelle.  
OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.  
OX NCBI\_TaxID=2762;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LB555 / PRINGSHEIM;  
RA Stirewalt V.L., Michalowski C.B., Luffelhardt W., Bohnert H.J.,  
RA Bryant D.A.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 407-432 FROM N.A.  
RC STRAIN-LB555 UTEX;  
RX MEDLINE-90092562; PubMed=2403527;  
RA Bryant D.A., Stirewalt V.L.;  
RT "The cyanelle genome of Cyanophora paradoxa encodes ribosomal  
proteins not encoded by the chloroplasts genomes of higher plants.";  
RL FEBS Lett. 259:273-280(1990).  
CC -!- CATALYTIC ACTIVITY: GLUTAMYL-TRNA (GLU) + NADPH = GLUTAMATE 1-  
SEMIALDEHYDE + NADP(+) + TRNA(GLU).  
CC -!- PATHWAY: FIRST STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY.  
CC INVOLVED IN CHLOROPHYLL BIOSYNTHESIS.  
CC -!- SIMILARITY: BELONGS TO THE GLUTAMYL-TRNA REDUCTASE FAMILY.  
CC -----  
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CC -----  
CC EMBL; U30821; AAA81194.1; -;  
CC EMBL; X17063; CAA34909.1; -;  
CC InterPro; IPR000343; -;  
CC Pfam; PF00745; Glutr; 1.  
CC PROSITE; PS00747; GLUTR; 1.  
CC Porphyrin biosynthesis; Chlorophyll biosynthesis; Oxidoreductase;  
KW NADP; Cyanelle.  
SQ SEQUENCE 432 AA: 48542 MW; F14378FC72FFD05B CRC64;

Query Match 82.1%; Score 23; DB 1; Length 432;  
Best Local Similarity 71.4%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
DB 94 QDAVMHL 100

RESULT 9  
HEMI\_PASMO  
ID HEMI\_PASMO STANDARD; PRT; 434 AA.  
AC P95525;  
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR).  
 GN HEMA.  
 OS Pasteurella multocida.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Pasteurella.  
 OX NCBI\_TaxID=747;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2.5;  
 RA Castrillon R.T.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: GLUTAMYL-TRNA(GLU) + NADPH = GLUTAMATE-1-  
 CC SMIALDEHYDE + NADP(+) + TRNA(GLU).  
 CC -1- PATHWAY: FIRST STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMYL-TRNA REDUCTASE FAMILY.  
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 CC -----  
 DR EMBL; Y10430; CAA71452.1; -.  
 DR InterPro; IPR000343; -.  
 DR Pfam; PF00745; Glutr; 1.  
 DR PROSITE; PS00747; GLUTR; 1.  
 KW porphyrin biosynthesis; Oxidoreductase; NADP.  
 SQ SEQUENCE 434 AA; 48460 MW; D4FF92E52CFFB2B3 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 434;  
 Best Local Similarity 71.4%; Pred. No. 78;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I  
 DB 99 QQAVLHL 105

RESULT 10  
 IFT2\_MOUSE STANDARD; PRT; 472 AA.  
 AC Q64112; Q62385;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE INTERFERON-INDUCED PROTEIN WITH TETRATRICOPEPTIDE REPEATS 2 (IFI-2)  
 DE (INTERFERON-INDUCED 54 KDA PROTEIN) (IFI-54K) (GLUCOCORTICOID-  
 DE ATTENUATED RESPONSE GENE 39 PROTEIN) (GARG-39).  
 GN IFI2 OR IFI54 OR GARG39.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95203869; PubMed=7896268;  
 RA Bluyssen H.A., Vlietstra R.J., Faber P.W., Smit E.M., Hagemeijer A.,  
 RA Trapman J.;  
 RT "Structure, chromosome localization, and regulation of expression of  
 RT the interferon-regulated mouse Ifi54/Ifi56 gene family";  
 RL Genomics 24:137-148(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96239145; PubMed=8660659;  
 RA Smith J.B., Herschman H.R.;  
 RT "The glucocorticoid attenuated response genes GARG-16, GARG-39, and  
 RT GARG-49/IRG2 encode inducible proteins containing multiple  
 RT tetratricopeptide repeat domains";

RL Arch. Biochem. Biophys. 330:290-300(1996).  
 CC -1- SIMILARITY: BELONGS TO THE IFIT FAMILY.  
 CC -1- SIMILARITY: CONTAINS TPR REPEATS.  
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 CC -----  
 DR EMBL; S77713; AAB33830.1; -.  
 DR EMBL; S77710; AAB33830.1; JOINED.  
 DR EMBL; U43085; AAC52626.1; -.  
 DR MGD; MGI:99449; Ifit2.  
 KW Repeat; TPR repeat; Interferon induction.  
 FT REPEAT 51 85 TPR 1.  
 FT REPEAT 87 128 TPR 2.  
 FT REPEAT 157 172 TPR 3B.  
 FT REPEAT 175 209 TPR 4.  
 FT REPEAT 210 244 TPR 5.  
 FT REPEAT 245 278 TPR 6.  
 FT REPEAT 279 289 TPR 7A.  
 FT REPEAT 317 332 TPR 7B.  
 FT REPEAT 333 366 TPR 8.  
 FT REPEAT 369 404 TPR 9.  
 FT REPEAT 428 461 TPR 10.  
 FT CONFLICT 10 11 VC -> ES (IN REF. 2).  
 FT CONFLICT 182 182 F -> N (IN REF. 2).  
 FT CONFLICT 223 224 MISSING (IN REF. 2).  
 FT CONFLICT 468 468 D -> A (IN REF. 2).  
 SQ SEQUENCE 472 AA; 55020 MW; 0C76034B1C0B2C41 CRC64;

Query Match 82.1%; Score 23; DB 1; Length 472;  
 Best Local Similarity 71.4%; Pred. No. 86;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I  
 DB 315 QLVNHL 321

RESULT 11  
 THDF\_TREPA STANDARD; PRT; 495 AA.  
 AC Q83561;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.  
 GN THDF OR TP0550.  
 OS Treponema pallidum  
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.  
 OX NCBI\_TaxID=160;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=NICHOLS;  
 RX STRAIN=NICHOLS;  
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,  
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,  
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,  
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,  
 RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
 RA Venter J.C.;  
 RT "Complete genome sequence of Treponema pallidum, the syphilis  
 RT spirochete";  
 RL Science 281:375-388(1998).  
 CC -1- FUNCTION: INVOLVED IN THIOPHENE OXIDATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ERA/THDF FAMILY OF GTP-BINDING  
 CC PROTEINS.

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CC -----
DR EMBL; AE001230; AAC65535.1; -
DR TIGR; TP0550; -
DR InterPro; IPR002086; -
DR InterPro; IPR002106; -
DR InterPro; IPR002917; -
DR Pfam; PF01926; MMR_HSR1; 1.
KW GTP-binding.
FT NP_BIND 230 237 GTP (BY SIMILARITY).
FT NP_BIND 277 281 GTP (BY SIMILARITY).
FT NP_BIND 337 340 GTP (BY SIMILARITY).
SQ SEQUENCE 495 AA; 53781 MW; C40681269E7AFD2F CRC64;

Query Match 82.1%; Score 23; DB 1; Length 495;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8
DB 150 QQAVLHL 156

RESULT 12
RECO_BAC50
ID RECO_BAC50 STANDARD; PRT; 496 AA.
AC P50729;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATP-DEPENDENT DNA HELICASE RECO (BC 3.6.1.-) (RECOMBINATION PROTEIN
DE S).
GN RECO OR RECS.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / MABURG;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA Serron P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kdg loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=98317281; PubMed=9642195;
RA Fernandez S., Sorokin A., Alonso J.C.;
RT "Genetic recombination in Bacillus subtilis 168: effects of recU and
RT recS mutations on DNA repair and homologous recombination.";
RL J. Bacteriol. 180:3405-3409(1998).
CC -!- FUNCTION: PROBABLE DNA HELICASE. REQUIRED FOR DNA REPAIR AND
CC INTRAMOLECULAR RECOMBINATION.
CC -!- SIMILARITY: BELONGS TO THE RECO SUBFAMILY OF HELICASES.
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DR EMBL; L47648; AAC83947.1; -
DR EMBL; Z99115; CAB14218.1; -
DR EMBL; Z99116; CAB14234.1; -
DR Subtilist; BG11407; recQ.
DR InterPro; IPR001410; -
DR InterPro; IPR001650; -
DR InterPro; IPR002464; -
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW Hydrolase; Helicase; DNA-binding; ATP-binding.
FT NP_BIND 38 45 ATP (POTENTIAL).
FT SITE 136 139 DEAH BOX.
SQ SEQUENCE 496 AA; 56508 MW; DDC2FED715875F2D CRC64;

Query Match 82.1%; Score 23; DB 1; Length 496;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8
DB 189 QHAVRHL 195

RESULT 13
TCPE_SCHPO
ID TCPE_SCHPO STANDARD; PRT; 546 AA.
AC Q9UTM4;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON).
GN CCT5 OR SPAC1420.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Aert R., Voickaert G., McDougall R.C., Rajandream M.A., Barral M.G.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
CC ACTIN AND TUBULIN (BY SIMILARITY).
CC -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KDA THAT
CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
CC -----
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CC -----
DR EMBL; AL121732; CAB57321.1; -
DR InterPro; IPR001844; -
DR InterPro; IPR002194; -
DR InterPro; IPR002423; -
DR Pfam; PF00118; cpn60_TCP1; 1.
DR PRINTS; PR00298; CHAPERONING60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00750; TCP1_1; 1.
DR PROSITE; PS00751; TCP1_2; 1.
DR PROSITE; PS00995; TCP1_3; 1.
KW Chaperone; ATP-binding; Multigene family.
SQ SEQUENCE 546 AA; 59377 MW; DAB279CF67BFDC94 CRC64;
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FT REPEAT 281 285 4 (APPROXIMATE).  
FT REPEAT 286 290 5 (APPROXIMATE).  
FT DOMAIN 579 593 5 X 3 AA TANDEM REPEATS OF P-Q-P.  
SQ SEQUENCE 910 AA; 93452 MW; A169871E20A2E7DB CRC64;

Query Match 82.1%; Score 23; DB 1; Length 910;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QXAVXHL 8  
| | | |  
Db 247 QGAVVHL 253

Search completed: October 25, 2001, 11:28:29  
Job time: 477 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:45 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-8  
Perfect score: 28  
Sequence: 1 QXAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-unclassified:\*  
13: sp-vertebrate:\*  
14: sp-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match %	Length	ID	Description
1	25	89.3	264	2 O07048	O07048 aeromonas h
2	25	89.3	424	11 Q92023	Q92023 mus musculus
3	25	89.3	432	3 O42654	O42654 schizosacch
4	24	85.7	179	2 Q92316	Q92316 schizobium s
5	24	85.7	237	2 Q9WZ25	Q9WZ25 thermotoga
6	24	85.7	257	2 Q9PPN8	Q9PPN8 ureaplasma
7	24	85.7	265	2 Q9RA67	Q9RA67 thermomonos
8	24	85.7	302	2 Q55655	Q55655 synechocyst
9	24	85.7	328	2 Q9L296	Q9L296 streptomyce
10	24	85.7	347	4 Q9HAF9	Q9HAF9 homo sapien
11	24	85.7	363	2 Q52936	Q52936 calothrix v
12	24	85.7	476	10 Q9M318	Q9M318 arabidopsis
13	24	85.7	513	5 Q9N8N9	Q9N8N9 trypanosoma
14	24	85.7	614	1 Q9HSB1	Q9HSB1 halobacteri
15	24	85.7	796	5 Q9VAP3	Q9VAP3 drosophila
16	24	85.7	929	2 O08235	O08235 erwinia car
17	24	85.7	1467	10 Q9M033	Q9M033 arabidopsis
18	24	85.7	2051	5 Q9NAW9	Q9NAW9 anopheles g
19	23	82.1	160	2 Q9K5G3	Q9K5G3 alcaligenes

# SUMMARIES

20	23	82.1	161	2	Q9K5G2	Q9K5G2 alcaligenes
21	23	82.1	166	2	Q9RV36	Q9RV36 alinococcus
22	23	82.1	174	2	O84729	O84729 thiamydial t
23	23	82.1	211	5	Q9VQF0	Q9VQF0 drosophila
24	23	82.1	228	5	Q9VKY4	Q9VKY4 drosophila
25	23	82.1	241	2	Q9X899	Q9X899 streptomyce
26	23	82.1	316	5	Q94483	Q94483 dictyostel
27	23	82.1	340	2	Q9KZU3	Q9KZU3 streptomyce
28	23	82.1	355	5	Q9VDL6	Q9VDL6 drosophila
29	23	82.1	366	1	Q93715	Q93715 drosophila
30	23	82.1	387	2	Q9S3M9	Q9S3M9 bordetella
31	23	82.1	404	5	Q9W170	Q9W170 drosophila
32	23	82.1	419	2	Q9KQ24	Q9KQ24 drosophila
33	23	82.1	453	5	Q9VLJ8	Q9VLJ8 drosophila
34	23	82.1	475	2	O52506	O52506 drosophila
35	23	82.1	475	2	P96956	P96956 drosophila
36	23	82.1	497	2	Q91751	Q91751 drosophila
37	23	82.1	540	4	O43353	O43353 homo sapien
38	23	82.1	573	2	Q9EWH6	Q9EWH6 streptomyce
39	23	82.1	595	14	O84421	O84421 parametium
40	23	82.1	714	2	Q9EYV9	Q9EYV9 klebsiella
41	23	82.1	822	5	O00901	O00901 leishmania
42	23	82.1	851	4	Q9ULM4	Q9ULM4 homo sapien
43	23	82.1	879	14	Q9W1U9	Q9W1U9 human immun
44	23	82.1	890	5	Q9VW12	Q9VW12 drosophila
45	23	82.1	905	2	Q9S6N0	Q9S6N0 bordetella

## ALIGNMENTS

RESULT 1	
O07048	
ID O07048	PRELIMINARY; PRT; 264 AA.
AC O07048	
DT 01-JUL-1997 (TREMBLrel. 04, Created)	
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)	
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)	
DE SIMILARITY WITH KNOWN PROKARYOTIC OR EUKARYOTIC PROTEINS.	
OS Aeromonas hydrophila.	
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;	
OC Aeromonas.	
OX NCBI_TaxID=644;	
ON [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=A6;	
RX MEDLINE=97315206; PubMed=9171380;	
RA Wong C.Y.F., Heuzenroeder M.W., Quinn D.M., Flower R.L.P.;	
RT "Cloning and characterization of two immunophilin-like genes, lipA and	
RT fkpA, on a single 3.9-kilobase fragment of Aeromonas hydrophi	
RT genomic DNA."	
RL J. Bacteriol. 179:3397-3403(1997).	
DR EMBL; U56832; AAC45361.1;	
SQ SEQUENCE 264 AA; 26815 MW; 8D2A5AB9CDE9681 CRC64;	

Query Match 89.3%; Score 25; DB 2; Length 264;  
Best Local Similarity 71.4%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 10 QAAVAHL 16

RESULT 2	
Q92023	
ID Q92023	PRELIMINARY; PRT; 424 AA.
AC Q92023	
DT 01-MAY-1999 (TREMBLrel. 10, Created)	
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE SCF COMPLEX PROTEIN SKP2.	

GN SKP2  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F1(C57/BL6XDBA); TISSUE=THYMUS;  
 RA Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.,  
 RA Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,  
 RA Nakayama K.-I.;  
 RT "Ubiquitin-dependent degradation of Ikb is mediated by a novel  
 RT ubiquitin ligase SCFFWDL";  
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1999).  
 DR EMBL; AF083215; AAD16037.1; -;  
 DR MGD; MGI:1351663; SKP2.  
 DR InterPro; IPR001810; -;  
 DR InterPro; IPR003592; -;  
 DR Pfam; PF00646; F-box; 1.  
 DR PROSITE; PS50181; FBOX; 1.  
 SMART; SM00370; LRR; 1.  
 SEQUENCE 424 AA; 47766 MW; 5B7945C979D26AF9 CRC64;

Query Match 89.3%; Score 25; DB 11; Length 424;  
 Best Local Similarity 71.4%; Pred. No. 98;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 I I I I I  
 DB 275 QAAVAHL 281

RESULT 3  
 O42654 PRELIMINARY; PRT; 432 AA.  
 ID O42654  
 AC O42654;  
 DT 01-JAN-1999 (TrEMBLrel. 09, Created)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE HYPOTHETICAL 49.4 KDA PROTEIN C10F6.15 IN CHROMOSOME I.  
 GN SPAC10F6.15.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Connor R., Churcher C.M., Barrell C.G., Rajandream M.A., Wood V.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: SOME, TO S.FOMBE SPAC4G9.07.  
 DR EMBL; AL009197; CAA15728.1; -;  
 DR KW Hypothetical protein.  
 SQ SEQUENCE 432 AA; 49448 MW; C6CAEB860CCFDE9F CRC64;

Query Match 89.3%; Score 25; DB 3; Length 432;  
 Best Local Similarity 71.4%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 I I I I I  
 DB 142 QTAVALHL 148

RESULT 4  
 Q923L6 PRELIMINARY; PRT; 179 AA.  
 ID Q923L6  
 AC Q923L6;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE NODULATION PROTEIN B (FRAGMENT).  
 OS Rhizobium sp. USDA 2061.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae gr  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=87208;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USDA 2061;  
 RX MEDLINE=99261640; PubMed=10331255;  
 RA Wernegreen J.J., Riley M.A.;  
 RT "Comparison of the evolutionary dynamics of symbiotic and housekeeping  
 RT loci: a case for the genetic coherence of rhizobial lineages";  
 RL Mol. Biol. Evol. 16:98-113(1999).  
 DR EMBL; AF063486; AAD11384.1; -;  
 DR InterPro; IPR002509; -;  
 DR Pfam; PF01522; Polysac\_deacet; 1.  
 DR NON\_TER I  
 FT NON\_TER I  
 SQ SEQUENCE 179 AA; 19262 MW; F66FA52E61942F13 CRC64;

Query Match 85.7%; Score 24; DB 2; Length 179;  
 Best Local Similarity 71.4%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I  
 DB 73 QAAVQHL 79

RESULT 5  
 Q9WZZ5 PRELIMINARY; PRT; 237 AA.  
 ID Q9WZZ5  
 AC Q9WZZ5;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE BACTIRACIN RESISTANCE PROTEIN.  
 GN TM0893.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogales; Thermotoga.  
 OX NCBI\_TaxID=2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB8 / DSM 3109;  
 RX MEDLINE=99287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linner K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of Thermotoga maritima";  
 RL Nature 399:323-329(1999).  
 DR EMBL; AE001754; AAD35974.1; -;  
 DR TIGR; TM0893;  
 SQ SEQUENCE 237 AA; 26036 MW; 759239335C5FE10F CRC64;

Query Match 85.7%; Score 24; DB 2; Length 237;  
 Best Local Similarity 71.4%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I  
 DB 38 QTAVALHL 44

RESULT 6  
 Q9PPN8 PRELIMINARY; PRT; 257 AA.  
 ID Q9PPN8  
 AC Q9PPN8;

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE DIMETHYLADENOSINE TRANSFERASE.  
 GN KSCA.  
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=SERVAR 3;  
 RC STRAIN=20500219; PubMed=11048724;  
 RX MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;  
 RT "The complete sequence of the mucosal pathogen Ureaplasma  
 RT urealyticum.";  
 RL Nature 407:757-762(2000).  
 DR EMBL; AE002158; AAF31015.1; -.  
 DR InterPro; IPR000051; -.  
 DR Pfam; PF00398; RrnaAD; 1.  
 DR PROSITE; PS01131; RRNA-A-DIMETH; 1.  
 SQ SEQUENCE 257 AA; 29781 MW; 85F54A69404ECC4C CRC64;

Query Match 85.7%; Score 24; DB 2; Length 257;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 | | | | |  
 Db 177 QSAVIHL 183  
 RESULT 7  
 Q9RA67 PRELIMINARY; PRT; 265 AA.  
 AC Q9RA67;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE PUTATIVE DIENELACTONE HYDROLASE.  
 GN DLHA.  
 OS Thermomonospora fusca.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptosporangineae; Thermomonosporaceae;  
 OC Thermobifida.  
 OX NCBI\_TaxID=2021;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP Spiridonov N.A., Wilson D.B.;  
 RA "PepA and dlhA genes from Thermobifida fusca.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF218823; AAF25687.1; -.  
 DR InterPro; IPR000379; -.  
 DR InterPro; IPR002925; -.  
 DR Pfam; PF01738; DLH; 2.  
 KW Hydrolase.  
 SQ SEQUENCE 265 AA; 29069 MW; 06C5A8E364BCDF8F CRC64;

Query Match 85.7%; Score 24; DB 2; Length 265;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 | | | | |  
 Db 97 QTAVDHL 103

RESULT 8  
 Q55655

ID Q55655 PRELIMINARY; PRT; 302 AA.  
 AC Q55655;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE HYPOTHETICAL 33.8 KDA PROTEIN.  
 GN SLL0310.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=PCC6803;  
 RC Tabata S.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 RA Suglura M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the  
 RT region from map positions 64% to 92% of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura  
 RA Miyajima N., Hirose M., Suglura M., Sasaki S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Ohta S.,  
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasui H.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL; D64000; BAA10175.1; -.  
 DR InterPro; IPR000182; -.  
 DR Pfam; PF00583; Acetyltransf; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 302 AA; 33760 MW; 62D74D7F5B74564E CRC64;  
 Query Match 85.7%; Score 24; DB 2; Length 302;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QXAVXHL 8  
 | | | | |  
 Db 90 QTAIAHL 96  
 RESULT 9  
 Q9L296 PRELIMINARY; PRT; 328 AA.  
 ID Q9L296;  
 AC Q9L296;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HYPOTHETICAL 37.4 KDA PROTEIN (FRAGMENT).  
 GN SCL2.01.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptococcaceae;  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=A3(2);  
 RC Seeger K.J., Harris D.;  
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);

RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RC SEQUENCE FROM N.A.  
RP STRAIN=A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb streptomycetes coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL; ALI37778; CAB70913.1; -;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 328 AA; 37352 MW; D60E937C5C48321F CRC64;

Query Match 85.7%; Score 24; DB 2; Length 328;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |  
Db 43 QTAVDHL 49

RESULT 10  
QHAF9 PRELIMINARY; PRT; 347 AA.  
AC QHAF9;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DE CDNA FLJ11703 FIS, CLONE HENBA1005075.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=WHOLE EMBRYO, MAINLY HEAD;  
RA Tsogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara K., Takeuchi K.,  
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;  
RT "NEDO human cDNA sequencing project.";  
BL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RI EMBL; AK021765; BAB13890.1; -;  
SQ SEQUENCE 347 AA; 37973 MW; DF68202D85E6EC48 CRC64;

Query Match 85.7%; Score 24; DB 4; Length 347;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | |  
Db 86 QAAVLHL 92

RESULT 11  
O52936 PRELIMINARY; PRT; 363 AA.  
AC O52936;  
DT 01-JUN-1998 (TReMBLrel. 06, Created)  
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)  
DE HYPOTHETICAL 43.1 KDA PROTEIN (FRAGMENT).  
OS Calothrix viguieri.  
OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Calothrix.  
OX NCBI\_TaxID=57746;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=D254;  
RA Evans I.M., Bown D., Gupta A., Morby A.P., Whittton B.A.,  
RA Gatehouse J.A.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y09899; CAA71029.1; -;  
KW Hypothetical protein.  
FT NON\_TER 1  
FT NON\_TER 363  
SQ SEQUENCE 363 AA; 43113 MW; FAE7DB281D7E1BC9 CRC64;

Query Match 85.7%; Score 24; DB 2; Length 363;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QXAVXHL 8  
| | | |  
Db 221 QEAVSHL 227

RESULT 12  
Q9M318 PRELIMINARY; PRT; 476 AA.  
AC Q9M318;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 51.9 KDA PROTEIN.  
GN F2A19.90.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X., Quetier F., Salanoubat M.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; ALI32962; CAB71079.1; -;  
DR InterPro; IPR000743; -;  
DR InterPro; IPR001066; -;  
DR Pfam; PF00295; Glyco\_hydro\_28; 1.  
DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 51939 MW; 48233D8B48A4BEDD CRC64;

Query Match 85.7%; Score 24; DB 10; Length 476;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QXAVXHL 8  
| | | |  
Db 65 QSAVDHL 71

RESULT 13  
Q9N8N9 PRELIMINARY; PRT; 513 AA.  
AC Q9N8N9;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE PROBABLE AXONEME CENTRAL APPARATUS PROTEIN.  
GN CHRI.235.  
OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

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OX NCBI_TaxID=5691;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajandream M.A., Barrall B.G.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL359782; CAB95504.1; -.
DR InterPro; IPR000225; -.
DR Pfam; PF00514; Armadillo_seg; 8.
DR SMART; SM00185; ARM; 1.
SQ SEQUENCE 513 AA; 56126 MW; 40BB4546A1B390C3 CRC64;

Query Match 85.7%; Score 24; DB 5; Length 513;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8
1 |||
208 QDAVTHL 214

RESULT 14
ID Q9HSB1 PRELIMINARY; PRT; 614 AA.
AC Q9HSB1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DOLICHOL-P-GLUCOSE SYNTHETASE.
GN DPG OR VNG0318G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitthaus B., Keller K., Cruz R., Hanson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Llang P., Riley M., Hood L., Dassarma S.;
RA "Genome sequence of Halobacterium species NRC-1."
DR EMBL; AE004992; AAG18896.1; -.
DR Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR InterPro; IPR001173; -.
DR Pfam; PF00535; Glycos.transf.2; 1.
SQ SEQUENCE 614 AA; 64802 MW; DAD585C50B14DAB2 CRC64;

Query Match 85.7%; Score 24; DB 1; Length 614;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8
1 |||
DB 65 QSAVRHL 71

RESULT 15
ID Q9VAP3 PRELIMINARY; PRT; 796 AA.
AC Q9VAP3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CG11880 PROTEIN.

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GN CG11880.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscophila;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.I.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie K.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Hendrix D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.,
RA Brandon R.C., Rogers Y.-H.C., Blazewicz R.G., Champe M., Pfeiffer J.,
RA Wan K.H., Doyle G., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Balschwey A.D.,
RA Balcer R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley H.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov A.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chao M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser F.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kettler J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen Y.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith I.,
RA Spires R., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang W.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Ye J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003768; AAF56859.1; -.
DR FlyBase; FBgn0039637; CG11880.
DR InterPro; IPR001662; -.
DR ProDom; PD006217; -.
SQ SEQUENCE 796 AA; 90628 MW; 20961DD89A3EE3B CRC64;

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Query Match 85.7%; Score 24; DB 5; Length 796;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels

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QY 2 QXAVXHL 8
1 |||
DB 587 QTAIVYHL 593

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Search completed: October 25, 2001, 11:27:45
Job time: 448 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:21 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: us-09-630-333-8  
Perfect score: 28  
Sequence: 1 QXAVXHL 8  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	89.3	432	2 T37509	hypothetical prote
2	24	85.7	237	2 F72321	bacitracin resista
3	24	85.7	257	2 E82871	dimethyladenosine
4	24	85.7	302	2 S76323	hypothetical prote
5	24	85.7	476	2 T47941	hypothetical prote
6	24	85.7	614	2 D84191	dolichol-P-glucose
7	24	85.7	1467	2 T48162	hypothetical prote
8	24	85.7	1510	2 D64120	cell division prot
9	23	82.1	85	1 WQECPH	phosphotransferase
10	23	82.1	85	1 WQEBPH	phosphotransferase
11	23	82.1	85	1 S12749	phosphotransferase
12	23	82.1	85	1 T64137	phosphotransferase
13	23	82.1	85	2 B85884	PRS system protein
14	23	82.1	166	2 A75426	hypothetical prote
15	23	82.1	174	2 G71478	hypothetical prote
16	23	82.1	241	2 T36184	hypothetical prote
17	23	82.1	276	2 T35693	DNA glycosylase -
18	23	82.1	320	2 S09639	variant surface gl
19	23	82.1	366	2 T44937	glucose 1-dehydrog
20	23	82.1	419	2 C82109	glutamyl-tRNA redu
21	23	82.1	432	2 T06831	glutamyl-tRNA redu
22	23	82.1	470	2 S71335	glucocorticoid-att
23	23	82.1	472	2 A55508	interferon alpha I
24	23	82.1	475	2 D83202	alginate biosynthe
25	23	82.1	495	2 B71311	probable thiophene
26	23	82.1	496	2 A69691	ATP-dependent DNA
27	23	82.1	497	2 F83634	hypothetical prote
28	23	82.1	546	2 T37665	probable t-complex
29	23	82.1	595	2 T17590	probable glutamine

30	23	82.1	687	2 T30958	hypothetical prote
31	23	82.1	822	2 T02824	hypothetical prote
32	23	82.1	910	2 A32560	outer membrane pro
33	23	82.1	1121	2 C82120	transcription acqu
34	23	82.1	1206	2 S24407	formil. form IV
35	23	82.1	1213	2 A41724	limb d. mity (ld
36	23	82.1	1231	2 S33089	protein, prosinc p
37	23	82.1	1468	2 S11515	formin - mouse
38	23	82.1	1735	1 S22812	DNA-directed RNA p
39	23	82.1	1749	2 S75071	hypothetical prote
40	23	82.1	2347	1 TVHURS	kinase-related p
41	23	82.1	4447	2 A69679	polyketide synth
42	22	78.6	14	1 BSTD	bombesin - fire-b
43	22	78.6	57	2 A82521	hypothetical prote
44	22	78.6	101	2 S29093	SMD3 protein - yea
45	22	78.6	107	1 BSTDY	bombesin precursor

ALIGNMENTS

RESULT 1  
T37509  
hypothetical protein SPAC10F6.15 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T37509  
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood V.  
submitted to the EMBL Data Library, November 1997  
A:Reference number: 221719  
A:Accession: T37509  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-432 <CON>  
A:Cross-references: EMBL:AL009197; PIDN:CAA15728.1; GSPDB:GN00066; SHUB.SPAC1  
A:Experimental source: strain 972h; cosmid c10F6  
C:Genetics:  
A:Gene: SPDB:SPAC10F6.15  
A:Map position: 1

Query Match 89.3%; Score 25; DB 2; Length 432;  
Best Local Similarity 71.4%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0  
Qy 2 QXAVXHL 8  
Db 142 QTAVSHL 148

RESULT 2  
F72321  
bacitracin resistance protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C:Accession: F72321  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; et al.  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A:Reference number: A72200; MUID:99287316  
A:Accession: F72321  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-237 <ARN>  
A:Cross-references: GB:AE001754; GB:AE000512; NID:g4981417; PIDN:AA015974.1, P110, P111  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0893  
C:Superfamily: Escherichia coli bacitracin resistance protein bar

Query Match 85.7%; Score 24; DB 2; Length 237;  
Best Local Similarity 71.4%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 38 QTAVALHL 44

RESULT 3  
EB2871  
dimethyladenosine transferase UU601 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
C:Accession: EB2871  
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
A:Reference number: A82870  
A:Accession: EB2871  
A:Molecule type: DNA  
A:Residues: 1-257 <GLA>  
A:Cross-references: GB:AE002158; GB:AF222894; NID:96899599; PIDN:AAF31015.1; GSPDB:GN001  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: ksgA; UU601  
A:Genetic code: SGC3  
C:Superfamily: rRNA (adenine-N6-)-methyltransferase

Query Match 85.7%; Score 24; DB 2; Length 257;  
Best Local Similarity 71.4%; Pred. No. 46;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 177 QSAVHL 183

RESULT 4  
S76323  
hypothetical protein sll0310 - Synecocystis sp. (strain PCC 6803)  
C:Species: Synecocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S76323  
R:Yaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis  
s.  
A:Reference number: S74322; MUID:97061201  
A:Accession: S76323  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-302 <RAN>  
A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAAI0175.1; PID:g100154  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 85.7%; Score 24; DB 2; Length 302;  
Best Local Similarity 57.1%; Pred. No. 56;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 90 QTAIAHL 96

RESULT 5  
T47941  
hypothetical protein F2A19.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T47941  
R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Meves, H.W.; Lemcke, K.; Mayer, K.F.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z24480  
A:Accession: T47941  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-476 <DEH>  
A:Cross-references: EMBL:AL132962  
A:Experimental source: cultivar Columbia; BAC clone F2A19  
C:Genetics:  
A:Map position: 3  
A:Introns: 155/1; 213/2; 237/1  
A:Note: F2A19.90

Query Match 85.7%; Score 24; DB 2; Length 476;  
Best Local Similarity 71.4%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 65 QSAVDHL 71

RESULT 6  
D84191  
dolichol-P-glucose synthetase [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: D84191  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, I.D.; Lasky  
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Mallocks, D.G.; Ja  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbard, H.; Lowe, I.  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483  
A:Accession: D84191  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-614 <STO>  
A:Cross-references: GB:AE004437; NID:g10579946; PIDN:AAG18896.1; GSPDB:GN00138  
C:Genetics:  
A:Gene: dpg

Query Match 85.7%; Score 24; DB 2; Length 614;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 65 QSAVRHL 71

RESULT 7  
T84162  
hypothetical protein T1008.110 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T48162  
R:Bevan, M.; Pohl, T.; Weizenecker, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer,  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24486  
A:Accession: T48162  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1467 <BEV>  
A:Cross-references: EMBL:AL161746  
A:Experimental source: cultivar Columbia; BAC clone T1008

## C:Genetics:

A:Map position: 5  
A:Introns: 68/2; 121/3; 152/3; 178/1; 234/2; 291/3; 331/3; 516/3; 698/3; 721/3; 760/3; 820/3  
A:Note: T1008.110

Query Match 85.7%; Score 24; DB 2; Length 1467;

Best Local Similarity 71.4%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QXAVXHL 8

I I I I I

Db 841 QSAVHHL 847

## RESULT 8

D64120 cell division protein mukB - Haemophilus influenzae (strain Rd KW20)

A:Species: Haemophilus influenzae

A:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 02-Feb-2001

A:Accession: D64120

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.H.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.B.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: D64120

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1510 <TIGR>

A:Cross-references: GB:U32817; GB:L42023; NID:gi574201; PIDN:AAC23022.1; PID:gi574208; TIGR

C:Genetics:

A:Gene: mukB

C:Function:

A:Description: required for chromosome partitioning

C:Superfamily: Escherichia coli mukB protein

C:Keywords: ATP; coiled coil; nucleotide binding; P-loop

F:75-82/Region: nucleotide-binding motif A (P-loop)

Query Match 85.7%; Score 24; DB 2; Length 1510;

Best Local Similarity 71.4%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 QXAVXHL 8

I I I I I

371 QSAVDHL 377

## RESULT 9

WQECFH

phosphotransferase system phosphohistidine-containing protein [validated] - Escherichia

A:Alternate names: phosphotransferase system HPR

C:Species: Escherichia coli

A:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 15-Sep-2000

C:Accession: A29785; A24035; A32345; G28181; F65015

R:Saffen, D.W.; Presper, K.A.; Doering, T.L.; Roseman, S.

J. Biol. Chem. 262, 16241-16253, 1987

A:Title: Sugar transport by the bacterial phosphotransferase system. Molecular cloning a

A:Reference number: A29785; MUID:88058992

A:Accession: A29785

A:Molecule type: DNA

A:Residues: 1-85 <SAE>

A:Cross-references: GB:J02796; NID:gl47397; PIDN:AAA24440.1; PID:gl47398

R:De Reuse, H.; Roy, A.; Danchin, A.

Gene 35, 199-207, 1985

A:Title: Analysis of the ptsH-ptsI-crr region in Escherichia coli K-12: nucleotide sequ

A:Reference number: A24035; MUID:85286351

A:Accession: A24035

A:Molecule type: DNA

A:Residues: 1-85 <DER1>

A:Cross-references: GB:M10425; NID:gl47394; PIDN:AAA24438.1; PID:gl47395

R:De Reuse, H.; Danchin, A.

J. Bacteriol. 170, 3827-3837, 1988

A:Title: The ptsH, ptsI, and crr genes of the Escherichia coli phosphoenolpyruvate-de

A:Reference number: A32345; MUID:88314869

A:Accession: A32345

A:Molecule type: DNA

A:Residues: 1-85 <DER2>

A:Cross-references: GB:M21994; NID:gl47261; PIDN:AAA24384.1; PID:gl47263

R:Byrne, C.R.; Monroe, R.S.; Ward, K.A.; Kredich, N.M.

J. Bacteriol. 170, 3150-3157, 1988

A:Title: DNA sequences of the cysK regions of Salmonella typhimurium and Escherichia

A:Reference number: A28181; MUID:88257033

A:Accession: G28181

A:Molecule type: DNA

A:Residues: 1-85 <BYR>

A:Cross-references: GB:M21451; NID:gl45684; PIDN:AAA23655.1; PID:gl45687

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burlingame, V.; Kelley, M.;

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: F65015

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-85 <BLAT>

A:Cross-references: GB:AB000329; GB:U00096; NID:g2367137; PIDN:AAC75468.1; PID:gl47487

A:Experimental source: strain K-12, substrain MG1655

R:Prasad, L.; Delbaere, L.T.J.; Quail, J.W.; Vandonselaar, M.

submitted to the Brookhaven Protein Data Bank, April 1993

A:Reference number: A52379; PDB:1JEL

A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 1-2, 'E', 4-44

R:Sharma, S.; Georges, F.; Delbaere, L.T.J.; Lee, J.S.; Klevit, R.E.; Waygood, E.B.

Proc. Natl. Acad. Sci. U.S.A. 88, 4877-4881, 1991

A:Title: Epitope mapping by mutagenesis distinguishes between the two tertiary struct

A:Reference number: A39710; MUID:91271296

A:Contents: annotation; site-directed mutagenesis

R:Jia, Z.; Quail, W.; Delbaere, L.

submitted to the Brookhaven Protein Data Bank, October 1993

A:Reference number: A51916; PDB:1POH

A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-85

R:Van Nuland, N.A.J.; Scheek, R.M.; Robillard, G.T.

submitted to the Brookhaven Protein Data Bank, February 1994

A:Reference number: A52354; PDB:1HDN

A:Contents: annotation; conformation by (1)H-, (13)C-, and (15)N NMR; residues 1-85

R:van Nuland, N.A.J.; Hangyi, I.W.; van Schaik, R.C.; Berendsen, H.J.; van Gunsteren

J. Mol. Biol. 237, 544-559, 1994

A:Title: The high-resolution structure of the histidine-containing phosphocarrier pro

Overhauser effect data.

A:Reference number: A58916; MUID:94210480

A:Contents: annotation; conformation by (1)H-, (13)C-, and (15)N NMR

R:van Nuland, N.A.J.; Groetzing, J.; Dijkstra, K.; Scheek, R.M.; Robillard, G.T.

Eur. J. Biochem. 210, 881-891, 1992

A:Title: Determination of the three-dimensional solution structure of the histidine-c

A:Reference number: A58912; MUID:93130914

A:Contents: annotation; conformation by (1)H-, (13)C-, and (15)N NMR

R:van Nuland, N.A.J.; Scheek, R.M.; Robillard, G.T.

submitted to the Brookhaven Protein Data Bank, August 1995

A:Reference number: A66357; PDB:1PFH

A:Contents: annotation; conformation by (1)H-, (13)C-, and (15)N NMR; residues 1-85

R:van Nuland, N.A.J.; Boelens, R.; Scheek, R.M.; Robillard, G.T.

J. Mol. Biol. 246, 180-193, 1995

A:Title: High-resolution structure of the phosphorylated form of the histidine-contai

A:Reference number: A58913; MUID:95156481

A:Contents: annotation; conformation by (1)H-, (13)C-, and (15)N NMR

R:Napper, S.; Delbaere, L.; Waygood, B.

submitted to the Brookhaven Protein Data Bank, August 1996

A:Reference number: A67665; PDB:1OPD

A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-2, 'E', 4-45,

R:Napper, S.; Anderson, J.W.; Georges, F.; Quail, J.W.; Delbaere, L.; Waygood, E.B.

Biochemistry 35, 11260-11267, 1996

A:Title: Mutation of serine-46 to aspartate in the histidine-containing protein of Escherichia coli  
 A:Reference number: A58915; MUID:96378616  
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms  
 C:Comment: This protein is phosphorylated by the phosphotransferase system enzyme I (see systems).

C:Genetics:  
 A:Gene: ptsH  
 A:Map position: 52 min  
 C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; phosphotransferase system phosphohistidine-containing protein homology <H  
 F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H  
 F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I) #s  
 F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
 I I I I I  
 Db 71 QKAVEHL 77

RESULT 10

WQEBPH

N:Alternate names: phosphocarrier protein - Salmonella typhimurium  
 C:Species: Salmonella typhimurium

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 16-Jul-1999

C:Accession: C28181; S04159; A22849

R:Byrne, C.R.; Monroe, R.S.; Ward, K.A.; Kredich, N.M.

J. Bacteriol. 170, 3150-3157, 1988

A:Title: DNA sequences of the cysK regions of Salmonella typhimurium and Escherichia coli

A:Reference number: A28181; MUID:88257033

A:Accession: C28181

A:Molecule type: DNA

A:Residues: 1-85 <BTR>

A:CROSS-references: GB:M21450; NID:g153933; PIDN:AAA27052.1; PID:g153936

R:Schlirow, B.J.; Yamada, M.; Sailer Jr., M.H.

Mol. Microbiol. 3, 113-118, 1989

A:Title: Partial nucleotide sequence of the pts operon in Salmonella typhimurium: comparison

A:Reference number: S04159; MUID:89237892

A:Accession: S04159

A:Molecule type: DNA

A:Residues: 1-85 <SCH>

A:CROSS-references: EMBL:X14737; NID:g47844; PIDN:CAA32865.1; PID:g47845

R:Powells, D.A.; Roseman, S.

J. Biol. Chem. 259, 15212-15214, 1984

A:Title: The primary structure of Salmonella typhimurium HPr, a phosphocarrier protein of

A:Reference number: A22849; MUID:85080006

A:Accession: A22849

A:Molecule type: protein

A:Residues: 1-20, 'G', '22-84', 'Z' <POW>

C:Comment: The phosphoenolpyruvate--glycose phosphotransferase system (PTS) comprises two subunits (II-A/II-B or III/III'), lipid, and divalent cation. The phosphoryl group is transferred to the substrate as it crosses the cell membrane.

C:Genetics:

A:Gene: ptsH

A:Map position: 49 min

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system

F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H

F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I) #s

F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I

Db 71 QKAVEHL 77

RESULT 11

S12749

phosphotransferase system phosphohistidine-containing protein - Klebsiella pneumoniae  
 C:Species: Klebsiella pneumoniae

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S12749

R:Titgemeyer, F.; Eisermann, R.; Hengstenberg, W.; Lengeler, J.W.

Nucleic Acids Res. 18, 1898, 1990

A:Title: The nucleotide sequence of ptsH gene from Klebsiella pneumoniae.

A:Reference number: S12749; MUID:90245592

A:Accession: S12749

A:Molecule type: DNA

A:Residues: 1-85 <TIT>

A:CROSS-references: EMBL:X51452; NID:g43910; PIDN:CAA35818.1; PID:g43911

C:Genetics:

A:Gene: ptsH

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system

F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H

F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I)

F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I

Db 71 QKAVEHL 77

RESULT 12

I64137

phosphotransferase system phosphohistidine-containing protein - Haemophilus influenza

C:Species: Haemophilus influenzae

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: I64137

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: I64137

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-85 <TIGR>

C:CROSS-references: GB:U32844; GB:L42023; NID:g1574563; PIDN:AAC23358.1; PID:g1574568

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotransferase system phosphocarrier protein; phosphohistidine; phosphoprotein; sugar transport system

F:8-84/Domain: phosphotransferase system phosphohistidine-containing protein homology <H

F:15/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme I)

F:46/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 82.1%; Score 23; DB 1; Length 85;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
 I I I I I

Db 71 QKAVEHL 77

RESULT 13

B85884

PTS system protein Hpr [imported] - Escherichia coli (strain O157:H7)

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
C:Accession: B85884  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B85884  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-85 <STO>  
A:Cross-references: GB:AE005174; NID:gi12516791; PIDN:AA057534.1; GSPDB:GN00145; UNCP:236  
A:Experimental source: strain O157:H7, substrain EDU933  
C:Genetics:  
A:Gene: ptsH

Query Match 82.1%; Score 23; DB 2; Length 85;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
| | | |  
Db 71 QXAVEHL 77

RESULT 14  
A75426  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
C:Accession: A75426  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896  
A:Accession: A75426  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-166 <WHI>  
A:Cross-references: GB:AE001968; GB:AE0000513; NID:g6458930; PIDN:AAF10769.1; PID:g645893  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1194  
A:Map position: 1  
C:Superfamily: Deinococcus radiodurans hypothetical protein DR1194

Query Match 82.1%; Score 23; DB 2; Length 166;  
Best Local Similarity 71.4%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
| | | |  
Db 144 QXAVIHL 150

RESULT 15  
G71478  
hypothetical protein CT724 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C>Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 08-Oct-1999  
C:Accession: G71478  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trad  
A:Reference number: A71570; MUID:99000809  
A:Accession: G71478  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-174 <ARN>

A:Cross-references: GB:AE001343; GB:AE001273; NID:g3329176; PIDN:AE001343; PID:g332  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: CT724

Query Match 82.1%; Score 23; DB 2; Length 174;  
Best Local Similarity 71.4%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
| | | |  
Db 113 QEAQVHL 119

Search completed: October 25, 2001, 11:25:22  
Job time: 335 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-8  
Perfect score: 28  
Sequence: 1 QXAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	85.7	9	1	US-08-263-905-12
2	24	85.7	9	5	PCT-US93-00183-12
3	23	82.1	8	1	US-08-168-390-12
4	23	82.1	8	6	5217955-35
5	23	82.1	8	6	5217955-36
6	23	82.1	9	6	5217955-13
7	23	82.1	9	6	5217955-14
8	23	82.1	9	6	5217955-15
9	23	82.1	9	6	5217955-22
10	23	82.1	540	3	US-09-019-942-1
11	23	82.1	910	4	US-08-460-269C-2
12	22	78.6	8	1	US-08-168-390-11
13	22	78.6	8	2	US-08-337-127-9
14	22	78.6	8	6	5217955-32
15	22	78.6	8	6	5217955-34
16	22	78.6	9	1	US-07-619-747B-1
17	22	78.6	9	1	US-07-619-747B-2
18	22	78.6	9	1	US-07-619-747B-4
19	22	78.6	9	1	US-07-619-747B-5
20	22	78.6	9	1	US-07-619-747B-9
21	22	78.6	9	1	US-07-619-747B-10
22	22	78.6	9	1	US-07-619-747B-12
23	22	78.6	9	1	US-07-619-747B-14
24	22	78.6	9	1	US-07-619-747B-15
25	22	78.6	9	1	US-07-619-747B-17
26	22	78.6	9	1	US-07-619-747B-18
27	22	78.6	9	1	US-07-619-747B-22

28	22	78.6	9	1	US-07-619-747B-23
29	22	78.6	9	1	US-07-619-747B-24
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32	22	78.6	9	1	US-07-619-747B-27
33	22	78.6	9	1	US-07-619-747B-28
34	22	78.6	9	1	US-07-619-747B-29
35	22	78.6	9	1	US-07-619-747B-30
36	22	78.6	9	1	US-07-619-747B-31
37	22	78.6	9	1	US-07-619-747B-32
38	22	78.6	9	1	US-07-619-747B-33
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41	22	78.6	9	1	US-07-619-747B-36
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44	22	78.6	9	1	US-07-619-747B-39
45	22	78.6	9	1	US-07-619-747B-40

ALIGNMENTS

RESULT 1  
US-08-263-905-12  
; Sequence 12, Application US/08263905  
; Patent No. 5428018  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Judson V  
; TITLE OF INVENTION: Phenylalanine Analogs of Bombesin  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marion Merrell Dow Inc.  
; STREET: 2110 East Galbraith Rd.  
; CITY: Cincinnati P. O. Box 156300  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45215-6300  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/263,905  
; FILING DATE: 22-JUN-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/833,834  
; FILING DATE: 07-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collier, Kenneth J  
; REGISTRATION NUMBER: 34,982  
; REFERENCE/DOCKET NUMBER: M01614 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (513) 948-7834  
; TELEFAX: (513) 948-7961  
; TELEX: 214320  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-263-905-12

Query Match 85.7%; Score 24; DB 1; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels

QY 2 QXAVXHL 8

Db 3 QTAUGH 9

RESULT 2  
PCT-US93-00183-12  
; Sequence 12, Application PC/US9300183  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Judson V  
; TITLE OF INVENTION: Phenylalanine Analogs of Bombesin  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marion Merrell Dow Inc.  
; STREET: 2110 East Galbraith Rd.  
; CITY: Cincinnati P. O. Box 156300  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45215-6300  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00183  
; FILING DATE: 19930107  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collier, Kenneth J  
; REGISTRATION NUMBER: 34,982  
; REFERENCE/DOCKET NUMBER: W01614 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (513) 948-7834  
; TELEFAX: (513) 948-7961  
; TELEX: 214320  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-00183-12

Query Match 85.7%; Score 24; DB 5; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 QXAVXHL 8  
1 1 1 1 1  
Db 3 QTAUGH 9

RESULT 3  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end cap.  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "The alanine at position 6  
; OTHER INFORMATION: is dextrorotatory alanine."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-12

Query Match 82.1%; Score 23; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1 1 1 1 1  
Db 2 QWAVHL 8

RESULT 4  
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; Patent No. 5217955  
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 35:  
; SEQUENCE LENGTH: 8  
5217955-35

Query Match 82.1%; Score 23; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1 1 1 1 1

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Db      2 QWAVAHL 8
RESULT  5
5217955-36
;PATENT NO. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
;OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
;SEQ ID NO:36:
; LENGTH: 8
;955-36
Query Match      82.1%; Score 23; DB 6; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 QXAVXHL 8
      | | | |
Db      2 QWAVAHL 8
RESULT  6
5217955-13
;PATENT NO. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
;OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
;SEQ ID NO:13:
; LENGTH: 9
;955-13
Query Match      82.1%; Score 23; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 QXAVXHL 8
      | | | |
Db      2 QWAVAHL 8
RESULT  7
5217955-14
;PATENT NO. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
;OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
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; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
;SEQ ID NO:14:
; LENGTH: 9
5217955-14
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Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 QXAVXHL 8
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Db      2 QWAVAHL 8
RESULT  8
5217955-15
;PATENT NO. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
;OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
;SEQ ID NO:15:
; LENGTH: 9
5217955-15
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Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 QXAVXHL 8
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Db      2 QWAVAHL 8
RESULT  9
5217955-22
;PATENT NO. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
;OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
;SEQ ID NO:22:
; LENGTH: 9
5217955-22
Query Match      82.1%; Score 23; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 QXAVXHL 8
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Db      2 QWAVAHL 8
RESULT  9
5217955-22
;PATENT NO. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
;OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
;SEQ ID NO:22:
; LENGTH: 9
5217955-22
Query Match      82.1%; Score 23; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 QXAVXHL 8
      | | | |
Db      2 QWAVAHL 8
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RESULT 10  
US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-019-942-1

Query Match 82.1%; Score 23; DB 3; Length 540;  
Best Local Similarity 71.4%; Pred. No. 3.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
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Db 43 QVAVKHL 49

RESULT 11  
US-08-460-269C-2  
; Sequence 2, Application US/08460269C  
; Patent No. 6197548  
; GENERAL INFORMATION:  
; APPLICANT: CLARE, JEFFREY J.  
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN  
; YEAST  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
; STREET: 2200 Clarendon Blvd., Suite 1400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,269C  
; FILING DATE: 02-Jun-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lebovitz, Richard M.  
; REGISTRATION NUMBER: 37,067  
; REFERENCE/DOCKET NUMBER: Popov-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 243-6333  
; TELEFAX: (703) 243-6410  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 910 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-460-269C-2

Query Match 82.1%; Score 23; DB 4; Length 910;  
Best Local Similarity 71.4%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXAVXHL 8  
| | | | |  
Db 247 QGAVVHL 253

RESULT 12  
US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "The amino-terminal residue
; OTHER INFORMATION: comprises one of several chemical end caps."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "The carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-11
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Query Match 78.6%; Score 22; DB 1; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 QXAVXHL 8
Db 2 QWAVGHL 8
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## RESULT 13

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US-08-337-127-9
; Sequence 9, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
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; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/009000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an methylester C-terminus (i.e., COOCH3),
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).
US-08-337-127-9
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Query Match 78.6%; Score 22; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QXAVXHL 8
Db 2 QWAVGHL 8

RESULT 14
5217955-32
; Patent No. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:32:
; LENGTH: 8
5217955-32
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Query Match 78.6%; Score 22; DB 6; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 QXAVXHL 8
Db 2 QWAVGHL 8
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RESULT 15
5217955-34
; Patent No. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
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;  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 34  
; LENGTH: 8  
5217955-34

Query Match 78.6%; Score 22; DB 6; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QXAVXHL 8  
| | | |  
Db 2 QWAVGHL 8

Search completed: October 25, 2001, 11:23:56  
Job time: 269 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:22 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-9  
Perfect score: 40  
Sequence: 1 QMXVGH 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
1 number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	14	1 BSTD	bombesin - fire-be
2	38	95.0	107	1 BSTDY	bombesin precursor
3	38	95.0	119	2 A39261	bombesin precursor
4	36	90.0	232	2 S32963	hypothetical prote
5	36	90.0	256	2 T48787	hypothetical prote
6	34	85.0	9	2 S07204	litorin I - Austr
7	34	85.0	13	2 A60409	bombesin-like pept
8	34	85.0	82	2 B28945	ranatensin precurs
9	33	82.5	10	2 P00177	neuromedin C - lau
10	33	82.5	10	2 A06647	neuromedin C - bov
11	33	82.5	25	2 S06263	gastrin-releasing
12	33	82.5	27	1 RHFGA	gastrin-releasing
13	33	82.5	27	1 RHGPGA	gastrin-releasing
14	33	82.5	27	1 RHCHA	gastrin-releasing
15	33	82.5	120	2 A47201	bombesinlike pepti
16	33	82.5	134	2 I47010	gastrin-releasing
17	33	82.5	138	2 A26182	gastrin-releasing
18	33	82.5	147	2 A40922	gastrin-releasing
19	33	82.5	148	1 B26182	gastrin-releasing
20	33	82.5	155	2 A42437	gastrin-releasing
21	33	82.5	308	1 QRECLH	leucine transport
22	33	82.5	308	2 H66012	hypothetical prote
23	33	82.5	372	2 G83074	glutamate 5-kinase
24	33	82.5	700	2 A56976	transfer complex p
25	33	82.5	721	2 C84073	DNA topoisomerase
26	33	82.5	1121	1 NCCEXV	exodeoxyribonuclea
27	33	82.5	1122	2 A85934	hypothetical prote
28	32	80.0	195	1 MFIV2	matrix protein M2
29	32	80.0	195	1 MFIV2B	matrix protein M2

30 32 80.0 195 1 MFIV2C  
31 32 80.0 195 1 MFIV2W  
32 32 80.0 484 2 G72395  
33 32 80.0 780 2 T50315  
34 31 77.5 9 2 S07205  
35 31 77.5 563 2 B70682  
36 31 77.5 651 2 B43963  
37 31 77.5 1951 2 B43963  
38 31 77.5 2150 2 S13553  
39 31 77.5 2151 1 S16449  
40 30 75.0 150 2 T03977  
41 30 75.0 198 1 A64822  
42 30 75.0 198 2 E85594  
43 30 75.0 293 2 T49734  
44 30 75.0 295 2 T16231  
45 30 75.0 306 2 A54717

matrix protein  
matrix protein  
alpha-2-crystallin  
hypothetical prote  
litorin - Glu  
probabli litorin  
DNA topoisomerase  
RNA viral polymerase  
hypothetical prote  
genome protein  
hypothetical prote  
probabli lactorin  
hypothetical prote  
probabli methyltr  
hypothetical prote  
palmitic protein

## ALIGNMENTS

## RESULT 1

BSTD  
bombesin - fire-bellied toad  
C:Species: Bombina bombina (fire-bellied toad)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change  
C:Accession: A01564

R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin from the fire-bellied toad  
A:Reference number: A01564; MUID:72163516  
A:Accession: A01564

A:Molecule type: protein  
A:Residues: 1-14 <ANA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuromedin C  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 95.0%; Score 38; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 0.076;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

Qy 2 QMXVGH 8  
Db 7 QNAVGH 13

## RESULT 2

BSTDY  
bombesin precursor - yellow-bellied toad  
C:Species: Bombina variegata (yellow-bellied toad)  
C:Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 06-Dec-2000  
C:Accession: S09095; B01564; A01564  
R:Richter, K.; Egger, R.; Krell, G.  
FEBS Lett. 262, 353-355, 1990

A:Title: Molecular cloning of a cDNA encoding the bombesin precursor in the yellow-bellied toad  
A:Reference number: S09095; MUID:90242964  
A:Accession: S09095

A:Molecule type: mRNA  
A:Residues: 1-107 <RIC>

R:Anastasi, A.; Erspamer, V.; Bucci, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A:Title: Isolation and amino acid sequences of alytesin and bombesin from the yellow-bellied toad

A:Reference number: A01564; MUID:72163516

A:Accession: B01564

A:Molecule type: protein

A:Residues: 42-55 <ANA>

C:Superfamily: ranatensin

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuromedin C

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-41/Domain: amino-terminal propeptide #status predicted <PRO>

F:42-55/Product: bombesin #status experimental <MAT>  
F:56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
F:42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
F:55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 95.0%; Score 38; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 0.65;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWXXVGH 8  
|||  
Db 48 QWAVGH 54

RESULT 3  
A39261  
bombesin precursor - Bombina orientalis  
C:Species: Bombina orientalis  
C:Accession: A39261  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999  
R:Schmid, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990  
A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet  
A:Reference number: A39261; MUID:91088602  
A:Accession: A39261  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <SPI>  
A:Cross-references: GB:W55255; NID:g211016; PIDN:AAA48551.1; PID:g211017  
C:Superfamily: ranatensin  
C:Keywords: neuropeptide

Query Match 95.0%; Score 38; DB 2; Length 119;  
Best Local Similarity 85.7%; Pred. No. 0.72;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWXXVGH 8  
|||  
Db 51 QWAVGH 57

RESULT 4  
S32963  
hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YBR1729  
C:Species: Saccharomyces cerevisiae  
C:Accession: S32963  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
A:Reference number: S32963; S46142  
R:Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
Yeast 9, 189-199, 1993  
A:Title: The complete sequence of a 19,482 bp segment located on the right arm of chromo  
A:Reference number: S29348; MUID:93220397  
A:Accession: S32963  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-232 <DOI>  
A:Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; PID:g296560  
R:Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45940  
A:Accession: S46142  
A:Molecule type: DNA  
A:Residues: 1-232 <AIG>  
A:Cross-references: EMBL:Z36130; NID:g536688; PIDN:CAA85224.1; PID:g536689; MIPS:YBR261c  
C:Genetics:  
A:Map position: 2R  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 90.0%; Score 36; DB 2; Length 232;  
Best Local Similarity 85.7%; Pred. No. 3.7;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWXXVGH 8  
|||  
Db 139 QWCVGH 145

RESULT 5  
T48787  
hypothetical protein 13E11.350 [imported] - Neurospora crassa  
C:Species: Neurospora crassa  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 28-Jul-2000  
C:Accession: T48787  
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24541  
A:Accession: T48787  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-256 <SCH>  
A:Cross-references: EMBL:AL353820; GSPDB:GNO0112; NCSP:13E11.350  
A:Experimental source: cosmid contig 13E11; strain 74  
C:Genetics:  
A:Gene: NCSP:13E11.350  
A:Map position: 2  
A:Introns: 213/2  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 90.0%; Score 36; DB 2; Length 256;  
Best Local Similarity 85.7%; Pred. No. 4.1;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWXXVGH 8  
|||  
Db 162 QWCVGH 168

RESULT 6  
S07204  
Litorin I - Australian tree frog (Litoria aurea)  
C:Species: Litoria aurea  
C:Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
C:Accession: S07204  
R:Anastasi, A.; Erspamer, V.; Endean, R.  
Experientia 31, 510-511, 1975  
A:Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide f  
A:Reference number: S07204; MUID:75187011  
A:Accession: S07204  
A:Molecule type: protein  
A:Residues: 1-9 <ANA>  
C:Superfamily: gastrin-releasing peptide  
C:Keywords: amidated carboxyl end; neuropeptide; pyrrolutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 85.0%; Score 34; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWXXVGH 7  
|||  
Db 2 QWAVGH 7

RESULT 7  
A60409  
bombesin-like peptide L - frog (Pseudophryne guentheri)  
C:Species: Pseudophryne guentheri  
C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
C:Accession: A60409  
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; W.



A;Title: Neuromedin C: a bombesin-like peptide identified in porcine spinal cord.  
A;Reference number: A32738; MUID:84153890  
A;Accession: A32738  
A;Molecule type: protein  
A;Residues: 18-27 <MIN>  
C;Superfamily: gastrin-releasing peptide  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; spinal cord; stomach  
F;1-27/Product: gastrin-releasing peptide #status experimental <MAT>  
F;18-27/Product: neuromedin C #status experimental <NEU>  
F;27/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 82.5%; Score 33; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 1.7;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXVGHL 8  
| | | | |  
Db 21 WVGHL 26

## RESULT 13

RHGPGA  
gastrin-releasing peptide - guinea pig  
N;Contains: neuromedin C  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 20-Mar-1998  
C;Accession: A60206  
R;Shaw, C.; Thim, L.; Conlon, J.M.  
J. Neurochem. 49, 1348-1354, 1987  
A;Title: Primary structure and tissue distribution of guinea pig gastrin-releasing peptide  
A;Reference number: A60206; MUID:88034997  
A;Accession: A60206  
A;Molecule type: protein  
A;Residues: 1-27 <SHA>  
A;Note: the carboxyl-terminal residue was not determined directly, but an alpha-amidated ion times

C;Superfamily: gastrin-releasing peptide  
C;Keywords: amidated carboxyl end; brain; hormone; intestine; neuropeptide; stomach  
F;18-27/Product: neuromedin C #status predicted <NEU>  
F;27/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 82.5%; Score 33; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 1.7;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXVGHL 8  
| | | | |  
Db 21 WVGHL 26

## RESULT 14

RHCHA  
gastrin-releasing peptide - chicken (fragment)  
N;Contains: proventricular peptide  
C;Species: Gallus gallus (chicken)  
C;Date: 28-Feb-1981 #sequence\_revision 19-Apr-1996 #text\_change 19-Apr-1996  
C;Accession: A01563; S08150  
R;McDonald, T.J.; Jornvall, H.; Gbatei, M.; Bloom, S.R.; Mutt, V.  
FEBS Lett. 122, 45-48, 1980  
A;Title: Characterization of an avian gastric (proventricular) peptide having sequence F  
A;Reference number: A01563; MUID:81164953  
A;Accession: A01563  
A;Molecule type: protein  
A;Residues: 1-27 <MCD>  
R;Campbell, B.J.; Young, J.; Dimaline, R.; Dockray, G.J.  
Biochim. Biophys. Acta 1048, 66-71, 1990

A;Title: Isolation, sequence and biosynthetic significance of a novel fragment of gastrin  
A;Reference number: S08150; MUID:90122926  
A;Accession: S08150  
A;Molecule type: protein  
A;Residues: 1-27 <CAM>

C;Superfamily: gastrin-releasing peptide  
C;Keywords: amidated carboxyl end; neuropeptide  
F;1-27/Product: proventricular peptide #status experimental <PVPT>  
F;27/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 82.5%; Score 33; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 1.7;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WXVGHL 8  
| | | | |  
Db 21 WVGHL 26

## RESULT 15

A47201  
bombesinlike peptide - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998  
C;Accession: A47201  
R;Wechselberger, C.; Kreil, G.; Richter, K.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9819-9822, 1992  
A;Title: Isolation and sequence of a cDNA encoding the precursor of a bombesin like peptide  
A;Reference number: A47201; MUID:93028554  
A;Accession: A47201  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-120 <WEC>  
A;Note: sequence inconsistent with the nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:115857, NCBIIP:115858)  
C;Superfamily: ranatensin

Query Match 82.5%; Score 33; DB 2; Length 120;  
Best Local Similarity 66.7%; Pred. No. 7.8;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWXXVGH 7  
| | | | |  
Db 47 QWAIGH 52

Search completed: October 25, 2001, 11:25:22  
Job time: 335 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-9  
Perfect score: 40  
Sequence: 1 XQWXXVGH 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

1 number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	38	95.0	8	2	Sequence 9, Appl
3	38	95.0	8	6	Patent No. 5217955
4	38	95.0	8	6	Patent No. 5217955-32
5	38	95.0	9	1	Sequence 1, Appl
6	38	95.0	9	1	Sequence 2, Appl
7	38	95.0	9	1	Sequence 4, Appl
8	38	95.0	9	1	Sequence 5, Appl
9	38	95.0	9	1	Sequence 9, Appl
10	38	95.0	9	1	Sequence 10, Appl
11	38	95.0	9	1	Sequence 12, Appl
12	38	95.0	9	1	Sequence 14, Appl
13	38	95.0	9	1	Sequence 15, Appl
14	38	95.0	9	1	Sequence 17, Appl
15	38	95.0	9	1	Sequence 18, Appl
16	38	95.0	9	1	Sequence 22, Appl
17	38	95.0	9	1	Sequence 23, Appl
18	38	95.0	9	1	Sequence 24, Appl
19	38	95.0	9	1	Sequence 25, Appl
20	38	95.0	9	1	Sequence 26, Appl
21	38	95.0	9	1	Sequence 27, Appl
22	38	95.0	9	1	Sequence 28, Appl
23	38	95.0	9	1	Sequence 29, Appl
24	38	95.0	9	1	Sequence 30, Appl
25	38	95.0	9	1	Sequence 31, Appl
26	38	95.0	9	1	Sequence 32, Appl
27	38	95.0	9	1	Sequence 33, Appl

28	38	95.0	9	1	US-07-619-747B-34	Sequence 14, Appl
29	38	95.0	9	1	US-07-619-747B-35	Sequence 35, Appl
30	38	95.0	9	1	US-07-619-747B-36	Sequence 36, Appl
31	38	95.0	9	1	US-07-619-747B-37	Sequence 37, Appl
32	38	95.0	9	1	US-07-619-747B-38	Sequence 38, Appl
33	38	95.0	9	1	US-07-619-747B-39	Sequence 39, Appl
34	38	95.0	9	1	US-07-619-747B-40	Sequence 40, Appl
35	38	95.0	9	1	US-08-031-325A-37	Sequence 37, Appl
36	38	95.0	9	1	US-08-263-905-4	Sequence 4, Appl
37	38	95.0	9	1	US-08-263-905-5	Sequence 5, Appl
38	38	95.0	9	1	US-08-263-905-6	Sequence 6, Appl
39	38	95.0	9	1	US-08-263-905-7	Sequence 7, Appl
40	38	95.0	9	1	US-08-263-905-10	Sequence 10, Appl
41	38	95.0	9	1	US-08-263-905-11	Sequence 11, Appl
42	38	95.0	9	1	US-07-919-731-3	Sequence 3, Appl
43	38	95.0	9	1	US-08-287-957-116	Sequence 116, Appl
44	38	95.0	9	1	US-08-240-711-6	Sequence 6, Appl
45	38	95.0	9	1	US-08-240-711-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end "

US-08-168-390-11  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."

```
Query Match          95.0%; Score 38; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8
   || |||
Db 2 QWVGHL 8

RESULT 2
US-08-337-127-9
; Sequence 9, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy. David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/009000D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than
; OTHER INFORMATION: and has an methyl ester C-terminus (i.e.,
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e.,
US-08-337-127-9

Query Match          95.0%; Score 38; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8
   || |||
Db 2 QWVGHL 8

RESULT 3
5217955-32
; Patent No. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:32:
; LENGTH: 8
5217955-32

Query Match          95.0%; Score 38; DB 6; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8
   || |||
Db 2 QWVGHL 8

RESULT 4
5217955-34
; Patent No. 5217955
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:34:
; LENGTH: 8
5217955-34

Query Match          95.0%; Score 38; DB 6; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 QWVGH 8  
II IIII  
Db 2 QWVGH 8

## RESULT 5

US-07-619-747B-1  
; Sequence 1, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-1

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGH 8  
II IIII  
Db 2 QWVGH 8

## RESULT 6

US-07-619-747B-2  
; Sequence 2, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi

; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-2

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGH 8  
II IIII  
Db 2 QWVGH 8

## RESULT 7

US-07-619-747B-4  
; Sequence 4, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 360K Diskette
COMPUTER: IBM PC
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WP 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/619,747B
FILING DATE: 19901129
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5244883e
FILING DATE: N/A
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Behr, Omri M.
REGISTRATION NUMBER: 22,940
REFERENCE/DOCKET NUMBER: SHAL3.0-011
TELEPHONE: (908)494-5240
TELEFAX: 1-908-494-0428
TELEX: 511642 BEPATEDIN
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: Position 1 is 5F-D-Trp
OTHER INFORMATION: Position 8 is a reduced
OTHER INFORMATION: isostere of named aminoacid
US-07-619-747B-4

```

```

Query Match 95.08; Score 38; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 2 QWVXVGH 8
Db 2 QWVXVGH 8

```

```

RESULT 8
US-07-619-747B-5
Sequence 5, Application US/07619747B
Patent No. 5244883
GENERAL INFORMATION:
APPLICANT: Cai, Ren Zhi
APPLICANT: Schally, Andrew V.,
TITLE OF INVENTION: No. 5244883apeptide Bombesin
TITLE OF INVENTION: Antagonists
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Andrew V. Schally
STREET: 5025 Kawanne Avenue
CITY: Metairie
STATE: Louisiana
COUNTRY: USA
ZIP: 70002
COMPUTER READABLE FORM:
MEDIUM TYPE: 360K Diskette
COMPUTER: IBM PC
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WP 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/619,747B
FILING DATE: 19901129
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5244883e

```

```

FILING DATE: N/A
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Behr, Omri M.
REGISTRATION NUMBER: 22,940
REFERENCE/DOCKET NUMBER: SHAL3.0-011
TELEPHONE: (908)494-5240
TELEFAX: 1-908-494-0428
TELEX: 511642 BEPATEDIN
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: Position 1 is D-Tpi
OTHER INFORMATION: Position 8 is a reduced
OTHER INFORMATION: isostere of named aminoacid
US-07-619-747B-5

```

```

Qy 2 QWVXVGH 8
Db 2 QWVXVGH 8

```

```

RESULT 9
US-07-619-747B-9
Sequence 9, Application US/07619747B
Patent No. 5244883
GENERAL INFORMATION:
APPLICANT: Cai, Ren Zhi
APPLICANT: Schally, Andrew V.,
TITLE OF INVENTION: No. 5244883apeptide Bombesin
TITLE OF INVENTION: Antagonists
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Andrew V. Schally
STREET: 5025 Kawanne Avenue
CITY: Metairie
STATE: Louisiana
COUNTRY: USA
ZIP: 70002
COMPUTER READABLE FORM:
MEDIUM TYPE: 360K Diskette
COMPUTER: IBM PC
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WP 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/619,747B
FILING DATE: 19901129
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5244883e
FILING DATE: N/A
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Behr, Omri M.
REGISTRATION NUMBER: 22,940
REFERENCE/DOCKET NUMBER: SHAL3.0-011
TELEPHONE: (908)494-5240
TELEFAX: 1-908-494-0428

```

TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is NH2CO-Trp  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-9

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 QWXXVGH 8  
|| ||||  
2 QWAVGH 8

RESULT 10  
US-07-619-747B-10  
Sequence 10, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren Zhi  
APPLICANT: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Trp  
OTHER INFORMATION: Position 8 is a reduced

OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-10

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 QWXXVGH 8  
|| ||||  
2 QWAVGH 8

RESULT 11  
US-07-619-747B-12  
Sequence 12, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren Zhi  
APPLICANT: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Tpi  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-12

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 QWXXVGH 8  
|| ||||  
2 QWAVGH 8

```
RESULT 12
US-07-619-747B-14
; Sequence 14, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BPATEDIN
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: Position 1 is Hca
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: Isostere of named aminoacid
; OTHER INFORMATION: Position 9 is Tpi
US-07-619-747B-14

Query Match 95.0%; Score 38; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

QY 2 QWVXVGH 8
Db 2 QWVXVGH 8

RESULT 13
US-07-619-747B-15
; Sequence 15, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
```

```
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BPATEDIN
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: Position 1 is D-pGlu
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: Isostere of named aminoacid
; OTHER INFORMATION: Position 9 is Tpi
US-07-619-747B-15

Query Match 95.0%; Score 38; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

QY 2 QWVXVGH 8
Db 2 QWVXVGH 8

RESULT 14
US-07-619-747B-17
; Sequence 17, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; APPLICANT: Schally, Andrew V.,
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
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MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Phe  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-17

Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGHL 8  
DB 2 QWVGHL 8

RESULT 15  
US-07-619-747B-18  
Sequence 18, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren zhi  
APPLICANT: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanee Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Tip  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
OTHER INFORMATION: Position 9 is Tpi  
US-07-619-747B-18  
Query Match 95.0%; Score 38; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGHL 8  
DB 2 QWVGHL 8

Search completed: October 25, 2001, 11:23:56  
Job time: 269 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: us-09-630-333-9  
Perfect score: 40  
Sequence: 1 XQXVGHLL 8

Scoring table:  
BLOSOM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

1 number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	95.0	7	22 AAB48341	Bombesin/gastrin-r
2	38	95.0	8	11 AAR04531	Non-cyclic analogu
3	38	95.0	8	12 AAR11224	Linear litorin ana
4	38	95.0	8	12 AAR11240	Linear litorin ana
5	38	95.0	8	12 AAR14877	Peptide analogue #
6	38	95.0	8	13 AAR28456	Bombesin antagonist
7	38	95.0	8	13 AAR28459	Bombesin antagonist
8	38	95.0	8	16 AAW64910	Bombesin receptor
9	38	95.0	8	19 AAW50941	Bombesin antagonist
10	38	95.0	8	20 AAW92740	Bombesin peptide a
11	38	95.0	8	21 AAB08302	Amino acid sequenc

12	38	95.0	8	22 AAB72406	Bombesin analogue.
13	38	95.0	9	11 AAR04526	Non-cyclic analogu
14	38	95.0	9	11 AAR04527	Non-cyclic analogu
15	38	95.0	9	11 AAR04529	Non-cyclic analogu
16	38	95.0	9	11 AAR04528	Non-cyclic analogu
17	38	95.0	9	11 AAR04530	Non-cyclic analogu
18	38	95.0	9	11 AAR08345	Peptide analogue #
19	38	95.0	9	12 AAR11520	Peptide analogue #
20	38	95.0	9	12 AAR11521	Peptide analogue #
21	38	95.0	9	12 AAR11522	Peptide analogue #
22	38	95.0	9	12 AAR11529	Peptide analogue #
23	38	95.0	9	12 AAR12033	Peptide analogue #
24	38	95.0	9	12 AAR14860	Peptide analogue #
25	38	95.0	9	12 AAR14861	Peptide analogue #
26	38	95.0	9	12 AAR14862	Peptide analogue #
27	38	95.0	9	12 AAR14863	Peptide analogue #
28	38	95.0	9	12 AAR14864	Peptide analogue #
29	38	95.0	9	12 AAR14872	Peptide analogue #
30	38	95.0	9	12 AAR14876	Peptide analogue #
31	38	95.0	9	12 AAR14880	Cyclic peptide #1
32	38	95.0	9	12 AAR15038	Cyclic peptide #3
33	38	95.0	9	13 AAR24483	[psi]-pseudo; NO
34	38	95.0	9	13 AAR24484	[psi]-pseudo; NO
35	38	95.0	9	13 AAR24486	[psi]-pseudo; NO
36	38	95.0	9	13 AAR24490	[psi]-pseudo; NO
37	38	95.0	9	13 AAR24491	[psi]-pseudo; NO
38	38	95.0	9	13 AAR24492	[psi]-pseudo; NO
39	38	95.0	9	13 AAR24487	[psi]-pseudo; NO
40	38	95.0	9	13 AAR24488	[psi]-pseudo; NO
41	38	95.0	9	13 AAR24489	[psi]-pseudo; NO
42	38	95.0	9	13 AAR24493	[psi]-pseudo; NO
43	38	95.0	9	13 AAR28447	[psi]-pseudo; NO
44	38	95.0	9	13 AAR28448	[psi]-pseudo; NO
45	38	95.0	9	13 AAR28450	[psi]-pseudo; NO

## ALIGNMENTS

RESULT 1  
AAB48341  
ID AAB48341 standard; peptide; 7 AA.  
XX  
AC AAB48341;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Bombesin/gastrin-releasing peptide receptor-recognising pep  
XX  
KW Cancer; chemotherapy; heparin; thrombospondin; drug resistan  
XX  
KW toxicity; tumour; cytostatic; metalloprotease.  
XX  
OS Synthetic.  
XX  
PN WO200078359-A2.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-US16955.  
XX  
PR 21-JUN-1999; 99US-0140310.  
XX  
PA (TUSZ/) TUSZYNSKI G.  
PA (WILL/) WILLIAMS T.  
XX (ACTO/) ACTOR P.  
XX  
Tuszynski G, Williams T, Actor P;  
WPI; 2001-080760/09.  
Treating cancer involves administering chemotherapy agent  
a peptide or co-administering chemotherapy agent and the peptide

PS Disclosure; Page 6; 44pp; English.

XX The invention relates to a method of treating a patient suffering from  
CC cancer that comprises administering a chemotherapy agent conjugated to a  
CC peptide, or co-administering the agent and the peptide. The peptides can  
CC be selected from heparin binding domains of the thrombospondin protein.  
CC The method and compositions comprising the agent and the peptide are  
CC useful for treating a patient with drug resistant cancer, and for  
CC treating a patient with cancer to prevent drug resistance from occurring.  
CC Toxic chemotherapeutic agent can also be used, as peptide conjugation and  
CC co-administration can considerably reduce the toxicity of the agent and  
CC allow less composition to be administered due to increased efficacy. More  
CC effective treatment at lower doses is achieved by targeting the  
CC chemotherapeutic agents to the tumour cells. The present sequence represents  
CC bombesin/gastrin-releasing peptide receptor-recognising peptide.

XX Sequence 7 AA;

Query Match 95.0%; Score 38; DB 22; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QMXVGH 8  
DB 1 | | | | | 7

RESULT 2

AAR04531  
ID AAR04531 standard; protein; 8 AA.

AC AAR04531;

XX 24-SEP-1990 (first entry)

XX Non-cyclic analogue of amphibian bombesin and mammalian GRP.

XX Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
KW therapeutic peptides.

XX Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /label= D-phenylalanine

FT WO9003980-A.

XX 19-APR-1990.

XX 13-OCT-1989; 89WO-US00416.

XX 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.

XX (TULA ) TULANE E FUND ADMINISTRA.

XX Coy DH, Moreau J-P, Taylor JE, Kim SH;

XX WPI; 1990-147822/19.

XX New non-cyclic analogues of mammalian gastrin releasing peptide -  
PT and amphibian bombesin, used for cancer treatment eg small  
PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.

PS Claim 21; Page 55; 68pp; English.

XX C-terminal = ethylamide or amide.

XX The peptide has an active site and a binding site for binding to a  
CC target cell receptor, and has one of the following modifications:

CC (a) a deletion of a residue within the active site and a  
CC modification of a residue outside of the active site; and  
CC (b) a replacement of 1 or 2 residues within the active site with a

CC synthetic amino acid.  
CC On binding to its receptor, the analogue acts as a competitor;  
CC inhibitor of the naturally occurring peptide but due to the  
CC modifications, fails to exhibit the normal in vivo biological activity.  
CC The peptides are useful for the treatment of benign or malignant  
CC proliferation of tissues, eg cancers of the gastrointestinal  
CC tract, pancreatic cancer, colon cancer, lung cancer or breast  
CC cancer; for the treatment of atherosclerosis; and disorders of  
CC gastrointestinal tissues.  
CC This peptide is a claimed example of a highly generic formula;  
CC See also AAR04525-R04533.

XX Sequence 8 AA;

Query Match 95.0%; Score 38; DB 11; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QMXVGH 8  
DB 2 | | | | | 8

RESULT 3

AAR11224  
ID AAR11224 standard; Protein; 8 AA.

XX AAR11224;

XX 17-MAY-1991 (first entry)

XX Linear litorin analogue.

XX Bombesin; litorin analogue; linear; receptor affinity; cancer;  
KW diabetes.

XX Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 1..1 /label= D-p-chloro-phenylalanine

FT WO9102746-A.

XX 07-MAR-1991.

XX 17-AUG-1990; 90WO-US04646.

XX 21-AUG-1989; 89US-0397169.

XX 30-MAR-1990; 90US-0502438.

XX (TULA ) ADMIN TULANE EDUCATIONAL.

XX (BIOM-) BIOMEASURE INC.

XX Coy DH, Moreau JP, Kim SH;

XX WPI; 1991-087241/12.

XX New linear peptide analogues of bombesin - modified to eliminate  
PT biological activity while retaining receptor affinity, for treating  
PT cancer, diabetes, etc.

PS Claim 13; Page 53; 58pp; English.

XX This peptide is a specifically claimed example of a generic  
CC formula. The C-terminal amino acid (Met) of the naturally occurring  
CC peptide has been converted to an amide and Phe 8 has been replaced  
CC by statine.

CC The peptide is useful for treating benign or malignant tissue  
CC proliferation, atherosclerosis, gastrointestinal disorders and  
CC diabetes. They act as competitive inhibitors of natural peptide,  
CC since they bind to the cell receptors but have no biological

CC activity.  
XX  
SQ Sequence 8 AA;

Query Match 95.0%; Score 38; DB 12; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 8  
II IIII  
DB 2 qwvghl 8

RESULT 4

AAR11240  
ID AAR11240 standard; Protein; 8 AA.  
XX  
AC AAR11240;

17-MAY-1991 (first entry)

Linear litorin analogue (II).

Bombesin; litorin analogue; linear; receptor affinity; cancer;  
diabetes.  
XX  
OS Synthetic.

Key Location/Qualifiers  
FT Modified-site 1.1  
/label= D-p-chloro-phenylalanine

W09102746-A.  
XX  
PD 07-MAR-1991.

17-AUG-1990; 90WO-US04646.

21-AUG-1989; 89US-0397169.

30-MAR-1990; 90US-0502438.

(TULA ) ADMIN TULANE EDUCATIONAL.  
PA (BIOM-) BIOMEASURE INC.

Coy DH, Moreau JP, Kim SH;

WPI; 1991-087241/12.

New linear peptide analogues of bombesin - modified to eliminate biological activity while retaining receptor affinity, for treating cancer, diabetes, etc.

Claim 17; Page 53; 58pp; English.

This peptide is a specifically claimed example of a generic formula. The C-terminal amino acid (Met) of the naturally occurring peptide has been converted to an amide and Phe 8 has been replaced by beta-Leu.

The peptide is useful for treating benign or malignant tissue proliferation, arteriosclerosis, gastrointestinal disorders and diabetes. They act as competitive inhibitors of natural peptides, since they bind to the cell receptors but have no biological activity.

The analogue may also be of a naturally occurring peptide terminating at the C-terminus with a Met residue, such as the 10 amino acid C-terminal region of mammalian GRP or amphibian bombesin.

See also AAR11239-242.

Sequence 8 AA;

Query Match 95.0%; Score 38; DB 12; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGHL 8  
II IIII  
DB 2 qwvghl 8

RESULT 5

AAR14877  
ID AAR14877 standard; Protein; 8 AA.

XX  
AC AAR14877;

14-FEB-1992 (first entry)

Peptide analogue #18 of litorin, GRP, neuromedin or bombesin;  
tissue proliferation; gastrin related peptide; peptide hormone.  
XX  
OS Synthetic.

Key Location/Qualifiers  
FT Modified-site 1  
/label= D-Phe  
FT Modified-site 8  
/label= OTHER  
FT /note= "Leu-propylamide"

W09117181-A.

14-NOV-1991.

09-MAY-1991; 91WO-0003265.

09-MAY-1990; 90US-0520226.

(TULA ) TULANE E FUND ADMINISTRATION.  
PA (BIOM-) BIOMEASURE INC.

Coy DH, Kim SH, Moreau JP;

WPI; 1991-353721/48.

Peptide agonists of litorin, gastrin releasing peptide - neuromedin B or C or bombesin, for treating cancer, preventing smooth muscle proliferation and suppressing appetite and alcohol craving

Claim 20; Page 19; 25pp; English.

This peptide is one of 27 specific examples of a highly generic formula. The peptides are all analogues of either litorin; the 10 amino acid C-terminal region of mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid C-terminal region of amphibian bombesin. They act as at least partial agonists of the natural peptides. The peptide analogues are made by standard methods synthesis and can be cyclised.

See AAR14860-R14880 and AAR15035-R15040.

Sequence 8 AA;

Query Match 95.0%; Score 38; DB 12; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 QWVGHL 8  
II IIII  
DB 2 qwvghl 8

RESULT 6  
 AAR28456  
 ID AAR28456 standard; Protein; 8 AA.  
 XX AC AAR28456;  
 XX DT 09-DEC-1992 (first entry)  
 XX DE Bombesin antagonist (24).  
 XX KW Bombesin; GRP; gastrin releasing peptide.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Hca-Gln; Hca= hydrocinnamic acid"  
 FT Modified-site 7  
 FT /label= psi  
 FT /note= "residues 7-8 are linked via a pseudo  
 peptide bond"  
 FT Modified-site 8  
 FT /label= psi  
 FT /note= "residues 7-8 are linked via a pseudo  
 peptide bond"  
 XX PN W09209626-A.  
 XX PD 11-JUN-1992.  
 XX PF 15-NOV-1991; 91WO-US08534.  
 XX PR 29-NOV-1990; 90US-0619747.  
 XX PA (TULA ) TULANE EDUCATIONAL FUND.  
 XX PI Cai RZ, Schally AV;  
 XX WPI; 1992-217019/26.  
 XX New nona:peptide bombesin antagonists - used for treating  
 PT hypergastrinaemic states, such as pernicious anaemia and  
 PT Zollinger-Ellison syndrome and also used against lung and gastric  
 PT cancer, etc.  
 XX PS Disclosure; Page 8; 50pp; English.  
 XX The C-terminal is amidated. The peptide is an example of a highly  
 CC generic formula for bombesin antagonists which are [psi8-9 pseudo]  
 CC nonapeptides contg. D- or L-tryptophan or tryptophan analog  
 CC 2,3,4,9-tetrahydro-1H-pyrido[3,4-b]-indol-3-carboxylic acid (Tpi)  
 CC at the N- and/or C-terminal.  
 CC The peptide is a bombesin/GRP (gastrin releasing peptide) antagonist  
 CC and is useful for treatment of states of hypergastrinemia, e.g.  
 CC pernicious anaemia, chronic atrophic gastritis, Zollinger-Ellison  
 CC syndrome and vitiligo, associated with diffuse hyperplasia of  
 CC gastric enterochromaffin-like cells, and with an increased risk of  
 CC developing multifocal gastric carcinoma tumours. The peptide can  
 CC also be used to treat lung, colon and gastric cancers. Dosage is  
 CC 1- 1000 microg/kg parenterally.  
 XX Sequence 8 AA;  
 SQ

Query Match 95.0%; Score 38; DB 13; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVXVGH 8  
 DB 1 qvavghl 7

RESULT 7  
 AAR28459  
 ID AAR28459 standard; Protein; 8 AA.  
 XX AC AAR28459;  
 XX DT 09-DEC-1992 (first entry)  
 XX DE Bombesin antagonist (27).  
 XX KW Bombesin; GRP; gastrin releasing peptide.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Mpp-Gln; Mpp= 3-(4-methoxyphenyl)  
 propionic acid"  
 FT Modified-site 7  
 FT /label= psi  
 FT /note= "residues 7-8 are linked via a pseudo  
 peptide bond"  
 FT Modified-site 8  
 FT /label= psi  
 FT /note= "Trp(For), For= formyl; residues 7-8 are  
 linked via a pseudo peptide bond"  
 XX PN W09209626-A.  
 XX PD 11-JUN-1992.  
 XX PF 15-NOV-1991; 91WO-US08534.  
 XX PR 29-NOV-1990; 90US-0619747.  
 XX PA (TULA ) TULANE EDUCATIONAL FUND.  
 XX PI Cai RZ, Schally AV;  
 XX WPI; 1992-217019/26.  
 XX New nona:peptide bombesin antagonists - used for treating  
 PT hypergastrinaemic states, such as pernicious anaemia and  
 PT Zollinger-Ellison syndrome and also used against lung and gastric  
 PT cancer, etc.  
 XX PS Disclosure; Page 8; 50pp; English.  
 XX The C-terminal is amidated. The peptide is an example of a highly  
 CC generic formula for bombesin antagonists which are [psi8-9 pseudo]  
 CC nonapeptides contg. D- or L-tryptophan or tryptophan analog  
 CC 2,3,4,9-tetrahydro-1H-pyrido[3,4-b]-indol-3-carboxylic acid (Tpi)  
 CC at the N- and/or C-terminal.  
 CC The peptide is a bombesin/GRP (gastrin releasing peptide) antagonist  
 CC and is useful for treatment of states of hypergastrinemia, e.g.  
 CC pernicious anaemia, chronic atrophic gastritis, Zollinger-Ellison  
 CC syndrome and vitiligo, associated with diffuse hyperplasia of  
 CC gastric enterochromaffin-like cells, and with an increased risk of  
 CC developing multifocal gastric carcinoma tumours. The peptide can  
 CC also be used to treat lung, colon and gastric cancers. Dosage is  
 CC 1- 1000 microg/kg parenterally.  
 XX Sequence 8 AA;  
 SQ

Query Match 95.0%; Score 38; DB 13; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVXVGH 8  
 DB 1 qvavghl 7

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Query Match          95.0%; Score 38; DB 16; Length 8;
Best Local Similarity 85.7%; Pred. NO. 3.4e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
QY      2 QWVGHL 8
        |||||
DB      2 qwvghl 8

RESULT 9
AAW50941
ID ID AAW50941 standard; peptide; 8 AA.
XX AC
XX AAW50941;
DT 31-JUL-1998 (first entry)
XX DE
XX Bombesin antagonist (BOM1).
XX KW
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin, bombesin,
XX Substance P; cancer; inhibition.
XX OS
XX Synthetic.
XX FH
XX Key Location/Qualifiers
FT FT Misc-difference 1
FT FT Misc /note= "D-form residue"
FT FT Modified-site 8 /note= "Leu-NH2"
FT FT
XX EP835662-A2.
XX PN
XX 15-APR-1998.
XX PD
XX 11-DEC-1996; 96EP-0309012.
XX PF
XX 08-OCT-1996; 96US-0727679.
XX PR
XX 16-AUG-1996; 96IN-0001822.
XX XX
XX (NAIM-) NAT INST IMMUNOLOGY.
XX PA
XX Jaggi M, Mukherjee R;
XX PI
XX WPI: 1998-208959/19.
XX DR
XX Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)
XX PS
XX Claim 1; Page 4; 49pp; English.
XX CC
XX The invention relates to a new composition which comprises: (i) the
XX somatostatin analogue SOM2 AGCKNPFDMKTPSDC (3-14 disulphide bridge)
XX and (ii) at least 4 of the peptides: antagonist of vasoactive
XX intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX more general compositions containing peptide analogues of somatostatin,
XX VIP, bombesin and substance P. The compositions are used in human or
XX veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
XX or cancer cells, particularly for treatment of leukaemia, lymphoma,
XX adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
XX breast, kidney or particularly rectum and colon, and (b) to prevent,
XX inhibit or modulate over-expression of, e.g. VIP. A wide range of can-
XX cells express receptors for VIP, somatostatin, bombesin and/or substa-
XX P. The present sequence represents bombesin antagonist (BOM1).
XX SQ
Sequence 8 AA;

```

CC	Asn, Glu, Gln, p-X-Phe, Trp, Cys, Met, Pro, Hyp or cyclohexylAla; V
CC	Orn, Arg, Lys, Ile, Val, Phe, Thr, Ser, Gly, Ala, Asp, Glu, Aspartic acid,
CC	Ala, Gly, Leu, Tyr, His, Pro, Arg, Lys, Ile, Val, Phe, Thr, Ser, Gly, Ala,
CC	naphthyl(lower alkyl); R1, R2 = H, 112C alkyl, 7-10C phenylalkyl or
CC	COEt; where R1 and R2 are bonded to the N-terminal amino acid of the
CC	peptide; R1 = 1-20C alkyl, 3-20C alkenyl, 3-20C alkynyl, Ph, naphthyl
CC	or 7-10C phenylalkyl; provided that when 1 of R1 and R2 is COEt, 11
CC	other must be H. The peptides can be used for treating benign or
CC	malignant proliferation of tissue e.g. small-cell lung carcinoma,
CC	atherosclerosis, gastrointestinal disorders, and diabetes or diabetic
CC	related retinopathy. AA92735-W92742 represent bombesin peptide
CC	analogues used in the method of the invention.
XX	
SQ	Sequence 8 AA;
Query Match 95.0%; Score 38; DB 20; Length 6;	
Best Local Similarity 85.7%; Pred. No. 3.4e+05;	
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps	
OY	2 QWVGHGL 8
	II IIII
DB	2 qwvghl 8
RESULT 11	
AAB08302	ID AAB08302 standard; peptide; 8 AA.
XX	
AC	AAB08302;
XX	
DT	04-DEC-2000 (first entry)
XX	
DE	Amino acid sequence of bombesin analogue BOM1.
KX	
KW	Vasoactive intestinal peptide; VIP; analogue; somatostatin;
KW	VIP2; VIP3; BOM1; bombesin; SPI; substance P; MJJ-7; 11
KW	tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
KW	leukaemia; lymphoma.
XX	
OS	Synthetic.
XX	
FEH	Key Location/Qualifiers
FT	Misc-difference 1 /note= "D-form residue"
FT	Modified-site 8
FT	/note= "residue is Leu-NHet"
XX	
WO	2000047221-A1.
PD	17-AUG-2000.
XX	
PFP	11-FEB-2000; 2000WO-US03559.
XX	
PFR	11-FEB-1999; 99US-0248381.
XX	
PPA	(NAIN-) NAT INST IMMUNOLOGY.
PPA	(DABU-) DABUR RES FOUND.
PPA	(CORD/) CORD J I.
XX	
PPI	Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Kumar A;
PPI	Singh AT;
XX	
ORR	WPT; 2000-549083/50.
XX	
PPPT	Novel therapeutically active composition comprising at least 6
PPPT	peptides, useful for treating angiogenesis especially as a result of
PPPT	adenocarcinomas -
XX	
PS	Disclosure; Page 8; 42pp; English.
XX	
CCC	The present sequence represents an analogue of bombesin. The
CCC	specification describes therapeutically active compositions
CCC	at least one analogue of somatostatin (chosen from SOM1 and
CCC	2), and

CC	Asn, Glu, Gln, p-X-Phe, Trp, Cys, Met, Pro, Hyp or cyclohexylAla; V
CC	Orn, Arg, Lys, Ile, Val, Phe, Thr, Ser, Gly, Ala, Asp, Glu, Aspartic acid,
CC	Ala, Leu, Tyr, His, Pro, Arg, Lys, Ile, Val, Phe, Thr, Ser, Gly, Ala, Asp,
CC	naphthyl(lower alkyl); R1, R2 = H, 112C alkyl, 7-10C phenylalkyl or
CC	COEt; where R1 and R2 are bonded to the N-terminal amino acid of the
CC	peptide; R1 = 1-20C alkyl, 3-20C alkenyl, 3-20C alkynyl, Ph, naphthyl
CC	or 7-10C phenylalkyl; provided that when 1 of R1 and R2 is COEt, 11
CC	other must be H. The peptides can be used for treating benign or
CC	malignant proliferation of tissue e.g. small-cell lung carcinoma,
CC	atherosclerosis, gastrointestinal disorders, and diabetes or diabetic
CC	related retinopathy. AA92735-W92742 represent bombesin peptide
CC	analogues used in the method of the invention.
XX	
SQ	Sequence 8 AA;
Query Match 95.0%; Score 38; DB 20; Length 6;	
Best Local Similarity 85.7%; Pred. No. 3.4e+05;	
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps	
OY	2 QWVGHGL 8
	II IIII
Dd	2 qwvghl 8
RESULT 11	
AAB08302	ID AAB08302 standard; peptide; 8 AA.
XX	
AC	AAB08302;
XX	
DT	04-DEC-2000 (first entry)
XX	
DE	Amino acid sequence of bombesin analogue BOM1.
KX	Vasopressin
KW	Vasoactive intestinal peptide; VIP; analogue; somatostatin;
KW	VIP2; VIP3; BOM1; bombesin; SPI; substance P; MJJ-7; 11
KW	tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
KW	leukaemia; lymphoma.
XX	
OS	Synthetic.
XX	
FEH	Key Location/Qualifiers
FT	Misc-difference 1 /note= "D-form residue"
FT	Modified-site 8
FT	/note= "residue is Leu-NHet"
XX	
WO	2000047221-A1.
PD	17-AUG-2000.
XX	
PFP	11-FEB-2000; 2000WO-US03559.
XX	
PFR	11-FEB-1999; 99US-0248381.
XX	
PPA	(NAIN-) NAT INST IMMUNOLOGY.
PPA	(DABU-) DABUR RES FOUND.
PPA	(CORD/) CORD J I.
XX	
PPI	Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Kumar A;
PPI	Singh AT;
XX	
ORR	WPT; 2000-549083/50.
XX	
PPPT	Novel therapeutically active composition comprising at least 6
PPPT	peptides, useful for treating angiogenesis especially as a result of
PPPT	adenocarcinomas -
XX	
PS	Disclosure; Page 8; 42pp; English.
XX	
CCC	The present sequence represents an analogue of bombesin. The
CCC	specification describes therapeutically active compositions
CCC	at least one analogue of somatostatin (chosen from SOM1 and
CCC	2), and

CC at least four analogues chosen from vasoactive intestinal peptide (VIP) 1  
 CC (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a VIP  
 CC receptor antagonist), BOM1 (a bombesin antagonist), and SP1 (a substance  
 CC P antagonist). The combination of these 7 analogues is known as MuJ-7.  
 CC MuJ-7 is used as an anticancer drug to restrict tumour growth and spread  
 CC by inhibiting tumour angiogenesis. MuJ-7, in addition, inhibits  
 CC metastasis through its antiangiogenic activity in all cancers. The  
 CC peptides are useful for the treatment and prevention of angiogenesis,  
 CC especially as a result of adenocarcinomas of the colon, breast, lung,  
 CC prostate, kidney, leukemias or lymphomas.  
 XX  
 SQ Sequence 8 AA;

Query Match 95.0%; Score 38; DB 21; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHGL 8  
 || ||||  
 2 qwavghl 8

## RESULT 12

AAB72406  
 ID AAB72406 standard; peptide; 8 AA.

XX  
 AC AAB72406;

XX  
 DT 03-MAY-2001 (first entry)

XX  
 DE Bombesin analogue.

XX  
 KW Gene therapy; gene transfer; gastrin releasing peptide receptor; GRPr;  
 KW bombesin analogue; BBN.

XX  
 OS Unidentified.

XX  
 PN WO200112234-A1.

XX  
 PD 22-FEB-2001.

XX  
 PF 16-AUG-2000; 2000WO-US22456.

XX  
 PR 16-AUG-1999; 99US-0374972.

PR  
 01-JUN-2000; 2000US-0585194.

XX  
 (UABR-) UAB RES FOUND.

XX  
 Buchsbaum DJ, Curriel DT, Zinn KR, Rogers BE;

XX  
 WPI; 2001-218310/22.

XX  
 PT Monitoring therapeutic gene transfer and expression into a subject, by  
 PT administering vector encoding the gene and gene for membrane expressed  
 PT targeting molecule, and a radiolabeled ligand, and imaging gene  
 PT transfer -

PS  
 Example 10; Page 33; 107pp; English.

XX  
 CC The present invention relates to a method for monitoring therapeutic gene  
 CC transfer and expression into a subject, comprising administering a vector  
 CC encoding a therapeutic gene and a gene for a membrane expressed targeting  
 CC molecule (TM), and a radiolabeled ligand (RL) having high affinity for  
 CC TM, and detecting the binding of RL with TM. The binding is directly  
 CC proportional to the transfer and expression of the therapeutic gene.  
 CC Preferably, the TM is gastrin releasing peptide receptor (GRPr). A  
 CC technique was developed to image GRPr expression using a 99mTc-labelled  
 CC bombesin (BBN) analogue (the present sequence).  
 XX

SQ Sequence 8 AA;

Query Match 95.0%; Score 38; DB 22; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHGL 8  
 || ||||  
 Db 1 qwavghl 7

## RESULT 13

AAR04526  
 ID AAR04526 standard; protein; 9 AA.

XX  
 AC AAR04526;

XX  
 DT 24-SEP-1990 (first entry)

XX  
 DE Non-cyclic analogue of amphibian bombesin and mammalian GRP

XX  
 KW Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
 KW therapeutic peptides.

XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "D-p-Cl"

FT Modified-site 8

FT /label=beta-homoleucine

XX  
 PN WO9003980-A.

XX  
 PD 19-APR-1990.

XX  
 PF 13-OCT-1989; 89WO-US00416.

XX  
 PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.

XX  
 (TULA ) TULANE E FUND ADMINISTRA.

XX  
 PI Coy DH, Moreau J-P, Taylor JE, Kim SH;

XX  
 WPI; 1990-147822/19.

XX  
 PT New non-cyclic analogues of mammalian gastrin releasing peptide -  
 PT and amphibian bombesin, used for cancer treatment eg small  
 PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.

XX  
 Claim 8; Page 49; 68pp; English.

XX  
 C-terminal - NH2.

XX  
 CC The peptide has an active site and a binding site for binding to a  
 CC target cell receptor, and has one of the following modifications:

XX  
 CC (a) a deletion of a residue within the active site and a

XX  
 CC modification of a residue outside of the active site; and

XX  
 CC (b) a replacement of 1 or 2 residues within the active site with a  
 CC synthetic amino acid.

XX  
 CC On binding to its receptor, the analogue acts as a competitive  
 CC inhibitor of the naturally occurring peptide but due to the

XX  
 CC modifications, fails to exhibit the normal in vivo biological activity.

XX  
 CC The peptides are useful for the treatment of benign or malignant

XX  
 CC proliferation of tissues, eg cancers of the gastrointestinal tract,

XX  
 CC cancer; pancreatic cancer, colon cancer, lung cancer or breast

XX  
 CC cancer; for the treatment of atherosclerosis; and disorders of the

XX  
 CC gastrointestinal tissues.  
 CC This peptide is a claimed example of a highly generic formula.  
 XX  
 See also AAR04525-R04533.

SQ Sequence 9 AA;

Query Match 95.0%; Score 38; DB 11; Length 9;

Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVXGHL 8  
| | | | |  
Db 3 qvavghl 9

RESULT 14  
AAR04527  
ID AAR04527 standard; protein; 9 AA.  
XX AC AAR04527;  
XX DT 24-SEP-1990 (first entry)  
XX DE Non-cyclic analogue of amphibian bombesin and mammalian GRP.  
XX KW Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
XX OS therapeutic peptides.  
XX CS Synthetic.

XX FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 8 /label= D-beta-naphthylalanine  
FT Modified-site 8  
FT Modified-site 9 /label=leucine psi[CH2NH]  
XX WO9003980-A.  
XX PD 19-APR-1990.  
XX PF 13-OCT-1989; 89WO-US00416.  
XX PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.  
XX PA (TULA ) TULANE E FUND ADMINISTRA.  
XX PI Coy DH, Moreau J-P, Taylor JE, Kim SH;  
XX WPI: 1990-147822/19.

XX PT New non-cyclic analogues of mammalian gastrin releasing peptide -  
XX PT and amphibian bombesin, used for cancer treatment eg small  
XX PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.  
XX PS Claim 12; Page 52; 68pp; English.

XX CC C-terminal = NH2.  
XX CC The peptide has an active site and a binding site for binding to a  
XX CC target cell receptor, and has one of the following modifications:  
XX CC (a) a deletion of a residue within the active site and a  
XX CC modification of a residue outside of the active site; and  
XX CC (b) a replacement of 1 or 2 residues within the active site with a  
XX CC synthetic amino acid.  
XX CC On binding to its receptor, the analogue acts as a competitive  
XX CC inhibitor of the naturally occurring peptide but due to the  
XX CC modifications, fails to exhibit the normal in vivo biological activity.  
XX CC The peptides are useful for the treatment of benign or malignant  
XX CC proliferation of tissues, eg cancers of the gastrointestinal  
XX CC tract, pancreatic cancer, colon cancer, lung cancer or breast  
XX CC cancer; for the treatment of atherosclerosis; and disorders of the  
XX CC gastrointestinal tissues.  
XX CC This peptide is a claimed example of a highly generic formula.  
XX CC See also AAR04525-R04533.

XX SQ Sequence 9 AA;

Query Match 95.0%; Score 38; DB 11; Length 9;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVXGHL 8  
| | | | |  
Db 2 qvavghl 8

RESULT 15  
AAR04529  
ID AAR04529 standard; protein; 9 AA.  
XX AC AAR04529;  
XX DT 24-SEP-1990 (first entry)  
XX DE Non-cyclic analogue of amphibian bombesin and mammalian GRP.  
XX KW Mammalian gastrin releasing peptide; amphibian bombesin; cancer;  
XX OS therapeutic peptides.  
XX CS Synthetic.

XX FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 8 /label= D-phenylalanine  
FT Modified-site 9 /label=leucine psi[CH2NH]  
FT Modified-site 9 /label= D-phenylalanine  
XX WO9003980-A.  
XX PD 19-APR-1990.  
XX PF 13-OCT-1989; 89WO-US00416.  
XX PR 21-AUG-1989; 89US-0397169, US-257998; WO-U0416.  
XX PA (TULA ) TULANE E FUND ADMINISTRA.  
XX PI Coy DH, Moreau J-P, Taylor JE, Kim SH;  
XX WPI: 1990-147822/19.

XX PT New non-cyclic analogues of mammalian gastrin releasing peptide -  
XX PT and amphibian bombesin, used for cancer treatment eg small  
XX PT cell lung carcinoma, atherosclerosis and gastrointestinal disorders.  
XX PS Claim 15; Page 52; 68pp; English.

XX CC C-terminal = NH2.  
XX CC The peptide has an active site and a binding site for binding to a  
XX CC target cell receptor, and has one of the following modifications:  
XX CC (a) a deletion of a residue within the active site and a  
XX CC modification of a residue outside of the active site; and  
XX CC (b) a replacement of 1 or 2 residues within the active site with a  
XX CC synthetic amino acid.  
XX CC On binding to its receptor, the analogue acts as a competitive  
XX CC inhibitor of the naturally occurring peptide but due to the  
XX CC modifications, fails to exhibit the normal in vivo biological activity.  
XX CC The peptides are useful for the treatment of benign or malignant  
XX CC proliferation of tissues, eg cancers of the gastrointestinal  
XX CC tract, pancreatic cancer, colon cancer, lung cancer or breast  
XX CC cancer; for the treatment of atherosclerosis; and disorders of the  
XX CC gastrointestinal tissues.  
XX CC This peptide is a claimed example of a highly generic formula.  
XX CC See also AAR04525-R04533.

XX SQ Sequence 9 AA;

Query Match 95.0%; Score 38; DB 11; Length 9;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

Qy 2 QWVGHL 8  
|| ||||  
Db 2 qwvghl 8

Search completed: October 25, 2001, 11:22:46  
Job time: 219 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:45 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: us-09-630-333-9  
Perfect score: 40  
Sequence: 1 XQXVGH.L 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

1 number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	92.5	266	5 Q9VZF7	Q9vzf7 drosophila
2	36	90.0	224	4 Q9U128	Q9u128 homo sapien
3	36	90.0	232	3 Q9UVB4	Q9uve4 zygosacchar
4	36	90.0	256	3 Q9P6V1	Q9p6v1 neurospora
5	35	87.5	252	10 Q9FI20	Q9fi20 arabidopsis
6	34	85.0	119	13 Q90253	Q90253 bombina ori
7	34	85.0	276	5 Q9V5C9	Q9v5c9 drosophila
8	33	82.5	23	13 Q9PS30	Q9ps30 oncorhynchu
9	33	82.5	157	13 Q9I829	Q9i829 carassius a
10	33	82.5	211	2 Q9WMT3	Q9wmt3 pseudomonas
11	33	82.5	372	2 Q9HVL9	Q9hvl9 pseudomonas
12	33	82.5	387	2 Q9JN79	Q9jn79 streptomyce
13	33	82.5	396	4 Q99986	Q99986 homo sapien
14	33	82.5	399	5 Q9U0V1	Q9u0v1 leishmania
15	33	82.5	700	2 Q07111	Q07111 staphylococ
16	33	82.5	721	2 Q9K7H4	Q9k7h4 bacillus ha
17	33	82.5	822	2 Q33831	Q33831 thermotoga
18	33	82.5	1121	2 Q9RNX9	Q9rnx9 escherichia
19	32	80.0	109	14 Q9WD80	Q9wd80 influenza b

20	32	80.0	109	14	Q9WD79	Q9wd79 influenza i
21	32	80.0	109	14	Q9WD78	Q9wd78 influenza i
22	32	80.0	109	14	Q9WD77	Q9wd77 influenza b
23	32	80.0	109	14	Q9WD76	Q9wd76 influenza i
24	32	80.0	109	14	Q9WD75	Q9wd75 influenza b
25	32	80.0	109	14	Q9WD74	Q9wd74 influenza b
26	32	80.0	109	14	Q9W921	Q9w921 influenza b
27	32	80.0	109	14	Q9W9D0	Q9w9d0 influec b
28	32	80.0	109	14	Q9W8S3	Q9w8s3 influenza i
29	32	80.0	109	14	Q9W8S0	Q9w8s influenza b
30	32	80.0	109	14	Q9W8L9	Q9w8l9 influenza b
31	32	80.0	280	4	Q9H1A5	Q9h1a5 homo sapien
32	32	80.0	297	4	Q75213	Q75213 homo sapien
33	32	80.0	320	2	Q9ZBB0	Q9zbb0 sphingomon
34	32	80.0	370	10	Q9XEE0	Q9xee0 arabidop
35	32	80.0	484	2	Q9WYB7	Q9wyb7 thermotoga
36	32	80.0	780	3	Q9P7W8	Q9p7w8 thizosacch
37	31	77.5	109	14	Q9WD73	Q9wd73 influenza b
38	31	77.5	236	5	Q9N4D9	Q9n4d9 caenorhabdi
39	31	77.5	470	5	Q9GYB8	Q9gyb8 leishmania
40	31	77.5	487	5	Q9NI44	Q9ni44 trypanosoma
41	31	77.5	539	2	P72284	P72284 thizobium i
42	31	77.5	540	2	O06656	O06656 thizobium i
43	31	77.5	540	2	P72288	P72288 rhizobium i
44	31	77.5	540	2	Q9FDG4	Q9fdg4 rhizobium i
45	31	77.5	563	2	P71753	P71753 mycobacteri

## ALIGNMENTS

RESULT 1

ID	Q9VZF7	PRELIMINARY;	PRT;	266 AA.
AC	Q9VZF7;			
DT	01-MAY-2000 (TRENBLrel. 13, Created)			
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)			
DE	01-MAR-2001 (TRENBLrel. 16, Last annotation update)			
DE	IMPL2 PROTEIN.			
GN	IMPL2 OR CG15009.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov I.			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chaudhri I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Fierman P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,			
RA	Foster C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Liu X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson I.			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A			

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
DR EMBL: AE003480; AAF47866.2; -.  
DR HSSP: P56276; ITLK.  
DR FlyBase: FBgn0001257; ImpL2.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; ig; 4.  
SQ SEQUENCE 266 AA; 29823 MW; FC97694BDFE80F33 CRC64;

Query Match 92.5%; Score 37; DB 5; Length 266;

Best Local Similarity 85.7%; Pred. No. 5.1;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHL 8

Db 90 QWVVGHL 96

RESULT 2

ID Q9UI28 PRELIMINARY; PRT; 224 AA.

AC Q9UI28;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE ADRENAL GLAND PROTEIN AD-003.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,

RA Han Z., Wang Y., Chen Z., Fu G.;

RT "A novel gene expressed in human adrenal gland.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AFL10776; AAF14859.1; -.

DR InterPro: IPR000051; -.

DR InterPro: IPR001601; -.

SQ SEQUENCE 224 AA; 25474 MW; 8BB11B3FA7804CD3 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 224;

Best Local Similarity 71.4%; Pred. No. 6.8;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHL 8

Db 136 QWVVGHL 142

RESULT 3

ID Q9UVE4 PRELIMINARY; PRT; 232 AA.

AC Q9UVE4;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE HYPOTHETICAL 26.4 KDA PROTEIN.

OS Zygosaccharomyces rouxii (Candida mogii).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.

OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

OX NCBI\_TaxID=4956;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-CBS 732;

RA Sychrova H., Braun V., Potier S., Souciet J.L.;

RT "Genomic organization of *Pichia sorbitophila* and *Zygosaccharomyces* rouxii genomes: comparison with *Saccharomyces cerevisiae*.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: Y18560; CAB62288.1; -.

DR InterPro: IPR001601; -.

KW Hypothetical protein.

SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match 90.0%; Score 36; DB 3; Length 232;

Best Local Similarity 85.7%; Pred. No. 7.1;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHL 8

Db 140 QWVVGHL 146

RESULT 4

ID Q9P6Y1 PRELIMINARY; PRT; 256 AA.

AC Q9P6Y1;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE CONSERVED HYPOTHETICAL PROTEIN.

GN I3E11.350.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales; Sordariaceae; Neurospora.

OX NCBI\_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,

RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA German Neurospora genome project;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL353820; CAB88603.1; -.

DR InterPro: IPR001601; -.

SQ SEQUENCE 256 AA; 27789 MW; 5251FBC58B6BDD9 CRC64;

Query Match 90.0%; Score 36; DB 3; Length 256;

Best Local Similarity 85.7%; Pred. No. 7.8;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVVGHL 8

Db 162 QWVVGHL 168

RESULT 5

ID Q9FI20 PRELIMINARY; PRT; 252 AA.

AC Q9FI20;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE GENOMIC DNA, CHROMOSOME 5, PL CLONE:MFC16.

OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=COLUMBIA;  
 RX MEDLINE=99397451; PubMed=10470850;  
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,  
 RA Miyajima N., Tabata S.;  
 RA "Structural analysis of Arabidopsis thaliana chromosome 5, IX.  
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen  
 RT p1 and TAC clones"; 1999.  
 RL DNA Res. 6:183-195(1999).  
 DR EMBL; AB017065; BAB09152.1; -.  
 SQ SEQUENCE 252 AA; 28622 MW; F93F8EE657D284B2 CRC64;

Query Match 87.5%; Score 35; DB 10; Length 252;  
 Best Local Similarity 71.4%; Pred. No. 12;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVXGHL 8  
 Db 147 QWCIGHL 153  
 |||  
 |||

RESULT 6  
 Q90253 ID Q90253 PRELIMINARY; PRT; 119 AA.  
 AC Q90253;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE PHE-13 BOMBESIN PREPROHORMONE.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96205965; PubMed=8631814;  
 RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,  
 RA Dong J.Z., Spindel E.R.;  
 RT "There are three distinct forms of bombesin. Identification of  
 RT [Leu13]bombesin, [Phe13]bombesin, and [Ser3,Arg10,Phe13]bombesin in  
 RT the frog Bombina orientalis".  
 RL J. Biol. Chem. 271:7731-7737(1996).  
 DR EMBL; 049450; AAC59784.1; -.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 FT CHAIN 45 PHE-13 BOMBESIN.  
 SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 85.0%; Score 34; DB 13; Length 119;  
 Best Local Similarity 83.3%; Pred. No. 9.3;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVXGH 7  
 Db 51 QWAVGH 56  
 |||  
 |||

RESULT 7  
 Q9V5C9 ID Q9V5C9 PRELIMINARY; PRT; 276 AA.  
 AC Q9V5C9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE GASTRIN-RELEASING PEPTIDE, GRP.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 DE CG1675 PROTEIN.

GN CG1675.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gall J.R.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer E.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley L.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov A.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.F.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reiner T.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 FT "The genome sequence of Drosophila melanogaster".  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003831; AAF58883.1; -.  
 DR FlyBase; FBgn0033457; CG1675.  
 DR InterPro; IPR001601; -.  
 SQ SEQUENCE 276 AA; 30601 MW; 917222EFC544A385 CRC64;

Query Match 85.0%; Score 34; DB 5; Length 276;  
 Best Local Similarity 71.4%; Pred. No. 22;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVXGHL 8  
 Db 182 QWVLGHL 188  
 |||  
 |||

RESULT 8  
 Q9PS30 ID Q9PS30 PRELIMINARY; PRT; 23 AA.  
 AC Q9PS30;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE, GRP.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93126164; PubMed=1480521;  
RA Jensen J., Coulon J.M.;  
RT "Isolation and primary structure of gastrin-releasing peptide from a  
RT teleost fish, the trout (*Oncorhynchus mykiss*).";  
RL Peptides 13:995-999(1992).  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombsin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
SQ SEQUENCE 23 AA; 2479 MW; 94CD79F70E3DB637 CRC64;

Query Match 82.5%; Score 33; DB 13; Length 23;  
Best Local Similarity 83.3%; Pred. No. 2.8;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
3 WXVGH 8  
| | | | |  
Db 17 WAVGHL 22

RESULT 9  
Q91829  
ID Q91829 PRELIMINARY; PRT; 157 AA.  
AC Q91829;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE GASTRIN-RELEASING PEPTIDE PRECURSOR.  
GN GRP.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20336817; PubMed=10876046;  
RA Volkoff H., Peyon P., Lin X., Peter R.F.;  
RT "Molecular cloning and expression of cDNA encoding a brain  
RT bombesin/gastrin-releasing peptide-like peptide in goldfish.";  
RL Peptides 21:639-648(2000).  
DR EMBL; AF111028; AAF82387.1; -.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombsin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Signal.  
FT SIGNAL.  
FT CHAIN 1 27 POTENTIAL.  
SQ SEQUENCE 157 AA; 18201 MW; DD927EE19FD43117 CRC64;

Query Match 82.5%; Score 33; DB 13; Length 157;  
Best Local Similarity 83.3%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
3 WXVGH 8  
| | | | |  
Db 43 WAVGHL 48

RESULT 10  
Q9WWT3  
ID Q9WWT3 PRELIMINARY; PRT; 211 AA.  
AC Q9WWT3;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 23.6 KDA PROTEIN (FRAGMENT).

OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=PRS2000;  
RA Nichols N.N., Harwood C.S.;  
RT "Aerotaxis receptor of *Pseudomonas putida* PRS2000.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF079997; AAD22404.1; -.  
DR InterPro; IPR000014; -.  
DR InterPro; IPR000160; -.  
DR InterPro; IPR000700; -.  
DR InterPro; IPR001610; -.  
DR Pfam; PF00785; PAC; 1.  
DR Pfam; PF00989; PAS; 1.  
DR Pfam; PF00990; DUF9; 1.  
DR SMART; SM00267; DUF1; 1.  
KW Hypothetical protein.  
FT NON\_TER 211 211  
SQ SEQUENCE 211 AA; 23566 MW; F113AF955610BBE5 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 211;  
Best Local Similarity 83.3%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
2 QXVGH 7  
| | | | |  
Db 125 QWRVGH 130

RESULT 11  
Q9HVL9  
ID Q9HVL9 PRELIMINARY; PRT; 372 AA.  
AC Q9HVL9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE GLUTAMATE 5-KINASE.  
GN PROB OR PA4565.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
RT opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
DR EMBL; AE004870; AAG07953.1; -.  
DR InterPro; IPR001048; -.  
DR InterPro; IPR001057; -.  
DR InterPro; IPR002478; -.  
DR Pfam; PF00696; aakkinase; 1.  
DR Pfam; PF01472; PUA; 1.  
DR PRINTS; PF00474; GLU5KINASE.  
DR PROSITE; PS00902; GLUTAMATE\_5\_KINASE; UNKNOWN\_1.  
KW Kinase.  
SQ SEQUENCE 372 AA; 39845 MW; FAF2E81F6A8DEC36 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 372;  
Best Local Similarity 71.4%; Pred. No. 47;

```
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWVGHL 8
DB 271 QWLAGHL 277

RESULT 12
Q9JN79 PRELIMINARY; PRT; 387 AA.
AC Q9JN79;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PUTATIVE ENOYL REDUCTASE.
GN MYE.
OS Streptomyces coelicolor.
OG Plasmid pSCPl.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
CA Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=A3(2);
RA Bruton C.J.; Wietzorrek A., Hartley N., Woodburn L., Chater K.F.;
RT "Genes involved in methylenomycin biosynthesis from plasmid SCPl of
RL Streptomyces coelicolor A3(2).";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=A3(2);
RX MEDLINE=88112873; PubMed=2828187;
RA Neal R.J., Chater K.F.;
RT "Nucleotide sequence analysis reveals similarities between proteins
RL determining methylenomycin A resistance in Streptomyces and
RL tetracycline resistance in eubacteria.";
RN Gene 58:229-241(1987).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=A3(2);
RX MEDLINE=85284984; PubMed=2992952;
RA Chater K.F., Bruton C.J.;
RT "Resistance, regulatory and production genes for the antibiotic
RL methylenomycin are clustered.";
RN EMBO J. 4:1893-1897(1985).
DR EMBL; AJ276673; CAB82878.1; -.
DR InterPro; IPR001155; -.
DR Pfam; PF00724; oxidored_FMN; 1.
DR Plasmid.
SEQUENCE 387 AA; 40974 MW; 0149B42D0F6B90A3 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGHL 7
DB 246 QWVGHL 251

RESULT 13
Q99986 PRELIMINARY; PRT; 396 AA.
AC Q99986;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VRK1, COMPLETE CDS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

Query Match 82.5%; Score 33; DB 2; Length 399;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 4; Conservative 2; Mismatches 1; Indels 0;

QY 2 QWVGHL 8
DB 253 QWLGHL 259
```

```
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=LIVER;
RX MEDLINE=98008921; PubMed=9344656;
RA Nezu J., Oku A., Jones M.H., Shimane M.;
RT "Identification of two novel human putative serine/threonine kinases,
RL VRK1 and VRK2, with structural similarity to vaccinia virus p1K
RL kinase.";
RL Genomics 45:327-331(1997).
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB000449; BAA19108.1; -.
DR HSP; Q06486; 1CKT.
DR InterPro; IPR000719; -.
DR InterPro; IPR002290; -.
DR Pfam; PF00069; pkinase; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR SMART; SM00220; S_TKc; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 396 AA; 45476 MW; 5640C624BF059949 CRC64;

Query Match 82.5%; Score 33; DB 4; Length 396;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWVGHL 8
DB 253 QWLGHL 259

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=PRELIMINARY; PRT; 399 AA.
AC Q9UOV1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MITOCHONDRIAL CARRIER PROTEIN.
GN L8342.02.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Masuy D., Purnelle B., Coffeau A., Ivens A.C., Lawson D., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.N., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL122012; CAB58416.1; -.
DR InterPro; IPR000847; -.
DR InterPro; IPR001993; -.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SQ SEQUENCE 399 AA; 43755 MW; A3D4E510517865C8 CRC64;

Query Match 82.5%; Score 33; DB 5; Length 399;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 4; Conservative 2; Mismatches 1; Indels 0;

QY 2 QWVGHL 8
DB 253 QWLGHL 259
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Db 131 QWTLGHI 137

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RESULT 15
Q07711
AC Q07711 PRELIMINARY; PRT; 700 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
DE (UNTWISTING ENZYME) (SWIVELASE).
GN TRAI OR TRSI.
OS Staphylococcus aureus.
OG Plasmid pg01, and Plasmid pSV41.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RN [1] SEQUENCE FROM N.A.
PL PLASMID=PG01;
MEDLINE=93322322; PubMed=7687249;
RA Morton T.M., Eaton D.M., Johnston J.L., Archer G.L.;
RT "DNA sequence and units of transcription of the conjugative transfer
RT gene complex (trs) of Staphylococcus aureus plasmid pg01.";
RL J. Bacteriol. 175:4436-4447(1993).
RN [2]
RN [2] Analysis of a transfer region from the staphylococcal conjugative
RT plasmid pSK41.";
RL Gene 136:13-25(1993).
RN [3]
RN [3] SEQUENCE FROM N.A.
PL PLASMID=PSV41;
MEDLINE=94123990; PubMed=8293996;
RA Firth N., Ridgeway K.P., Byrne M.E., Fink P.D., Johnson L.,
RA Paulsen I.T., Skurray R.A.;
RT "Analysis of a transfer region from the staphylococcal conjugative
RT plasmid pSK41.";
RL Gene 136:13-25(1993).
RN [3]
RN [3] SEQUENCE FROM N.A.
PL PLASMID=PSV41;
MEDLINE=98389645; PubMed=9721269;
RA Berg T., Firth N., Apisiridej S., Hettiaratchi A., Leelaporn A.,
RA Skurray R.A.;
RT "Complete nucleotide sequence of pSK41: evolution of staphylococcal
RT conjugative multiresistance plasmids.";
RL J. Bacteriol. 180:4350-4359(1998).
DR EMBL; L11998; AA71960.1; .
DR EMBL; AF051917; AAC61961.1; .
DR InterPro; IPR000380; .
DR InterPro; IPR02936; .
DR Pfam; PF01131; Topoisom_bac; 1.
DR Pfam; PF01396; zf-C4_Topoisom; 1.
DR Pfam; PF01751; Toprim; 1.
DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; UNKNOWN_1.
DR SMART; SM00493; TOPRIM; 1.
KW Isomerase; Topoisomerase; DNA-binding; Plasmid.
SQ SEQUENCE 700 AA; 80742 MW; 1BB6BF2F2DB6142D CRC64;
```

```
Query Match 82.5%; Score 33; DB 2; Length 700;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WVGHL 8
   | | | | |
Db 45 WVGHL 50
```

Search completed: October 25, 2001, 11:27:45  
Job time: 448 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:28:29 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-9  
Perfect score: 40  
Sequence: 1 QWXXVGH 8

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	95.0	14	1	ALYT-ALYOB
2	38	95.0	107	1	BOMB-BOMVA
3	38	95.0	119	1	BOMB-BOMOR
4	37	92.5	263	1	IML2-DROME
5	36	90.0	232	1	YB9H-YEAST
6	34	85.0	9	1	LITO-LITAU
7	34	85.0	13	1	BOML-PSEGU
8	34	85.0	82	1	RANA-RANPI
9	33	82.5	10	1	GRP-RANRI
10	33	82.5	25	1	GRP-SCYCA
11	33	82.5	27	1	GRP-CANFA
12	33	82.5	27	1	GRP-CHICK
13	33	82.5	27	1	GRP-PIG
14	33	82.5	28	1	GRP-ALLMI
15	33	82.5	120	1	NEUB-XENLA
16	33	82.5	134	1	GRP-SHEEP
17	33	82.5	147	1	GRP-RAT
18	33	82.5	148	1	GRP-HUMAN
19	33	82.5	155	1	GRP-BOMOR
20	33	82.5	308	1	LIVH-ECOLI
21	33	82.5	391	1	HERP-HUMAN
22	33	82.5	1122	1	EX5C-ECOLI
23	32	80.0	195	1	VMT2-INBAC
24	32	80.0	195	1	VMT2-INBAC
25	32	80.0	195	1	VMT2-INBLE
26	32	80.0	195	1	VMT2-INBSI
27	31	77.5	366	1	YBAB-BACCI
28	31	77.5	651	1	TOP3-HAETN
29	31	77.5	2151	1	RRPL-HANTV
30	31	77.5	2151	1	RRPL-SEQ08
31	30	75.0	11	1	RANC-RANPI
32	30	75.0	17	1	RANC-RANRU
33	30	75.0	133	1	ECHA-ECOCA

34	30	75.0	192	1	CBIT-SALTY	Q05612
35	30	75.0	198	1	YB9G-ECOLI	P75806
36	30	75.0	282	1	AOP6-HUMAN	P13520
37	30	75.0	306	1	PPT-RAT	P45479
38	30	75.0	307	1	PPT-MOUSE	O85531
39	30	75.0	392	1	PO14-NASVI	Q03272
40	30	75.0	452	1	VE2-HPV17	Q03272
41	30	75.0	454	1	VE2-HPV37	Q03272
42	30	75.0	551	1	FIXN-AZOCA	Q03272
43	30	75.0	647	1	TOP3-VIBCH	Q03272
44	30	75.0	653	1	TOP3-ECOLI	Q03272
45	30	75.0	656	1	TOP3-YEAST	P14294

ALIGNMENTS

RESULT 1  
ALYT-ALYOB  
ID ALYT-ALYOB STANDARD; PRT; 14 AA.  
AC P08944;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE ALYTESIN.  
OS Alytes obstetricans (Midwife toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes  
OX NCBI\_TaxID=8443;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84131098; PubMed=6141890;  
RA Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
RT "Active peptides in the skins of one hundred amphibian species from  
RT Australia and Papua New Guinea";  
RL Comp. Biochem. Physiol. 77C:99-108(1984).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR InterPro: IPR000874;  
DR Pfam: PF02044; Bombesin; 1.  
DR PROSITE: PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 14 14 AMIDATION.  
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 95.0%; Score 38; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 0.078;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 2 QWXXVGH 8  
Db 7 QWAVGHL 13

RESULT 2  
BOMB-BOMVA  
ID BOMB-BOMVA STANDARD; PRT; 107 AA.  
AC P01296;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE BOMBESIN PRECURSOR.  
OS Bombina variegata (Yellow-bellied toad), and  
OS Bombina bombina (Fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8348, 8345;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.variegata; TISSUE=Skin;  
RX MEDLINE=90242964; PubMed=2335218;

RA Richter K., Egger R., Kreil G.;  
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
 RL of *Bombina variegata*.";  
 RN FEBS Lett. 262:353-355(1990).  
 RP [2]  
 RC SEQUENCE OF 42-55.  
 RX SPECIES=B.variegata, and B.bombina;  
 RA MEDLINE=72163516; PubMed=4537042;  
 RA Anastasi A., Erspaner V., Bucci M.;  
 RT "Isolation and amino acid sequences of alytesin and bombesin, two  
 RT analogous active tetradecapeptides from the skin of European  
 RT discoglossid frogs.";  
 RL Arch. Biochem. Biophys. 148:443-446(1972).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 CC OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
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 CC -----  
 DR EMBL; X52447; CAA36686.1; -;  
 DR PIR; A01564; BSTD.  
 DR PIR; B01564; BSTDY.  
 DR PIR; S09095; S09095.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT PEPTIDE 42 55 BOMBESIN.  
 FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;  
 -----  
 Query Match 95.0%; Score 38; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 0.52;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 -----  
 QY 2 QWVGHGL 8  
 DB 48 QWVGHGL 54  
 || |||||  
 -----  
 RESULT 3  
 BOMB\_BOMOR  
 ID BOMB\_BOMOR STANDARD; PRT; 119 AA.  
 AC P21591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE BOMBESIN PRECURSOR.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088602; PubMed=2263631;  
 RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;  
 RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
 RT relationship between bombesin and gastrin-releasing peptide.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 CC OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
 CC -!- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN  
 CC THE SKIN AND THE BRAIN.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
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 CC -----  
 DR EMBL; M55255; AAA48551.1; -;  
 DR PIR; A39261; A39261.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 ?  
 FT PEPTIDE 45 58 BOMBESIN.  
 FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2445A44A CRC64;  
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 Query Match 95.0%; Score 38; DB 1; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 0.57;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 QY 2 QWVGHGL 8  
 DB 51 QWVGHGL 57  
 || |||||  
 -----  
 RESULT 4  
 IML2\_DROME  
 ID IML2\_DROME STANDARD; PRT; 263 AA.  
 AC Q09024;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2 PRECURSOR.  
 GN IML2.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CANTON-S; TISSUE=Embryo;  
 RX MEDLINE=94139565; PubMed=8306886;  
 RA Garbe J.C., Yang E., Fristrom J.W.;  
 RT "IMP-L2: an essential secreted immunoglobulin family member  
 RT implicated in neural and ectodermal development in *Drosophila*.";  
 RL Development 119:1237-1250(1993).  
 CC -!- FUNCTION: ESSENTIAL DEVELOPMENTAL ROLE DURING EMBRYOGENESIS, IN  
 CC PARTICULAR THE NORMAL DEVELOPMENT OF THE NERVOUS SYSTEM. MAY BE  
 CC INVOLVED IN SOME ASPECT OF CELL ADHESION.  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: DETECTED IN SEVERAL SITES INCLUDING THE  
 CC VENTRAL NEUROECTODERM, THE TRACHEAL PITS, THE PHARYNX AND  
 CC OESOPHAGUS, AND SPECIFIC NEURONAL CELL BODIES, WHERE IT IS  
 CC PRIMARILY EXPRESSED.  
 CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT THE CELLULAR BLASTODERM  
 CC STAGE AND CONTINUES TO BE EXPRESSED THROUGH SUBSEQUENT  
 CC DEVELOPMENT.  
 CC -!- INDUCTION: BY 20-HYDROXYCYDSONE.  
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -----  
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DR EMBL; L23066; AAB59251.1; -;  
 DR HSSP; P56276; ITLK.  
 DR FlyBase; FBgn001257; Impl2.  
 DR InterPro; IPR003006; -;  
 DR Pfam; PF00047; Ig; 2.  
 KW Immunoglobulin domain; Cell adhesion; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 263  
 FT -----  
 FT DOMAIN 69 142  
 FT DOMAIN 184 247  
 FT DISULFID 76 135  
 FT DISULFID 191 240  
 FT VARIANT 173 173  
 FT V -> I.  
 SEQUENCE 263 AA; 29421 MW; 44AADB1B22DD1804 CRC64;

Query Match 92.5%; Score 37; DB 1; Length 263;  
 Best Local Similarity 85.7%; Pred. No. 1.9;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVGH 8  
 DB 87 QWVGH 93

RESULT 5  
 ID YB9H\_YEAST STANDARD; PRT; 232 AA.  
 AC P38340;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE HYPOTHETICAL 26.1 KDA PROTEIN IN POP4-SHML INTERGENIC REGION.  
 GN YBR261C OR YBR1729.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 STRAIN=S288C;  
 MEDLINE=93220397; PubMed=8465606;  
 RA Daignon F., Biteau N., Crouzet M., Aigle M.;  
 RT "The complete sequence of a 19,482 bp segment located on the right  
 RT arm of chromosome II from *Saccharomyces cerevisiae*.";  
 RL Yeast 9:189-199(1993).  
 CC -!- SIMILARITY: TO S.POMBE SPAC15E8.14C.  
 CC -----

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 CC -----

DR EMBL; X70529; CAA49926.1; -;  
 DR EMBL; Z36130; CAA85224.1; -;  
 DR PIR; S32963; S32963.  
 DR SGD; S0000465; YBR261C.  
 KW Hypothetical protein.  
 SQ SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 232;

Best Local Similarity 85.7%; Pred. No. 2.7;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWVGH 8  
 DB 139 QWVGH 145

RESULT 6  
 LITO\_LITAU STANDARD; PRT; 9 AA.  
 ID LITO\_LITAU  
 AC P08945;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LITORIN.  
 OS Litoria aurea (Australian frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 CC Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=75187011; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Amino acid composition and sequence of litorin, a bombesin-like  
 RT nonapeptide from the skin of the Australian leptodactylid frog  
 RT Litoria aurea";  
 RL Litoria aurea 31:510-511(1975).  
 RN [2]  
 RP SEQUENCE (METHYLATED VARIANT).  
 RX MEDLINE=78003546; PubMed=908397;  
 RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;  
 RT "Glu(Ome)3-litorin, the second bombesin-like peptide occurring in  
 RT methanol extracts of the skin of the Australian frog Litoria aurea".  
 RL Experientia 33:1289-1289(1977).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR; S07204; S07204.  
 DR PIR; S07205; S07205.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Methylation.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 2 2 METHYLATION (IN A VARIANT).  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1103 MW; D7CCC1E862CDC366 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+04;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 7  
 DB 2 QWVGH 7

RESULT 7  
 BOML\_PSEGU STANDARD; PRT; 13 AA.  
 ID BOML\_PSEGU  
 AC P42991;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE BOMBESIN-LIKE PEPTIDE L (PG-L).  
 OS Pseudophryne guentheri (Frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 CC Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]

```

RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Ersamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; A60409; A60409.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 13 13 AMIDATION.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.45;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGH 7
Db 6 QWVGH 11

RESULT 8
RANA_RANPI
ID RANA_RANPI STANDARD; PRT; 82 AA.
AC P08950;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RANATENSIN PRECURSOR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330837; PubMed=2459345;
RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;
RA "Molecular cloning of cDNAs encoding the human bombesin-like peptide
RT neuromedin B. Chromosomal localization and comparison to cDNAs
RT encoding its amphibian homolog ranatensin.";
J. Biol. Chem. 263:13317-13323(1988).
[2]
RP SEQUENCE OF 48-58.
RA Nakajima T., Tanimura T., Pisano J.J.;
RT "Isolation and structure of a new vasoactive polypeptide.";
Fed. Proc. 29:282-282(1970).
RL
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC
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CC
DR ENBL; M21552; AAA49533.1; -.
DR PIR; B28945; B28945.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation; Cleavage on pair of basic residues;
KW Signal.
FT SIGNAL 1 27 POTENTIAL.

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FT PROPEP 28 47
FT PEPTIDE 48 58
FT MOD_RES 58 58
SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 85.0%; Score 34; DB 1; Length 82;
Best Local Similarity 83.3%; Pred. No. 2.5;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWVGH 7
Db 51 QWVGH 56

RESULT 9
GRP_RANRI
ID GRP_RANRI STANDARD; PRT; 10 AA.
AC P23260;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE NEUROMEDIN C.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91315477; PubMed=1859413;
RA Conlon J.M., O'Harte F., Vaudry H.;
RT "Primary structures of the bombesin-like neuropeptides in frog brain
RT show that bombesin is not the amphibian gastrin-releasing peptide.";
RL Biochem. Biophys. Res. Commun. 178:526-530(1991).
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; PQ0177; PQ0177.
DR InterPro; IPR000874; -.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 10 10
FT MOD_RES 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;
SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 0.56;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WYVGH 8
Db 4 WYVGH 9

RESULT 10
GRP_SCYCA
ID GRP_SCYCA STANDARD; PRT; 25 AA.
AC P09472;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE GASTRIN-RELEASING PEPTIDE (GRP).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Ranioidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RX MEDLINE=88137922; PubMed=3436516;
RA Conlon J.M., Henderson I.W., Thim L.;
RT "Gastrin-releasing peptide from the intestine of the elasmobranch

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RT fish, Scyliorhinus canicula (common dogfish).";  
 RL Gen. Comp. Endocrinol. 68:415-420(1987).  
 CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR: S06263; S06263;  
 DR InterPro: IPR000874; -;  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 25 25  
 SQ SEQUENCE 25 AA: 2781 MW; B735F911B89007F8 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.3;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVGHL 8  
 | | | | |  
 DB 21 WVGHL 24

RESULT 11  
 GRP\_CANFA STANDARD; PRT; 27 AA.  
 AC P08989;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP-10)].  
 GN GRP.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83213518; PubMed=6853532;  
 RA Reeve J.R. Jr., Walsh J.H., Chew P., Clark B., Hawke D.,  
 RA Shively J.E.;  
 RT "Amino acid sequences of three bombesin-like peptides from canine  
 RT intestine extracts.";  
 RL J. Biol. Chem. 258:5582-5588(1983).  
 CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR InterPro: IPR000874; -;  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT PEPTIDE 18 27  
 FT MOD\_RES 27 27  
 SQ SEQUENCE 27 AA: 2889 MW; 9D9317261B7C7D65 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.4;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVGHL 8  
 | | | | |  
 DB 21 WVGHL 26

RESULT 12  
 GRP\_CHICK STANDARD; PRT; 27 AA.  
 AC P01295;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE (GRP) (PROVENTRICULAR PEPTIDE) [CONTAINS:  
 DE NEUROMEDIN C (GRP-10)].  
 GN GRP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81164953; PubMed=7215543;  
 RA McDonald T.J., Joernvall H., Gbatei M., Bloom S.R., Mutt V.;  
 RA "Characterization of an avian gastric (proventricular) peptide and its  
 RT sequence homology with the porcine gastrin-releasing peptide and the  
 RT amphibian peptides bombesin and aliytesin.";  
 RL FEBS Lett. 122:45-48(1980).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=90122926; PubMed=2297533;  
 RA Campbell B.J., Young J., Dimalline R., Dockray G.J.;  
 RA "Isolation, sequence and biosynthetic significance of a novel  
 RT fragment of gastrin-releasing peptide from chicken proventriculus.";  
 RL Biochim. Biophys. Acta 1048:66-71(1990).  
 CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
 CC GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR: A01563; RHCHA.  
 DR PIR: S08150; S08150.  
 DR InterPro: IPR000874; -;  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT PEPTIDE 18 27  
 FT MOD\_RES 27 27  
 SQ SEQUENCE 27 AA: 2842 MW; 3C121D0118D551C7 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 27;  
 Best Local Similarity 83.3%; Pred. No. 1.4;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVGHL 8  
 | | | | |  
 DB 21 WVGHL 26

RESULT 13  
 GRP\_PIG STANDARD; PRT; 27 AA.  
 AC P01294;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP 10)].  
 GN GRP.  
 OS Sus scrofa (Pig), and Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=9823, 10141;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Pig;  
 RX MEDLINE=80042433; PubMed=496973;  
 RA McDonald T.J., Joernvall H., Nilsson G., Vagne M., Gbatei M.,  
 RA Bloom S.R., Mutt V.;  
 RT "Characterization of a gastrin releasing peptide from porcine  
 RT non-antral gastric tissue.";  
 RL Biochem. Biophys. Res. Commun. 90:227-233(1979).  
 RN [2]  
 RP SEQUENCE OF 18-27.  
 RC SPECIES=Pig;

RX MEDLINE=84153890; PubMed=6546686;  
RA Minamino N., Kangawa K., Matsuo H.;  
RT "Neuromedin C: a bombesin-like peptide identified in porcine spinal  
RT cord.";  
RL Biochem. Biophys. Res. Commun. 119:14-20(1984).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=C.porcullus;  
RX MEDLINE=88034997; PubMed=3668528;  
RA Shaw C., Thim L., Conlon J.M.;  
RT "Primary structure and tissue distribution of guinea pig gastrin-  
RT releasing peptide.";  
RL J. Neurochem. 49:1348-1354(1987).  
CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
CC GASTROINTESTINAL HORMONES.  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR PIR: A01562; RHFGA.  
DR PIR: A60206; RHGPGA.  
DR InterPro: IPR000874; -.  
DR Pfam: PF02044; Bombesin; 1.  
DR PROSITE: PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT PEPTIDE 18 27 NEUROMEDIN C.  
FT MOD\_RES 27 27 AMIDATION.  
SQ SEQUENCE 27 AA; 2806 MW; FA1017260210410F CRC64;

Query Match 82.5%; Score 33; DB 1; Length 27;  
Best Local Similarity 83.3%; Pred. No. 1.4;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 WXVGH 8  
Db 21 WVGHL 26

RESULT 14  
GRP\_ALLMI STANDARD; PRT; 28 AA.  
AC P31886;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DE GASTRIN-RELEASING PEPTIDE (GRP) [CONTAINS: NEUROMEDIN C (GRP-10)].  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
NCBI\_TaxID=8496;  
[1]  
RP SEQUENCE.  
RC TISSUE=Stomach;  
RX MEDLINE=93324451; PubMed=8101369;  
RA Wang Y., Conlon J.M.;  
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain  
RT and stomach of the alligator.";  
RL Peptides 14:573-579(1993).  
CC -!- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER  
CC GASTROINTESTINAL HORMONES.  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR InterPro: IPR000874; -.  
DR Pfam: PF02044; Bombesin; 1.  
DR PROSITE: PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT PEPTIDE 19 28 NEUROMEDIN C.  
FT MOD\_RES 28 28 AMIDATION.  
SQ SEQUENCE 28 AA; 2786 MW; A74DB0487D844963 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 28;  
Best Local Similarity 83.3%; Pred. No. 1.5;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 WXVGH 8  
Db 22 WVGHL 27

RESULT 15  
NEUB\_XENLA STANDARD; PRT; 120 AA.  
AC P43443;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE NEUROMEDIN B PRECURSOR.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93028554; PubMed=1409705;  
RA Wehselberger C., Kreil G., Richter K.;  
RT "Isolation and sequence of a cDNA encoding the precursor of a  
RT bombesin-like peptide from brain and early embryos of Xenopus  
RT laevis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:9819-9822(1992).  
CC -!- FUNCTION: MAY BE A GROWTH FACTOR REQUIRED FOR THE HIGH RATE OF  
CC CELL DIVISION ENSUING AFTER FERTILIZATION, OR MAY HAVE A ROLE AS A  
CC SECRETAGOGUE THAT TRIGGERS THE RELEASE OF STORED COMPONENTS.  
CC -!- TISSUE SPECIFICITY: BRAIN, INTESTINE, AND OVARIES AND EARLY  
CC EMBRYOS (STAGES 2 AND 10).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.

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DR EMBL; L01530; AAA49912.1; -  
DR InterPro: IPR000874; -.  
DR Pfam: PF02044; Bombesin; 1.  
DR PROSITE: PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
KW Signal.  
FT SIGNAL 1 29 POTENTIAL.  
FT PROPEP 30 44  
FT PEPTIDE 45 54 NEUROMEDIN B.  
FT MOD\_RES 54 54 AMIDATION (G-55 PROVIDE AMIDE GROUP).  
SQ SEQUENCE 120 AA; 14384 MW; 2CB146BA082A2442 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 120;  
Best Local Similarity 66.7%; Pred. No. 5.6;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWVGH 7  
Db 47 QWAIGH 52

Search completed: October 25, 2001, 11:28:29  
Job time: 477 sec

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:45 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-10  
Perfect score: 38  
Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues 425026  
All number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16.\*  
1: sp-archaea.\*  
2: sp-bacteria.\*  
3: sp-fungi.\*  
4: sp-human.\*  
5: sp-invertebrate.\*  
6: sp-mammal.\*  
7: sp-mnc.\*  
8: sp-organelle.\*  
9: sp-phage.\*  
10: sp-plant.\*  
11: sp-rodent.\*  
12: sp-unclassified.\*  
13: sp-invertebrate.\*  
14: sp-virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	86.8	517	14 Q9DSP4	Q9dsp4 saint croix
2	32	84.2	174	10 Q9M2H1	Q9m2h1 arabidopsis
3	32	84.2	328	2 Q9X5G8	Q9x5g8 streptomyce
4	32	84.2	353	5 Q21051	Q21051 caenorhabdi
5	32	84.2	806	13 Q9DDL2	Q9ddl2 brachydanio
6	31	81.6	95	2 Q911X2	Q911x2 pseudomonas
7	31	81.6	98	14 Q64981	Q64981 artichoke l
8	31	81.6	119	13 Q90253	Q90253 bombina ori
9	31	81.6	183	2 Q9R251	Q9r251 deinococcus
10	31	81.6	216	11 Q9JM34	Q9jm34 mus musculus
11	31	81.6	232	3 Q90VE4	Q90ve4 zygosacchar
12	31	81.6	236	2 Q85726	Q85726 streptomyce
13	31	81.6	256	3 Q9P6Y1	Q9p6y1 neurospora
14	31	81.6	266	5 Q9VZF7	Q9vzf7 drosophila
15	31	81.6	273	8 Q9RTQ5	Q9rtq5 prototheca
16	31	81.6	309	5 Q27106	Q27106 trichomonas
17	31	81.6	325	2 Q9PAR1	Q9par1 xyella fas
18	31	81.6	357	10 Q65366	Q65366 antirrhinum
19	31	81.6	359	10 Q9FUK9	Q9fuk9 pisum sativ

20	31	81.6	675	10 Q9S9V7	Q9s9v7 rabidopsi
21	31	81.6	696	5 Q9VCU2	Q9vcu2 consoph a
22	31	81.6	703	10 Q9LYH3	Q9lyh3 rabidopsi
23	31	81.6	1273	4 Q9NU68	Q9nu68 homo sapien
24	31	81.6	1275	4 Q15057	Q15057 homo sapien
25	30	78.9	23	13 Q9PS30	Q9ps30 oncorhynch
26	30	78.9	132	2 Q9K3V3	Q9k3v3 streptomyce
27	30	78.9	157	13 Q9I829	Q9i829 rassius
28	30	78.9	170	2 P74711	P74711 streptocyst
29	30	78.9	224	4 Q9UI28	Q9ui28 homo sapien
30	30	78.9	252	1 Q26248	Q26248 rhodospirillum rubrum
31	30	78.9	252	10 Q9FI20	Q9fi20 rabidopsi
32	30	78.9	276	2 Q9LIQ5	Q9liq5 streptomyce
33	30	78.9	283	2 Q9PCE4	Q9pce4 xyella fas
34	30	78.9	291	14 Q72694	Q72694 arley mild
35	30	78.9	311	2 Q9PAE5	Q9pae5 xyella fas
36	30	78.9	318	2 Q9I066	Q9i066 pseudomonas
37	30	78.9	325	2 Q9KZG2	Q9kzg2 streptomyce
38	30	78.9	375	5 Q9TVM5	Q9tvm5 caenorhabdi
39	30	78.9	453	10 Q9M4A9	Q9m4a9 pisum sativ
40	30	78.9	520	10 Q65815	Q65815 nelianthus
41	30	78.9	691	2 Q55726	Q55726 streptocyst
42	30	78.9	700	2 Q07711	Q07711 streptocyst
43	30	78.9	719	14 P87541	P87541 bacillus h
44	30	78.9	721	2 Q9K7H4	Q9k7h4 bacillus h
45	30	78.9	858	5 Q17647	Q17647 caenorhabdi

## ALIGNMENTS

RESULT 1  
Q9DSP4 PRELIMINARY; PRT; 517 AA.  
AC Q9DSP4;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE NS1.  
OS Saint Croix river virus.  
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.  
OX NCBI\_TaxID=104581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Attoui H., De Micco P., de Lamballerie X.;  
RT "Complete nucleotide sequence of Saint Croix river virus.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF145403; AAG34262.1; -;  
SQ SEQUENCE 517 AA; 58030 MW; 0104A543FB2A1B1A CRC64;

Query Match 86.8%; Score 33; DB 14; Length 517  
Best Local Similarity 71.4%; Pred. No. 51;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps

QY 2 QWAVXHL 8  
|||: ||  
Db 500 QWALAH 506

RESULT 2  
Q9M2H1 PRELIMINARY; PRT; 174 AA.  
AC Q9M2H1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE HYPOTHEICAL 19.2 KDA PROTEIN.  
GN F14P22.40.

OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosii; II;  
OC Brassicales; Brassicaceae; Arabidopsis.

OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,  
 RA Lemecke K., Mayer K.F.X., Quetier F., Salanoubat M.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL137082; CAB68183.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 174 AA; 19189 MW; 4C27267C5E53B4DB CRC64;  
  
 Query Match 84.2%; Score 32; DB 10; Length 174;  
 Best Local Similarity 71.4%; Pred. No. 27;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 OC 2 QWAVXHL 8  
 RN :||| ||  
 RP 47 EWAVDHL 53  
  
 RESULT 3  
 Q9X5G8 PRELIMINARY; PRT; 328 AA.  
 ID Q9X5G8;  
 AC Q9X5G8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE PUTATIVE DEACETYLCEPHALOSPORIN C ACETYLTRANSFERASE.  
 GN CVM4.  
 OS Streptomyces clavuligerus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OC NCBI\_TaxID=1901;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL 3585;  
 RX MEDLINE=99240369; PubMed=10223939;  
 RA Mosher R.H., Paradkar A.S., Anders C., Barton B., Jensen S.E.;  
 RT "Genes specific for the biosynthesis of clavam metabolites antipodal  
 RT to clavulanic acid are clustered with the gene for clavaminase  
 RT synthase 1 in Streptomyces clavuligerus."  
 RL Antimicrob. Agents Chemother. 43:1215-1224(1999).  
 CC -1- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.  
 DR EMBL: AF124929; AAD30471.1; -;  
 RN InterPro: IPR000073; -;  
 KW Pfam: PF00561; abhydrolase; 1.  
 RN Transferase; Porin.  
 SQ SEQUENCE 328 AA; 34642 MW; 4CBC78DAD5215034 CRC64;  
  
 Query Match 84.2%; Score 32; DB 2; Length 328;  
 Best Local Similarity 83.3%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 2 QWAVXH 7  
 DB 133 QWAVSH 138  
  
 RESULT 4  
 Q21051 PRELIMINARY; PRT; 353 AA.  
 ID Q21051;  
 AC Q21051;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE CSMD1 F59G1.  
 GN F59G1.4.  
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peleoderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,  
 RA Snelson N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans."  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Latreille P.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U53332; AAC71158.1; -;  
 SQ SEQUENCE 353 AA; 40061 MW; 7961772B498E3052 CRC64;  
  
 Query Match 84.2%; Score 32; DB 5; Length 353;  
 Best Local Similarity 71.4%; Pred. No. 55;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 2 QWAVXHL 8  
 DB 201 EWAVNHL 207  
  
 RESULT 5  
 Q9DDL2 PRELIMINARY; PRT; 806 AA.  
 ID Q9DDL2;  
 AC Q9DDL2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE PARACASPASE.  
 OS Brachydanio rerio (Zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11090634;  
 RA Uren A.G., O'Rourke K., Aravind L., Pisabarro M.T., Seshagiri S.,  
 RA Koonin E.V., Dixit V.M.;  
 RT "Identification of Paracaspases and Metacaspases. Two Ancient Families  
 RT of Caspase-like Proteins, One of which Plays a Key Role in MALT  
 RT Lymphoma."  
 RL Mol. Cell 6:961-967(2000).  
 DR EMBL: AF316598; AAG38590.1; -;  
 SQ SEQUENCE 806 AA; 90754 MW; 589A8BC2013B0A51 CRC64;  
  
 Query Match 84.2%; Score 32; DB 13; Length 806;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||||| 1:  
Db 559 QWAIARV 565

RESULT 6  
Q911X2 PRELIMINARY: PRT; 95 AA.  
AC Q911X2;  
DT 01-MAR-2001 (TremBLrel. 16, Created)  
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE HYPOTHETICAL PROTEIN PA2143.  
GN PA2143.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
SEQUENCE FROM N.A.  
STRAIN=PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-O.T., Ervin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
RT opportunistic pathogen";  
RL Nature 406:959-964(2000).  
DR EMBL; AE004641; AAC05531.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 95 AA; 10821 MW; 5723E5D0CD08841F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 95;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||||| 1:  
Db 63 QWVHHL 69

RESULT 7  
Q64981 PRELIMINARY: PRT; 98 AA.  
Q64981;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TremBLrel. 07, Last annotation update)  
DE MRNA UNKNOWN FUNCTION (523BP) (FRAGMENT).  
OS Artichoke latent potyvirus  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
OX NCBI\_TaxID=46076;  
RN [1]  
SEQUENCE FROM N.A.  
RA Grieco F.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X87255; CAA60708.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 98 AA; 11570 MW; C4A6316685E31078 CRC64;

Query Match 81.6%; Score 31; DB 14; Length 98;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
||||| 1:  
Db 89 QWAVEH 94

RESULT 8  
Q90253 PRELIMINARY: PRT; 119 AA.  
AC Q90253;  
DT 01-NOV-1996 (TremBLrel. 01, Created)  
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE PHE-13 BOMBESIN PREPROHORMONE.  
OS Bombina orientalis (Oriental fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Bombina  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina  
OX NCBI\_TaxID=8346;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=96205965; PubMed=8631814;  
RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,  
RA Dong J.Z., Spindel E.R.;  
RT "There are three distinct forms of bombesin. Identification of  
RT [Leu13]bombesin, [Phe13]bombesin, and [Ser3,Arg10,Phe13]bombesin in  
RT the frog Bombina orientalis";  
RL J. Biol. Chem. 271:7731-7737(1996).  
DR EMBL; U49450; AAC59784.1; -.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
FT CHAIN 45 59 PHE-13 BOMBESIN  
SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 81.6%; Score 31; DB 13; Length 119;  
Best Local Similarity 83.3%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
||||| 1:  
Db 51 QWAVGH 56

RESULT 9  
Q9RZ51 PRELIMINARY: PRT; 183 AA.  
AC Q9RZ51;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 20.5 KDA PROTEIN.  
GN DRA0103.  
OS Deinococcus radiodurans.  
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus;  
OX NCBI\_TaxID=1299;  
RN [1]  
SEQUENCE FROM N.A.  
RP STRAIN=R1;  
RX MEDLINE=20036896; PubMed=10567266;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus  
RT radiodurans R1";  
RL Science 286:1571-1577(1999).  
DR EMBL; AE001862; AAF12366.1; -.  
DR TIGR; DRA0103; -.  
KW Hypothetical protein.  
SQ SEQUENCE 183 AA; 20468 MW; 6EEAB3B483DC1BB7 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;

Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 2 QWAVXHL 8  
:|||||  
Db 49 RWAVFHL 55

## RESULT 10

Q9JW34 PRELIMINARY; PRT; 216 AA.  
AC Q9JW34  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OLFACTORY RECEPTOR (FRAGMENT).  
OS Mus musculus domesticus (Western European house mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
QY NCBI\_TaxID=10092;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=20183981; PubMed=10706615;  
RA Rouquier S., Blancher A., Giorgi D.;  
RT "The olfactory receptor gene repertoire in primates and mouse:  
RT Evidence for reduction of the functional fraction in primates.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).  
RL EMBL: AF073967; AAD43416.1; -;  
DR InterPro: IPR000276; -;  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR; UNKNOWN\_1.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 216 216  
SQ SEQUENCE 216 AA; 24097 MW; B2732A1870584D47 CRC64;

Query Match 81.6%; Score 31; DB 11; Length 216;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHL 8  
:|||||  
Db 82 WAVSHL 87

## RESULT 11

Q9JVE4 PRELIMINARY; PRT; 232 AA.  
Q9JVE4  
Q9JVE4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE HYPOTHETICAL 26.4 KDA PROTEIN.  
OS Zygosaccharomyces rouxii (Candida mogii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.  
QY NCBI\_TaxID=4956;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=CBS 732;  
RA Sychrova H., Braun V., Potier S., Souciet J.L.;  
RT "Genomic organization of Pichia sorbitophila and Zygosaccharomyces  
RT rouxii genomes: comparison with Saccharomyces cerevisiae";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y18560; CAB62288.1; -;  
DR InterPro: IPR001601; -;  
KW Hypothetical protein.  
SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 232;  
Best Local Similarity 71.4%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
:|||||  
Db 140 QWCVGHL 146

## RESULT 12

O85726 PRELIMINARY; PRT; 236 AA.  
AC O85726  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE CEPHALOSPORIN HYDROXYLASE CMCI.  
GN CMCI.  
OS Streptomyces clavuligerus.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
QY NCBI\_TaxID=1901;  
[1]  
SEQUENCE FROM N.A.  
RX STRAIN=NRRL 3585;  
RX MEDLINE=98361893; PubMed=9696752;  
RA Alexander D.C., Jensen S.E.;  
RT "Investigation of the Streptomyces clavuligerus cephamycin C gene  
RT cluster and its regulation by the Ccar protein.";  
RL J. Bacteriol. 180:4068-4079(1998).  
RL EMBL: AF073896; AAC32491.1; -;  
DR EMBL: AF073896; AAC32491.1; -;  
SQ SEQUENCE 236 AA; 27584 MW; FD1EF1B650AF8070 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 236;  
Best Local Similarity 71.4%; Pred. No. 59;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
:|||||  
Db 170 KWAVDHL 176

## RESULT 13

Q9P6Y1 PRELIMINARY; PRT; 256 AA.  
AC Q9P6Y1  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE CONSERVED HYPOTHETICAL PROTEIN.  
GN 13E11.350.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Sordariaceae; Neurospora.  
QY NCBI\_TaxID=5141;  
[1]  
SEQUENCE FROM N.A.  
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., H. Lund R.,  
RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
SEQUENCE FROM N.A.  
RA German Neurospora genome project;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL353820; CAB88603.1; -;  
DR InterPro: IPR001601; -;  
SQ SEQUENCE 256 AA; 27789 MW; 5251FBC58B6BDD9 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 256;  
Best Local Similarity 71.4%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

```
Db 162 QMCVGH 168
|||||
RESULT 14
Q9VZF7 PRELIMINARY; PRT; 266 AA.
AC Q9VZF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IMPL2 PROTEIN.
GN IMPL2 OR CGI5009.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000)
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; AE003480; AAF47866.2; -.
CC HSSP; P56276; 1TLK.
CC FlyBase; FBgn0001257; ImpL2.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; ig: 4.
CC SEQUENCE 266 AA; 29823 MW; FC97694BDF80F33 CRC64;

Query Match 81.6%; Score 31; DB 5; Length 266;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
||| ||
Db 170 QWATLHL 176
```

Search completed: October 25, 2001, 11:27:45  
Job time: 448 sec

Query Match 81.6%; Score 31; DB 8; Length 273;

Best Local Similarity 71.4%; Pred. No. 68;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

||| ||  
Db 170 QWATLHL 176

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RA Richter K., Egger R., Kreil G.;  
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
 of Bombina variegata.";  
 RL FEBS Lett. 262:353-355(1990).  
 RN [2]  
 RP SEQUENCE OF 42-55.  
 RC SPECIES=B.variegata, and B.bombina;  
 RX MEDLINE=72163516; PubMed=4537042;  
 RA Anastasi A., Erspamer V., Buccì M.;  
 RT "Isolation and amino acid sequences of altyesin and bombesin, two  
 analogous active tetradecapeptides from the skin of European  
 discoglossid frogs.";  
 RL Arch. Biochem. Biophys. 148:443-446(1972).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
 GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X52447; CAA36686.1; -;  
 DR PIR; A01564; BSTD.  
 DR PIR; B01564; BSTDY.  
 DR PIR; S09095; S09095.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL. 1 24 POTENTIAL.  
 FT PEPTIDE 42 55 BOMBESIN.  
 FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;

Query Match 92.1%; Score 35; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 1.2;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 |||||  
 48 QWAVGHL 54

RESULT 3  
 BOMB\_BOMOR STANDARD; PRT; 119 AA.  
 ID BOMB\_BOMOR  
 AC P21591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE BOMBESIN PRECURSOR.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088602; PubMed=2263631;  
 RA Spindel E.R., Gibson B.W., Reeve J.R., Kelly M.;  
 RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
 relationship between bombesin and gastrin-releasing peptide.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
 CC -!- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR GLANDS IN  
 THE SKIN AND THE BRAIN.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
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 CC -----  
 DR EMBL; M55255; AAA48551.1; -;  
 DR PIR; A39261; A39261.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL. 1 58  
 FT PEPTIDE 45 58 BOMBESIN.  
 FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2445A44A CRC64;

Query Match 92.1%; Score 35; DB 1; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 1.3;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 |||||  
 51 QWAVGHL 57

RESULT 4  
 LITO\_LITAU STANDARD; PRT; 9 AA.  
 ID LITO\_LITAU  
 AC P08945;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LITORIN.  
 OS Litoria aurea (Australian frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75187011; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Amino acid composition and sequence of litorin, a bombesin-like  
 nonapeptide from the skin of the Australian leptodactylid frog  
 Litoria aurea.";  
 RL Experientia 31:510-511(1975).  
 RN [2]  
 RP SEQUENCE (METHYLATED VARIANT).  
 RX MEDLINE=78003546; PubMed=908397;  
 RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;  
 RT "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in  
 methanol extracts of the skin of the Australian frog Litoria aurea.";  
 RL Experientia 33:1289-1289(1977).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
 CC -----  
 DR PIR; S07204; S07204.  
 DR PIR; S07205; S07205.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Methylation.  
 FT MOD\_RES 1 1  
 OF PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 2 2 METHYLATION (IN A VARIANT).  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1103 MW; D7CC1E862CDC366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+04;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 Db 2 QWAVGH 7

## RESULT 5

BOML\_PSEGU STANDARD; PRT; 13 AA.  
 AC P42951;  
 DE 01-NOV-1995 (Rel. 32, Created)  
 DE BOMBESIN-LIKE PEPTIDE L (PG-L).  
 OS Pseudophryne guentheri (Frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.

## TISSUE-Skin;

RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.

DR PIR; A60409; A60409.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 13;  
 Best Local Similarity 83.3%; Pred. No. 1;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 Db 6 QWAVGH 11

## RESULT 6

RANA\_RANPI STANDARD; PRT; 82 AA.  
 AC P08950;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE RANATENSIN PRECURSOR.  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE FROM N.A.

## MEDLINE=88330837; PubMed=2458345;

RX krane I.N., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;

RT "Molecular cloning of cDNAs encoding the human bombesin-like peptide  
 neuromedin B. Chromosomal localization and comparison to cDNAs  
 encoding its amphibian homolog ranatensin.";  
 RL J. Biol. Chem. 263:13317-13323(1988).  
 RN [2]  
 RP SEQUENCE OF 48-58.  
 RA Nakajima T., Tanimura T., Pisano J.J.;  
 RT "Isolation and structure of a new vasoactive polypeptide.";  
 RL Fed. Proc. 29:282-282(1970).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M21552; AAA49533.1; -.

DR PIR; B28945; B28945.

DR InterPro; IPR000874; -.

DR Pfam; PF02044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.

KW Bombesin family; Amidation; Cleavage on pair of basic residues;

KW SIGNAL.

FT SIGNAL 1 27 POTENTIAL.

FT PROPEP 28 47

FT PEPTIDE 48 58 RANATENSIN.

FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).

SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 81.6%; Score 31; DB 1; Length 82;

Best Local Similarity 83.3%; Pred. No. 6.1;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 Db 51 QWAVGH 56

## RESULT 7

YB9H\_YEAST STANDARD; PRT; 232 AA.  
 AC P38340;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE HYPOTHETICAL 26.1 KDA PROTEIN IN POP4-SHM1 INTERGENIC REGION.  
 GN YBR261C OR YBR1729.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C.

RX MEDLINE=93220397; PubMed=8465606;

RA Dolignon F., Biteau N., Crouzet M., Aigle M.;

RT "The complete sequence of a 19,482 bp segment located on the right

arm of chromosome II from *Saccharomyces cerevisiae*.";

RL Yeast 9:189-199(1993).

CC -!- SIMILARITY: TO S.POMBE SPAC16E8.14C.

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CC -----
DR EMBL; X70529; CAA49926.1; -.
DR EMBL; Z36130; CAA85224.1; -.
DR PIR; S32963; S32963.
DR SGD; S0000465; YBR261C.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 232;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8
Db 139 QWCVGHL 145

RESULT 8
IML2_DROME STANDARD; PRT; 263 AA.
009024;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2 PRECURSOR.
GN IML2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S; TISSUE=Embryo;
RX MEDLINE=94139565; PubMed=8306886;
RA Garbe J.C., Yang E., Fristrom J.W.;
RT "IMP-L2: an essential secreted imaginal development in Drosophila.";
RL Development 119:1237-1250(1993).
CC -!- FUNCTION: ESSENTIAL DEVELOPMENTAL ROLE DURING EMBRYOGENESIS. IN
CC PARTICULAR THE NORMAL DEVELOPMENT OF THE NERVOUS SYSTEM. MAY BE
CC INVOLVED IN SOME ASPECT OF CELL ADHESION.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: DETECTED IN SEVERAL SITES INCLUDING THE
CC VENTRAL NEUROECTODERM, THE TRACHEAL PITS, THE PHARYNX AND
CC OESOPHAGUS, AND SPECIFIC NEURONAL CELL BODIES, WHERE IT IS
CC PRIMARILY EXPRESSED.
CC -!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT THE CELLULAR BLASTODERM
CC STAGE AND CONTINUES TO BE EXPRESSED THROUGH SUBSEQUENT
CC DEVELOPMENT.
CC -!- INDUCTION: BY 20-HYDROXYECDYSONE.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; L23066; AAB59251.1; -.
DR HSP; P56276; 1TLK.
DR FlyBase; FBgn0001257; ImpL2.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 2.
KW Immunoglobulin domain; Cell adhesion; Signal.
FT SIGNAL 1 23
FT CHAIN 24 263
FT DOMAIN 69 142
FT DOMAIN 184 247
FT DOMAIN IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN IG-LIKE C2-TYPE DOMAIN.

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FT DISULFID 76 135 BY SIMILARITY.
FT DISULFID 191 240 BY SIMILARITY.
FT VARIANT 173 173 V -> I.
SQ SEQUENCE 263 AA; 29421 MW; 44AADB1B22DD1804 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 263;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8
Db 87 QWVVGHL 93

RESULT 9
IHA_SHEEP STANDARD; PRT; 265 AA.
ID IHA_SHEEP
AC P38440;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INHIBIN ALPHA CHAIN (FRAGMENT).
GN INHA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Sadanandan S.L., Jeyaseelan K.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; L28815; AAA31553.1; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein
FT NON_TER 1 227 BY SIMILARITY.
FT DISULFID 161 262 BY SIMILARITY.
FT DISULFID 190 262 BY SIMILARITY.
FT DISULFID 194 264 BY SIMILARITY.
FT DISULFID 226 226 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 265 AA; 28754 MW; D880E9AB156B6656 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 265;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8
Db 74 RWAVLHL 80

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RESULT 10
IHA_BOVIN STANDARD; PRT; 360 AA.
AC F07994;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
GN INHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicular fluid;
RC MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
RA Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
RT "Cloning and sequence analysis of cDNA species coding for the two
RT subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
RN [2]
RP SEQUENCE OF 1-87 FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting.";
RT Eur. J. Biochem. 226:751-764(1994).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; M13273; AAA97414.1; -
CC EMBL; A14416; CAA01156.1; -
CC EMBL; U16237; AAB60262.1; -
CC PIR; A25732; A25732.
CC InterPro; IPR001839; -
CC InterPro; IPR002405; -
CC Pfam; PF00019; TGF-beta; 1.
CC PRINTS; PR00669; INHIBIN.
CC PROSITE; PS00250; TGF-BETA_1; 1.
CC Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 226
FT CHAIN 227 360
FT INHIBIN ALPHA CHAIN.
FT BY SIMILARITY.
FT DISULFID 256 322
FT BY SIMILARITY.
FT DISULFID 285 357
FT BY SIMILARITY.
FT DISULFID 289 359
FT BY SIMILARITY.
FT DISULFID 321 321
FT INTERCHAIN (BY SIMILARITY).
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 140 140
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 262 262
FT SEQUENCE 360 AA; 38809 MW; FBBF385DDIEFEF46 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 360;
Best Local Similarity 71.4%; Pred. No. 25;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 OWAVXHL 8
Db 169 RWAHL 175
:|||||
RESULT 11
IHA_PIG STANDARD; PRT; 364 AA.
AC P04087;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
GN INHA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86287350; PubMed=3016724;
RA Mayo K.E., Cerelli G.M., Spiess J., Rivier J., Rosenfeld M.G.,
RA Evans R.M., Vale W.;
RT "Inhibin A-subunit cDNAs from porcine ovary and human placenta.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 231-256.
RC TISSUE=Ovarian follicular fluid;
RC MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA Guillemin R., Niall H., Seeburg P.H.;
RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT precursor structure and homology with transforming growth
RT factor-beta.";
RL Nature 318:659-663(1985).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; M13980; AAA31057.1; -
CC EMBL; X03265; CAA27019.1; -
CC PIR; A01392; WPPGA.
CC PIR; A25947; A25947.
CC InterPro; IPR001839; -
CC InterPro; IPR002405; -
CC Pfam; PF00019; TGF-beta; 1.
CC PRINTS; PR00669; INHIBIN.
CC PROSITE; PS00250; TGF-BETA_1; 1.
CC Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 230
FT CHAIN 231 364
FT INHIBIN ALPHA CHAIN.
FT BY SIMILARITY.
FT DISULFID 260 326
FT BY SIMILARITY.
FT DISULFID 289 361
FT BY SIMILARITY.
FT DISULFID 293 363
FT BY SIMILARITY.
FT DISULFID 325 325
FT INTERCHAIN (BY SIMILARITY).
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 144 144
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 266 266
FT CONFLICT 120 120
FT CONFLICT 125 125
FT A -> T (IN REF. 2).

```

SQ SEQUENCE 364 AA; 39160 MW; BB595B9B7959A168 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 364;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
:|||||

Db 173 RWAUHL 179

RESULT 12

IDA\_MOUSE ID IHA\_MOUSE STANDARD; PRT; 366 AA.

AC Q04997; 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE INHIBIN ALPHA CHAIN PRECURSOR.

INHA.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RP ALBANO P.M., GROOMER N., SMITH J.C.;  
MEDLINE=93321614; PubMed=8330535;

RA "Activins are expressed in preimplantation mouse embryos and in ES  
and EC cells and are regulated on their differentiation.";

RT Development 117:711-723(1993).

[2]

SEQUENCE FROM N.A.

RP MEDLINE=92337610; PubMed=1632772;

RA SU J.G.W., HSUEH A.J.W.;  
"Characterization of mouse inhibin alpha gene and its promoter.";

RT Biochem. Biophys. Res. Commun. 186:293-300(1992).

[3]

SEQUENCE OF 49-366 FROM N.A.

RC STRAIN-SWISS WEBSTER;

RX MEDLINE=91071531; PubMed=2253839;

RA TONE S., KATCH Y., FUJIMOTO H., TOGASHI S., YANAZAWA M., KATO Y.,  
HIGASHINAKAGAWA T.;  
"Expression of inhibin alpha-subunit gene during mouse  
gametogenesis.";

RT Differentiation 44:62-68(1990).

RL -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE  
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND  
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN.

-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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-----

EMBL; X69618; CAA49324.1; -;  
DR EMBL; M95525; AAA39314.1; -;  
DR EMBL; M95526; AAA39314.1; JOINED.  
DR EMBL; X55957; CAA39424.1; -;  
DR PIR; S31439; S31439.  
DR PIR; JC1106; JC1106.  
DR MGI; MGI:96569; Inha.  
DR InterPro; IPR001839; -;  
DR InterPro; IPR002405; -;  
DR Pfam; PF00019; TGF-beta; 1.

PRINTS: PR00669; INHIBINA.

DR PROSITE; PS00250; TGF\_BETA\_1; 1.

KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Inhibin;  
FT SIGNAL 1 20  
FT PROPEP 21 233  
FT CHAIN 234 366  
FT DISULFID 263 328  
FT DISULFID 292 363  
FT DISULFID 296 365  
FT DISULFID 327 327  
FT CARBOHYD 147 147  
FT CARBOHYD 269 269  
FT CONFLICT 165 165  
FT CONFLICT 171 171  
FT CONFLICT 336 336  
SQ SEQUENCE 366 AA; 39536 MW; 8F3851B722FE0011 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
:|||||

Db 176 RWAUHL 182

RESULT 13

IDA\_MOUSE ID IHA\_MOUSE STANDARD; PRT; 366 AA.

AC P17490; 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE INHIBIN ALPHA CHAIN PRECURSOR.

GN INHA.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI\_TaxID=10116;

[1]

SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=90190649; PubMed=2628729;

RA FENG Z.-M., LI Y.-P., CHEN C.-L.C.;  
"Analysis of the 5'-flanking regions of rat inhibin alpha- and  
beta-B-subunit genes suggests two different regulatory mechanisms.";

RT Mol. Endocrinol. 3:1914-1925(1989).

RL -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE  
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND  
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN.

-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

-!- TISSUE SPECIFICITY: ALPHA- AND BETA-B-SUBUNITS ARE THE  
PREDOMINANT FORMS FOUND IN RAT TESTIS.

-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

-----

EMBL; X69618; CAA49324.1; -;  
DR EMBL; M95525; AAA39314.1; -;  
DR EMBL; M95526; AAA39314.1; JOINED.  
DR EMBL; X55957; CAA39424.1; -;  
DR PIR; S31439; S31439.  
DR PIR; JC1106; JC1106.  
DR MGI; MGI:96569; Inha.  
DR InterPro; IPR001839; -;  
DR InterPro; IPR002405; -;  
DR Pfam; PF00019; TGF-beta; 1.

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CC -----

DR EMBL; M32755; AAA41437.1; -.  
DR EMBL; M32754; AAA41437.1; JOINED.  
DR EMBL; M36453; AAA41435.1; -.  
DR PIR; A40905; A40905.  
DR PIR; A41398; A41398.  
DR PIR; A40056; A40056.  
DR InterPro; IPR001839; -.  
DR InterPro; IPR002405; -.  
DR Pfam; PF00019; TGF-beta; 1.  
DR PRINTS; PR00669; INHIBINA.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
DR Follitropin inhibitor; Contracptive; Hormone; Glycoprotein; Signal.  
DR SIGNAL 1 20  
DR PROPEP 21 233  
DR CHAIN 234 366  
DR DISULFID 263 328  
DR DISULFID 292 363  
DR DISULFID 296 365  
DR DISULFID 327 327  
DR CARBOHYD 147 147  
DR CARBOHYD 269 269  
DR SEQUENCE 366 AA; 39496 MW; 327A233B9FEDFDCD CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QWAVXHL 8  
Db 176 RNVVLHL 182

RESULT 14  
SWI6\_KLUJA  
ID SWI6\_KLUJA STANDARD; PRT; 769 AA.  
AC P40418;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE REGULATORY PROTEIN SWI6 (CELL-CYCLE BOX FACTOR, CHAIN SWI6) (TRANS-  
ACTING ACTIVATOR OF HO ENDONUCLEASE GENE) (MBF SUBUNIT P90).  
GN SWI6.  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE=93383264; PubMed=83723350;  
RA Koch C., Moll T., Neuberg M., Ahorn H., Nasmyth K.;  
RT "A role for the transcription factors Mbp1 and Swi4 in progression  
from G1 to S phase.";  
RL Science 261:1551-1557(1993).

CC -!- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT  
CC TRANSCRIPTION. SWI4 AND SWI6 ARE REQUIRED FOR FORMATION OF THE  
CC CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE  
CC UPSTREAM REGION OF HO (5'-CACGAAA-3') IS CALLED THE CELL CYCLE  
CC BOX (CCB).  
CC -!- SUBUNIT: MBF CONTAINS SWI6 AND MBP1; SBF CONTAINS SWI6 AND SWI4.  
CC -!- SIMILARITY: STRONG, TO S.POMBE CDC10.  
CC -!- SIMILARITY: CONTAINS 2 ANK REPEATS.  
CC -----

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CC -----

DR EMBL; M32755; AAA41437.1; -.  
DR EMBL; M32754; AAA41437.1; JOINED.  
DR EMBL; M36453; AAA41435.1; -.  
DR PIR; A40905; A40905.  
DR PIR; A41398; A41398.  
DR PIR; A40056; A40056.  
DR InterPro; IPR001839; -.  
DR InterPro; IPR002405; -.  
DR Pfam; PF00019; TGF-beta; 1.  
DR PRINTS; PR00669; INHIBINA.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
DR Follitropin inhibitor; Contracptive; Hormone; Glycoprotein; Signal.  
DR SIGNAL 1 20  
DR PROPEP 21 233  
DR CHAIN 234 366  
DR DISULFID 263 328  
DR DISULFID 292 363  
DR DISULFID 296 365  
DR DISULFID 327 327  
DR CARBOHYD 147 147  
DR CARBOHYD 269 269  
DR SEQUENCE 366 AA; 39496 MW; 327A233B9FEDFDCD CRC64;

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CC -----

DR EMBL; X74292; CAA52345.1; -.  
DR PIR; S36657; S36657.  
DR InterPro; IPR002110; -.  
DR Pfam; PF00023; ank; 2.  
DR PROSITE; PS50088; ANK\_REPEAT; 2.  
DR PROSITE; PS50297; ANK\_REPEAT; 2.  
DR Transcription regulation; DNA-binding; ANK repeat; Repeat.  
DR REPEAT 286 315  
DR REPEAT 422 451  
DR SEQUENCE 769 AA; 86669 MW; E3A5328B4DA084FB CRC64;

Query Match 81.6%; Score 31; DB 1; Length 769;  
Best Local Similarity 57.1%; Pred. No. 51;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 409 QWVITHL 415

RESULT 15  
GRP\_RANRI  
ID GRP\_RANRI STANDARD; PRT; 10 AA.  
AC P23260;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-APR-1993 (Rel. 25, Last annotation update)  
DE NEUROMEDIN C.  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; R. l.  
OX NCBI\_TaxID=8406;  
RN [1]  
RS SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=91315477; PubMed=1859413;  
RA Conlon J.M., O'Harte F., Vaudry H.;  
RT "Primary structures of the bombesin-like neuropeptides in frog brain  
show that bombesin is not the amphibian gastrin-releasing peptide.";  
RL Biochem. Biophys. Res. Commun. 178:526-530(1991).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
DR PIR; PQ0177; PQ0177.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
DR Bombesin family; Amidation.  
DR MOD\_RES 10 10  
DR SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.3;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
QY 3 WAVXHL 8  
Db 4 WAVGHL 9

Search completed: October 25, 2001, 11:28:30  
Job time: 478 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:22 ; Search time 76.25 seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-10

Perfect score: 38

Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: piri:\*

2: piri2:\*

3: piri3:\*

4: piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	14	1 BSTDY	bombesin - fire-be
2	35	92.1	107	1 BSTDY	bombesin precursor
3	35	92.1	119	2 A39261	bombesin precursor
4	32	84.2	174	2 T45665	hypothetical prote
5	32	84.2	353	2 T34312	hypothetical prote
6	31	81.6	9	2 S07204	litorin I - Austr
7	31	81.6	13	2 A60409	bombesin-like pept
8	31	81.6	82	2 B28945	ranatensin precurs
9	31	81.6	95	2 H83378	hypothetical prote
10	31	81.6	193	2 A75605	hypothetical prote
11	31	81.6	232	2 S32963	hypothetical prote
12	31	81.6	256	2 T48787	hypothetical prote
13	31	81.6	309	2 S41427	cysteine proteinas
14	31	81.6	325	2 F82558	lipopolysaccharide
15	31	81.6	357	2 T17027	WFB-related transc
16	31	81.6	360	1 A25732	inhibin alpha chai
17	31	81.6	364	1 WFPGA	inhibin alpha chai
18	31	81.6	366	1 JC1106	inhibin alpha chai
19	31	81.6	366	1 A40056	inhibin alpha chai
20	31	81.6	703	2 T48559	probable receptor-
21	31	81.6	769	2 S36657	SW16 protein - yea
22	30	78.9	10	2 PQ0177	neuromedin C - lau
23	30	78.9	10	2 A60647	gastrin-releasing
24	30	78.9	25	2 S06263	gastrin-releasing
25	30	78.9	27	1 RHPGA	gastrin-releasing
26	30	78.9	27	1 RHGPGA	gastrin-releasing
27	30	78.9	27	1 RHCHA	gastrin-releasing
28	30	78.9	120	2 A47201	bombesinlike pepti
29	30	78.9	134	2 I47010	gastrin-releasing

30 30 78.9 138 2 A26182 gastrin releasing  
31 30 78.9 147 2 A40922 gastrin releasing  
32 30 78.9 148 1 B26182 gastrin releasing  
33 30 78.9 155 2 A42437 gastrin releasing  
34 30 78.9 170 2 S76918 hypothetical prote  
35 30 78.9 250 2 T07902 MADS box protein  
36 30 78.9 252 2 A69060 conserved hypothet  
37 30 78.9 283 2 B82631 hypothetical prote  
38 30 78.9 311 2 H82541 conserved hypothet  
39 30 78.9 318 2 H83298 conserved hypothet  
40 30 78.9 366 1 A24248 inhibin alpha chai  
41 30 78.9 375 2 T43049 hypothetical prote  
42 30 78.9 453 2 T50645 glucan endo-1,3-be  
43 30 78.9 458 2 S56816 GTPase-activating  
44 30 78.9 505 2 T10896 cytochrome P450 (E  
45 30 78.9 691 1 S76521 hypothetical prote

#### ALIGNMENTS

RESULT 1

BSTDY

bombesin - fire-bellied toad

C:Species: Bombina bombina (fire-bellied toad)

C>Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20

C:Accession: A01564

R:Anastasi, A.; Erspamer, V.; Bucci, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A:Title: Isolation and amino acid sequences of alytesin and bombesin, two anal.

A:Reference number: A01564; MUID:72163516

A:Accession: A01564

A:Molecule type: protein

A:Residues: 1-14 <ANA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyroglutam

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 92.1%; Score 35; DB 1; Length 14;

Best Local Similarity 85.7%; Pred. No. 0.33;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

DB 7 QWAVGHL 13

RESULT 2

BSTDY

bombesin precursor - yellow-bellied toad

C:Species: Bombina variegata (yellow-bellied toad)

C>Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 08-Dec-2000

C:Accession: S09095; B01564; A01564

R:Richter, K.; Egger, R.; Kreil, G.

FEBS Lett. 262, 353-355, 1990

A:Title: Molecular cloning of a cDNA encoding the bombesin precursor in skin

A:Reference number: S09095; MUID:90242964

A:Accession: S09095

A:Molecule type: mRNA

A:Residues: 1-107 <RIC>

R:Anastasi, A.; Erspamer, V.; Bucci, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A:Title: Isolation and amino acid sequences of alytesin and bomb.

A:Reference number: A01564; MUID:72163516

A:Accession: B01564

A:Molecule type: protein

A:Residues: 42-55 <ANA>

C:Superfamily: ranatensin

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neur.

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-41/Domain: amino-terminal propeptide #status predicted <PRO>

F:42-55/Product: bombesin #status experimental <MAT>  
F:56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
F:42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
F:55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 92.1%; Score 35; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	QWAVXHL	8
Dp	48	QWAVGHL	54

### RESULT

A39261  
bombesin precursor - Bombina orientalis  
C:Species: Bombina orientalis  
Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999  
Accession: A39261  
R:Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990  
A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet  
A:Reference number: A39261; MUID:91088602  
A:Accession: A39261  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <SPI>  
A:Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017  
C:Superfamily: ranatensin  
C:Keywords: neuropeptide

Query Match 92.1%; Score 35; DB 2; Length 119;  
Best Local Similarity 85.7%; Pred. No. 2.8;  
Matches 6. Conservative 0: Mismatches 1: Indels

QY 2 QWAVXHL 8  
db 51 QWAVGHL 57

## RESULT 4

T45665  
hypothetical protein F14P22.40 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
Accession: T45665  
Submitted by: Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.  
Submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z23011  
A:Accession: T45665  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-174 <DAN>  
A:Cross-references: EMBL:AL137082  
A:Experimental source: cultivar Columbia; BAC clone F14P22  
C:Genetics:  
A:Map position: 3  
A:Introns: 90/1; 126/3; 166/2  
A>Note: F14P22.40

Query Match 84.2%; Score 32; DB 2; Length 174;  
Best Local Similarity 71.4%; Pred. No. 17;  
Matches 5. Conservative 1. Mismatches 1. Indels

QY 2 QWAVXHL 8  
Db 47 FWAVDHL 53

RESULT 5

T34312  
 hypothetical protein F59G1.4 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T34312

R; Latreille, P.  
A; Description: The sequence of *C. elegans* cosmid F59C1.  
A; Reference number: Z21504

A;Accession: T34312

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-353 <LAT>

A;Cross-references: EMBL:U53332; PIDN:AA71158.1; GSP

A; Experimental source

C;Genetics:

A;Gene: CESP:F59G

A;Map position: 2  
 A;Tat+pos: 22/1. 17/2. 93/3. 114/3. 151/1. 187/2. 229/3. 257/3. 316/1

C. superfamily v: Caenorhabditis elegans hypothetical protein F59G1.4  
A; ILMF0HS: 23/1; 41/2; 83/3; I14/3; I31/1; I81/2; 223/3; 231/3; 31

Query Match 84.2%; Score 32; DB 2; Length 353;  
Best Local Similarity 71.4%; Pred. No. 33;  
Matches 5: Conservative 1; Mismatches 1; Indels

2. OWAVXHL 8

**P**

Db 201 EWAVNHL 207

## RESULT

S07204  
 litlorin I - Australian tree frog (*Litoria aurea*)  
 C:Species: *Litoria aurea*  
 C:date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
 C:Accession: S07204  
 R:Anastasi, A.; Erspamer, V.; Eudean, R.  
 Experientia 31, 510-511, 1975  
 A:title: Aminoacid composition and sequence of litlorin, a bombesin like nonapeptide  
 A:Reference number: S07204; MUID:75187011

A;Molecule type: pr

A; Residues: 1-9 <ANA>

C; Superfamily: gastrin-releasing peptide

**C;Keywords:** amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experiment!!

F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels

OY 2 QWAVXH 7

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—  
—  
—  
—

7x

## RESULT

A60409  
bombesin-like peptide L - frog (Pseudophryne guentheri)  
C:Species: Pseudophryne guentheri  
C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
C:Accession: A60409  
R:Stimmaco, M.; Severini, C.; De Blase, D.; Barra, D.; Bossa, F.; Roberts, J. D. Tech  
Peptides 11, 299-304, 1990  
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aus  
A:Reference number: A60409; MUID:90287814  
A:Accession: A60409  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>

C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
Db 6 QWAVGH 11

RESULT 8  
B28945  
ranatensin precursor - northern leopard frog  
C;Species: Rana pipiens (northern leopard frog)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
C;Accession: B28945  
J. Krane, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.  
J. Biol. Chem. 263, 13317-13323, 1988  
A;Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromedin  
A;Reference number: A92667; MUID:88330837  
A;Accession: B28945  
A;Molecule type: mRNA  
A;Residues: 1-82 <KRA>  
A;Cross-references: GB:M21552; GB:J03948; NID:q213693; PIDN:AAA49533.1; PID:q213694  
C;Superfamily: ranatensin  
C;Keywords: neuropeptide

Query Match 81.6%; Score 31; DB 2; Length 82;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
Db 51 QWAVGH 56

RESULT 9  
H83378  
hypothetical protein PA2143 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: H83378  
Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
han, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337  
A;Accession: H83378  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-95 <STO>  
A;Cross-references: GB:AE004641; GB:AE004091; NID:g9948150; PIDN:AAG05531.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA2143

Query Match 81.6%; Score 31; DB 2; Length 95;  
Best Local Similarity 71.4%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXH 8  
|||||  
Db 63 QWVHHL 69

RESULT 10  
A75605  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28 Jul 2000  
C;Accession: A75605  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson,  
; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans  
A;Reference number: A75250; MUID:20036896  
A;Accession: A75605  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-183 <WHI>  
A;Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAH1 0.1; PII: 0.1  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DRA0103  
A;Map position: 2  
C;Superfamily: Deinococcus radiodurans hypothetical protein DRA0103

Query Match 81.6%; Score 31; DB 2; Length 183;  
Best Local Similarity 71.4%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
|||||  
Db 49 RWAFFHL 55

RESULT 11  
S32963  
hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YBR1729  
C;Species: Saccharomyces cerevisiae  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul 2000  
C;Accession: S32963; S46142  
R;Doignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
Yeast 9, 189-199, 1993  
A;Title: The complete sequence of a 19,482 bp segment located on the right arm of chr  
A;Reference number: S29348; MUID:93220397  
A;Accession: S32963  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-232 <DOI>  
A;Cross-references: EMBL:X70529; NID:gl907246; PIDN:CAA49926.1; PID:q296560  
R;Aigle, M.; Baciuet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45940  
A;Accession: S46142  
A;Molecule type: DNA  
A;Residues: 1-232 <AIG>  
A;Cross-references: EMBL:Z36130; NID:g536688; PIDN:CAA85224.1; PID:g536688; MUID: 2  
C;Genetics:  
A;Map position: 2R  
C;Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 232;  
Best Local Similarity 71.4%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
|||||  
Db 139 QWCVGHL 145

RESULT 12  
T48787  
hypothetical protein 13E11.350 [imported] - Neurospora crassa

RESULT 14  
F82558  
lipopolysaccharide core biosynthesis protein XF2434 [imported] - Xylella fastidiosa (strain  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: F82558  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: F82558  
A:Status: preliminary

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:56 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-10  
Perfect score: 38  
Sequence: 1 XQMAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	8	1	US-08-168-390-12
2	36	94.7	8	6	5217955-35
3	36	94.7	8	6	5217955-36
4	36	94.7	9	6	5217955-13
5	36	94.7	9	6	5217955-14
6	36	94.7	9	6	5217955-15
7	36	94.7	9	6	5217955-22
8	35	92.1	8	1	US-08-168-390-11
9	35	92.1	8	2	US-08-337-127-9
10	35	92.1	8	6	5217955-32
11	35	92.1	8	6	5217955-34
12	35	92.1	9	1	US-07-619-747B-1
13	35	92.1	9	1	US-07-619-747B-2
14	35	92.1	9	1	US-07-619-747B-4
15	35	92.1	9	1	US-07-619-747B-5
16	35	92.1	9	1	US-07-619-747B-9
17	35	92.1	9	1	US-07-619-747B-10
18	35	92.1	9	1	US-07-619-747B-12
19	35	92.1	9	1	US-07-619-747B-14
20	35	92.1	9	1	US-07-619-747B-15
21	35	92.1	9	1	US-07-619-747B-17
22	35	92.1	9	1	US-07-619-747B-18
23	35	92.1	9	1	US-07-619-747B-22
24	35	92.1	9	1	US-07-619-747B-23
25	35	92.1	9	1	US-07-619-747B-24
26	35	92.1	9	1	US-07-619-747B-25
27	35	92.1	9	1	US-07-619-747B-26

28	35	92.1	9	1	US-07-619-747B-27
29	35	92.1	9	1	US-07-619-747B-28
30	35	92.1	9	1	US-07-619-747B-29
31	35	92.1	9	1	US-07-619-747B-30
32	35	92.1	9	1	US-07-619-747B-31
33	35	92.1	9	1	US-07-619-747B-32
34	35	92.1	9	1	US-07-619-747B-33
35	35	92.1	9	1	US-07-619-747B-34
36	35	92.1	9	1	US-07-619-747B-35
37	35	92.1	9	1	US-07-619-747B-36
38	35	92.1	9	1	US-07-619-747B-37
39	35	92.1	9	1	US-07-619-747B-38
40	35	92.1	9	1	US-07-619-747B-39
41	35	92.1	9	1	US-07-619-747B-40
42	35	92.1	9	1	US-08-031-325A-37
43	35	92.1	9	1	US-08-263-905-4
44	35	92.1	9	1	US-08-263-905-5
45	35	92.1	9	1	US-08-263-905-6

ALIGNMENTS

RESULT 1  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end co;  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "The alanine at position 6  
; OTHER INFORMATION: is dextrorotatory alanine."  
; FEATURE:

; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-12

Query Match 94.7%; Score 36; DB 1; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVXHL 8

RESULT 2  
5217955-35  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 35:  
; LENGTH: 8  
5217955-35

Query Match 94.7%; Score 36; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVXHL 8

RESULT 3  
5217955-36  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 36:  
; LENGTH: 8  
5217955-36

Query Match 94.7%; Score 36; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVXHL 8

RESULT 4  
5217955-13  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 13:  
; LENGTH: 9  
5217955-13

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVXHL 8

RESULT 5  
5217955-14  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 14:  
; LENGTH: 9  
5217955-14

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVXHL 8

RESULT 6  
5217955-15  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125

; FILING DATE: 15-SEP-1989  
; SEQ ID NO:15:  
; LENGTH: 9  
5217955-15

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
IIIIII  
Db 2 QWAVAHL 8

## RESULT 7

5217955-22  
; Patent No. 5217955  
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989

; SEQ ID NO:22:  
; LENGTH: 9  
5217955-22

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
IIIIII  
Db 2 QWAVAHL 8

## RESULT 8

US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK

; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1

; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-11

Query Match 92.1%; Score 35; DB 1; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 2 QWAVXHL 8  
IIIIII  
Db 2 QWAVGHL 8

## RESULT 9

US-08-337-127-9  
; Sequence 9, Application US/08337127  
; Patent No. 5877277  
; GENERAL INFORMATION:  
; APPLICANT: Coy, David H.  
; APPLICANT: Moreau, Jacques-Pierre  
; APPLICANT: Kim, Sun H.  
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
; TITLE OF INVENTION: ANALOGS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,127  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/779,039  
; FILING DATE: 10/18/91  
; APPLICATION NUMBER: 07/502,438  
; FILING DATE: 03/30/90  
; APPLICATION NUMBER: 07/397,169  
; FILING DATE: 08/21/89  
; APPLICATION NUMBER: 07/376,555  
; FILING DATE: 07/07/89  
; APPLICATION NUMBER: 07/317,941  
; FILING DATE: 03/02/89  
; APPLICATION NUMBER: 07/282,328  
; FILING DATE: 12/09/88  
; APPLICATION NUMBER: 07/257,998

;; FILING DATE: 10/14/88  
;; APPLICATION NUMBER: 07/248,771  
;; FILING DATE: 09/23/88  
;; APPLICATION NUMBER: 07/207,759  
;; FILING DATE: 06/16/88  
;; APPLICATION NUMBER: 07/204,171  
;; FILING DATE: 06/08/88  
;; APPLICATION NUMBER: 07/173,311  
;; FILING DATE: 03/25/88  
;; APPLICATION NUMBER: 07/100,571  
;; FILING DATE: 09/24/87  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00537/00900D  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The sequence contains at  
; position 1 a pyroglutamate, rather than a glutamate,  
; and has an methylester C-terminus (i.e., COOCH3),  
; rather than a carboxyl C-terminus (i.e., COOH).  
US-08-337-127-9

Query Match 92.1%; Score 35; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVGHL 8

RESULT 10  
5217955-32  
; Patent No. 5217955  
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 32:  
; LENGTH: 8  
5217955-33

Query Match 92.1%; Score 35; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVGHL 8

RESULT 11  
5217955-34

; Patent No. 5217955  
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO: 34:  
; LENGTH: 8  
5217955-34

Query Match 92.1%; Score 35; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVGHL 8

RESULT 12  
US-07-619-747B-1  
; Sequence 1, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide

;  
;  
;  
; FEATURE:  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-1

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||||||  
Db 2 QWAVGHL 8

RESULT 13  
US-07-619-747B-2  
; Sequence 2, Application US/07619747B  
; Patent No. 5244883

GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-2

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8

Db 2 QWAVGHL 8  
||||||  
; Sequence 4, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: Position 1 is 5F-D-Trp  
; OTHER INFORMATION: Position 8 is a reduced  
; OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-4

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||||||  
Db 2 QWAVGHL 8

RESULT 15  
US-07-619-747B-5  
; Sequence 5, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,

; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
 ; TITLE OF INVENTION: Antagonists  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dr. Andrew V. Schally  
 ; STREET: 5025 Kawanne Avenue  
 ; CITY: Metairie  
 ; STATE: Louisiana  
 ; COUNTRY: USA  
 ; ZIP: 70002  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 360K Diskette  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: DOS 5.0  
 ; SOFTWARE: WP 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/619,747B  
 ; FILING DATE: 19901129  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: No. 5244883e  
 ; FILING DATE: N/A  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Behr, Omri M.  
 ; REGISTRATION NUMBER: 22,940  
 ; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908)494-5240  
 ; TELEFAX: 1-908-494-0428  
 ; TELEX: 511642 BEPATEDIN  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9  
 ; TYPE: AMINO  
 ; STRANDEDNESS: Unknown  
 ; TOPOLOGY: Unknown  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; OTHER INFORMATION: Position 1 is D-Tpi  
 ; OTHER INFORMATION: Position 8 is a reduced  
 ; OTHER INFORMATION: Isostere of named aminoacid  
 ; US-07-619-747B-5

Query Match 92.1%; Score 35; DB 1; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 Db 2 QWAVGHL 8

Search completed: October 25, 2001, 11:23:57  
 Job time: 270 sec

GenCore version 4.5  
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OM protein - protein search, using SW model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-10  
Perfect score: 38  
Sequence: 1 XQWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	7	10 AAP91147	Sequence of new ne
2	36	94.7	7	13 AAR20585	Antagonist of bomb
3	36	94.7	7	13 AAR32998	{D-Ala11}-bombesin
4	36	94.7	7	20 AAW94610	Bombesin/gastrin r
5	36	94.7	8	3 AAF20294	Bombesin analog pe
6	36	94.7	8	12 AAR11241	Linear litorin ana
7	36	94.7	8	12 AAR11242	Linear litorin ana
8	36	94.7	8	13 AAR29155	Bombesin analogue
9	36	94.7	8	13 AAR29157	Bombesin analogue
10	36	94.7	8	16 AAW64911	Bombesin receptor
11	36	94.7	9	11 AAR09335	Sequence of Bombes

12	36	94.7	9	12 AAR11522	Example of peptide
13	36	94.7	9	12 AAR14865	Peptide analogue #
14	36	94.7	9	12 AAR14866	Peptide analogue #
15	36	94.7	9	12 AAR14867	Peptide analogue #
16	36	94.7	9	12 AAR14873	Peptide analogue
17	36	94.7	9	14 AAR40903	Bombesin analogue
18	36	94.7	9	19 AAW51195	Peptide derived fr
19	36	94.7	9	19 AAW51201	Peptide derived fr
20	36	94.7	10	10 AAP96113	Sequence of new ne
21	35	92.1	7	22 AAB48341	Bombesin/gastrin r
22	35	92.1	8	11 AAR04531	Non-cyclic analog
23	35	92.1	8	12 AAR11224	Linear litorin ana
24	35	92.1	8	12 AAR11240	Linear litorin ana
25	35	92.1	8	12 AAR14877	Peptide analogue #
26	35	92.1	8	13 AAR28456	Bombesin antagonist
27	35	92.1	8	13 AAR28459	Bombesin antagonist
28	35	92.1	8	16 AAW64910	Bombesin receptor
29	35	92.1	8	19 AAW50941	Bombesin antagonist
30	35	92.1	8	20 AAW92740	Bombesin peptide a
31	35	92.1	8	21 AAB08302	Amino acid sequenc
32	35	92.1	8	21 AAB08308	Amino acid sequenc
33	35	92.1	8	22 AAB72406	Bombesin analogue
34	35	92.1	9	11 AAR04526	Non-cyclic analog
35	35	92.1	9	11 AAR04527	Non-cyclic analog
36	35	92.1	9	11 AAR04529	Non-cyclic analog
37	35	92.1	9	11 AAR04528	Non-cyclic analog
38	35	92.1	9	11 AAR04530	Non-cyclic analog
39	35	92.1	9	11 AAR08345	Peptide bombesin a
40	35	92.1	9	12 AAR11520	Example of peptide
41	35	92.1	9	12 AAR11521	Example of peptide
42	35	92.1	9	12 AAR11529	Example of peptide
43	35	92.1	9	12 AAR12033	Bombesin antagonist
44	35	92.1	9	12 AAR12033	Peptide analogue #
45	35	92.1	9	12 AAR14860	

## ALIGNMENTS

RESULT 1  
AAP91147  
ID AAP91147 standard; protein; 7 AA.  
XX  
AC AAP91147;  
XX  
DT 13-MAY-1990 (first entry)  
DT 22-DEC-1990 (corrected)  
XX  
DE Sequence of new neuromedin C deriv.  
XX  
KW Bombesin antagonist; malignant disease; therapy; gastric acid secretion.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /label=OTHER  
FT /note="Ac-D-Gln"  
FT Misc-difference 5 /label=OTHER  
FT /note="D-Ala"  
FT Misc-difference 7 /label=OTHER  
FT /note="Leu-OMe"

EP315367-A.  
XX  
PN Antagonist of bomb  
XX {D-Ala11}-bombesin  
PD Bombesin/gastrin r  
XX Bombesin analog pe  
PF Linear litorin ana  
XX Linear litorin ana  
PR Bombesin analogue  
XX Bombesin analogue  
XX Bombesin receptor  
XX Sequence of Bombes

CC	5-200 mg/dose.
XX	
SQ	Sequence 7 AA;
Query Match	94.7%; Score 36; DB 13; Length 7;
Best Local Similarity	85.7%; Pred. No. 3.4e+05;
Matches	6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	2 QWAVXHL 8 
Db	1 qwavahl 7
RESULT 3	
AAR32998	ID AAR32998 standard; peptide; 7 AA.
XX	
AC	AAR32998;
XX	
DT	13-APR-1993 (first entry)
XX	
DE	[D-Ala <sup>11</sup> ]-bombesin(7-13)amide derivs.
XX	Intracellular signal; inhibition; gastrointestinal tract;
KW	litorin; Gastrin Releasing Peptide; GRP.
KW	
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1
FT	/label= OTHER
FT	/note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,
FT	N-alpha-lauryl-Gln or N-alpha-palmityl-Gln"
FT	Misc-difference 5
FT	/note= "D-Ala"
FT	Modified-site 7
FT	/note= "amidated"
XX	
PN	WO9220707-A.
XX	
PD	26-NOV-1992.
XX	
Pf	21-APR-1992; 92WO-US03287.
XX	
PR	23-MAY-1991; 91US-0704863.
XX	
PA	(RICH ) MERRELL DOW PHARM INC.
XX	
PI	Edwards JV, Fanger BO;
XX	
DR	WPI; 1992-415707/50.
XX	
XX	New bombesin peptide agonists and antagonists - stimulate or
PT	inhibit digestion, increase susceptibility of tumours to
PT	chemotherapeutic agents, treat gastric ulcers and tumours etc
XX	
PS	Example; Page 40; 64pp; English.
XX	
CC	The peptides in this example are bombesin analogues. The peptides
CC	were tested in a competitive binding assay and a phosphatidyl Inositol
CC	(PI)-turnover assay in mouse pancreas. None of the peptides
CC	demonstrated agonist activity but all inhibited PI-turnover (c.f.
CC	stimulation produced by 100nM GRP). Analogues of bombesin are
CC	potentially useful for growth therapy and the treatment of digestive
CC	disorders, e.g. for stimulating digestion, stimulating growth of
CC	tissue in the lung, pancreas and intestine, stimulating NK cell
CC	activity against tumour cells and stimulating growth of tumours to
CC	increase susceptibility to chemotherapeutic agents.
XX	
SQ	Sequence 7 AA;

PI	Camble R, Cotton R, Dutta AS, Hayward CF;
XX	
DR	WPI; 1989-139341/19.
XX	
PT	New Neuromedin C polypeptide derivs. -
PT	are potent bombesin antagonist used for treating malignant
PT	disease and conditions associated with gastrin or gastric acid
PT	secretion
XX	
PS	Disclosure; Page 929; 49pp; English.
XX	
CC	It is a potent bombesin antagonist. It may be used for the treatment of
CC	e.g. malignant disease, conditions associated with the over-prodn. of
CC	bombesin and conditions associated with failure of normal physiological
CC	control of the regulation of gastric acid secretion.
XX	
SQ	Sequence 7 AA;
Query Match	94.7%; Score 36; DB 10; Length 7;
Best Local Similarity	85.7%; Pred. No. 3.4e+05;
Matches	6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	2 QWAVXHL 8 
Db	1 qwavahl 7
RESULT 2	
AAR20585	ID AAR20585 standard; Peptide; 7 AA.
XX	
AC	AAR20585;
XX	
DT	07-MAY-1992 (first entry)
XX	
DE	Antagonist of bombesin/GRP.
XX	
KW	Antitumour agent; leukaemia.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 5
FT	/note= "D-Ala"
XX	
PN	EP468497-A.
XX	
PF	29-JAN-1992.
XX	
PR	25-JUL-1991; 91EP-0112504.
XX	
XX	26-JUL-1990; 90US-0558031.
XX	
PA	(RICH ) MERRELL DOW PHARM INC.
XX	
PI	Kristenansky JL;
XX	
DR	WPI; 1992-034251/05.
XX	
PT	New peptide bombesin-GRP antagonists - used as antitumour agents
PT	to treat e.g. leukaemia, small cell lung and prostatic carcinoma
PT	and to inhibit gastric acid secretion.
XX	
PS	Claim 7; Page 12; 14pp; English.
XX	
CC	The peptide is modified at the N-terminal with a lauryl, palmitoyl
CC	or esp. an octanoyl gp. The Leu at position 7 may be absent. The
CC	C-terminal (Ileu or His) is amidated. The peptides and derived
CC	salts can be used to treat small cell lung carcinoma, prostatic
CC	carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-
CC	ciated conditions, and to effect antagonism of bombesin/gastrin
CC	releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at

Query Match 94.7%; Score 36; DB 13; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 1 qwavahl 7

RESULT 4

AAW94610  
ID AAW94610 standard; peptide; 7 AA.

XX AC AAW94610;

DT 27-APR-1999 (first entry)

XX Bombesin/gastrin releasing peptide type inhibitor peptide #2.

XX Bombesin; gastrin releasing peptide; GRP; inhibitor; antagonist;  
KW small cell lung carcinoma; tumour; frog; antimitotic; antisecretory;  
XX peptic ulcer.

XX Synthetic.

OS Bombina bombina.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "optionally modified by octanoyl, lauroyl or  
FT palmitoyl"

FT Modified-site 7

FT /note= "amidated"

XX US5834433-A.

XX 10-NOV-1998.

XX 23-FEB-1996; 96US-0960130.

XX 24-JUL-1991; 91US-0735402.

PR 26-JUL-1990; 90US-0558031.

PR 21-JUL-1994; 94US-0278692.

PR 23-MAY-1995; 95US-0447528.

PR 23-FEB-1996; 96US-0960130.

XX (RICH ) MERRELL PHARM INC.

XX Krstenansky JL;

XX WPI; 1999-141255/12.

XX New peptide antagonists of bombesin or gastrin releasing peptide -  
PT are useful as antimitotic and antisecretory agents in treating,  
PT e.g., small cell lung carcinoma or peptic ulcers

XX Claim 5; Column 14; 9pp; English.

XX The present sequence represents a bombesin/gastrin releasing peptide,  
CC type inhibitor peptide. The peptide may be used as an antimitotic and  
CC antisecretory peptide. It can control growth of small cell lung and  
CC prostatic carcinomas, and it can also inhibit gastric secretions which  
CC are causative and symptomatic of peptic ulcers. Administration may be  
CC oral but is preferably subcutaneous, intravenous, intramuscular or  
CC intraperitoneal, by depot injection, by implant preparation or by  
CC application to the mucous membranes (e.g. of the nose or bronchial  
CC tubes) by aerosol.

XX Sequence 7 AA;

Query Match 94.7%; Score 36; DB 20; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 1 qwavahl 7

RESULT 5

AAP20294  
ID AAP20294 standard; peptide; 8 AA.

XX AC AAP20294;

DT 09-DEC-1992 (first entry)

XX Bombesin analog peptide.

XX Bombesin; hypothermic; analgesic.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1

FT /label= D-Glu

FT Misc-difference 5

FT /label= D-Ala

XX US4331661-A.

XX 25-MAY-1982.

XX 03-OCT-1980; 80US-0193621.

XX 03-OCT-1980; 80US-0193621.

XX (SALK-) SALK INST BIOLOGICA.

XX Marki WE, Brown MR, Rivier JEF;

XX WPI; 1982-48049E/23 (48049E).

XX Octa-peptide bombesin analogues - having hypothermic and  
PT analgesic props.

XX Claim 8; Column 8; 5pp; English.

XX The peptide may be preceded by a formyl, acetyl, propionyl, acrylyl  
CC or benzoyl group at its C-terminal. The peptide may be used for  
CC reducing the body temp. of a mammal, as well as for inducing  
CC analgesia. It produces hypothermia when injected i.v., but not  
CC when given i.v. or s.c. See also AAP20291-3.

XX Sequence 8 AA;

Query Match 94.7%; Score 36; DB 3; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 1 qwavahl 7

RESULT 6

AAR11241  
ID AAR11241 standard; Protein; 8 AA.

XX AC AAR11241;

XX 17-MAY-1991 (first entry)

XX Linear litorin analogue (III).

KW Bombesin; litorin analogue; linear; receptor affinity; cancer;  
XX diabetes.  
XX

OS Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 1..1  
FT /label= D-p-chloro-phenylalanine  
FT  
XX

PN W09102746-A.

XX 07-MAR-1991.

XX 17-AUG-1990; 90WO-US04646.

XX 21-AUG-1989; 89US-0397169.

XX 30-MAR-1990; 90US-0502438.

XX (TULA ) ADMIN TULANE EDUCATIONAL.

XX (BIOM-) BIOMEASURE INC.

XX Coy DH, Moreau JP, Kim SH;

XX WPI; 1991-087241/12.

XX New linear peptide analogues of bombesin - modified to eliminate

XX biological activity while retaining receptor affinity, for treating

XX cancer, diabetes, etc.

XX Claim 18; Page 54; 58pp; English.

XX This peptide is a specifically claimed example of a generic

XX formula. The C-terminal amino acid (Met) of the naturally occurring

XX peptide has been converted to an amide and Phe 8 has been replaced

XX by beta-leu. Gly 6 has also been replaced by D-Ala.

XX The peptide is useful for treating benign or malignant tissue

XX proliferation, arteriosclerosis, gastrointestinal disorders and

XX diabetes. They act as competitive inhibitors of natural peptides,

XX since they bind to the cell receptors but have no biological

XX activity.

XX The analogue may also be of a naturally occurring peptide

XX terminating at the C-terminus with a Met residue, such as the

XX 10 amino acid C-terminal region of mammalian GRP or amphibian

XX bombesin.

XX See also AAR11239-242.

XX Sequence 8 AA;

XX Query Match 94.7%; Score 36; DB 12; Length 8;

XX Best Local Similarity 85.7%; Pred. No. 3.4e+05;

XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Qy 2 QWAVXHL 8

XX Db 2 qwavahl 8

XX RESULT 7

XX AAR11242

XX ID AAR11242 standard; Protein; 8 AA.

XX AC AAR11242;

XX 17-MAY-1991 (first entry)

XX Linear litorin analogue (IV).

XX Bombesin; litorin analogue; linear; receptor affinity; cancer;

XX diabetes.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1 /note= "D-form residue"

XX Modified-site 6 /note= "NMe-D-Ala"

XX

FH Key Location/Qualifiers  
FT Modified-site 1..1  
FT /label=D-Phe, pentafluoro-Phe  
FT Modified-site 6..6  
FT /label= N-methyl-D-Ala

XX W09102746-A.

XX 07-MAR-1991.

XX 17-AUG-1990; 90WO-US04646.

XX 21-AUG-1989; 89US-0397169.

XX 30-MAR-1990; 90US-0502438.

XX (TULA ) ADMIN TULANE EDUCATIONAL.

XX (BIOM-) BIOMEASURE INC.

XX Coy DH, Moreau JP, Kim SH;

XX WPI; 1991-087241/12.

XX New linear peptide analogues of bombesin - modified to eliminate

XX biological activity while retaining receptor affinity, for treating

XX cancer, diabetes, etc.

XX Claim 20+21; Page 54; 58pp; English.

XX These peptides are specifically claimed examples of a generic

XX formula. The C-terminal amino acid (Met) of the naturally occurring

XX peptide has been converted to a methylester.

XX The peptide is useful for treating benign or malignant tissue

XX proliferation, arteriosclerosis, gastrointestinal disorders and

XX diabetes. They act as competitive inhibitors of natural peptides,

XX since they bind to the cell receptors but have no biological

XX activity.

XX The analogue may also be of a naturally occurring peptide

XX terminating at the C-terminus with a Met residue, such as the

XX 10 amino acid C-terminal region of mammalian GRP or amphibian

XX bombesin.

XX See also AAR11239-242.

XX Sequence 8 AA;

XX Query Match 94.7%; Score 36; DB 12; Length 8;

XX Best Local Similarity 85.7%; Pred. No. 3.4e+05;

XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Qy 2 QWAVXHL 8

XX Db 2 qwavahl 8

XX RESULT 8

XX AAR29155

XX ID AAR29155 standard; peptide; 8 AA.

XX AC AAR29155;

XX 16-APR-1993 (first entry)

XX Bombesin analogue (5).

XX Hepatoma; liver cancer; antagonist.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1 /note= "D-form residue"

XX Modified-site 6 /note= "NMe-D-Ala"

XX

FT Modified-site 8 /note= "Leu-OMe"  
 XX  
 PN W09220363-A.  
 XX  
 PD 26-NOV-1992.  
 XX  
 PF 11-MAY-1992; 92WO-US03916.  
 XX  
 PR 10-MAY-1991; 91US-0698681.  
 XX  
 PA (BIOM-) BIOMEASURE INC.  
 PA (TULA ) TULANE EDUCATIONAL FUND.  
 XX  
 PI Bodgen AE, Coy DH, Kim SH, Moreau J;  
 XX WPI; 1992-415466/50.  
 XX  
 DR Treatment of hepatoma - by admin. of admixed bombesin analogue  
 XX with carrier  
 XX  
 PS Claim 14; Page 48; 54pp; English.  
 XX  
 CC The peptide is an example of a highly generic formula. It is used  
 CC in a medicament for treating hepatoma. The cpd. acts as antagonist  
 CC to bombesin, which has been detected in a number of human cancer  
 CC lines.  
 XX  
 SQ Sequence 8 AA;  
 XX  
 Query Match 94.7%; Score 36; DB 13; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 DB |||||  
 2 qwavahl 8  
 RESULT 9  
 AAR29157  
 ID AAR29157 standard; peptide; 8 AA.  
 XX  
 AC AAR29157;  
 XX  
 16-APR-1993 (first entry)  
 Bombesin analogue (6).  
 XX  
 KW Hepatoma; liver cancer; antagonist.  
 XX  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "D-F5-Phe"  
 FT Misc-difference 6  
 FT /note= "D-form residue"  
 FT Modified-site 8  
 FT /note= "Leu-OMe"  
 XX  
 PN W09220363-A.  
 XX  
 PD 26-NOV-1992.  
 XX  
 PF 11-MAY-1992; 92WO-US03916.  
 XX  
 PR 10-MAY-1991; 91US-0698681.  
 XX  
 PA (BIOM-) BIOMEASURE INC.  
 PA (TULA ) TULANE EDUCATIONAL FUND.  
 XX

PI Bodgen AE, Coy DH, Kim SH, Moreau J;  
 XX WPI; 1992-415466/50.  
 XX  
 PD Treatment of hepatoma - by admin. of admixed bombesin analogue  
 XX with carrier  
 XX  
 PS Claim 15; Page 48; 54pp; English.  
 XX  
 CC The peptide is an example of a highly generic formula. It is used  
 CC in a medicament for treating hepatoma. The cpd. acts as antagonist  
 CC to bombesin, which has been detected in a number of human car  
 CC lines.  
 XX  
 SQ Sequence 8 AA;  
 XX  
 Query Match 94.7%; Score 36; DB 13; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps  
 QY 2 QWAVXHL 8  
 DB |||||  
 2 qwavahl 8  
 RESULT 10  
 AAW64911  
 ID AAW64911 standard; peptide; 8 AA.  
 XX  
 AC AAW64911;  
 XX  
 06-JUL-1999 (first entry)  
 Bombesin receptor antagonist.  
 DE  
 XX  
 KW Bombesin; antagonist; chlorambucil; peptic ulcer; pancreatitis;  
 KW eating disorder; diabetes; acromegaly; enterocutaneous fistula;  
 KW psoriasis; growth retardation; gastrointestinal motility disorder;  
 KW antitumour.  
 XX  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "The amino terminal is acylated with acetyl,  
 FT bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-amino]-  
 FT L-phenylalanine or a chlorambucil group"  
 FT Modified-site 8  
 FT /note= "The carboxy terminal is in the form of an  
 FT ethyl ester"  
 XX  
 PN W09500542-A1.  
 XX  
 PD 05-JAN-1995.  
 XX  
 PF 15-JUN-1994; 94WO-US06757.  
 XX  
 PR 17-DEC-1993; 93US-0168390.  
 PR 18-JUN-1993; 93US-0078062.  
 XX  
 PA (PEPT-) PEPTIDE TECHNOLOGIES CORP.  
 XX  
 PI Chandrasekhar B, Knight M, Takahashi K;  
 XX WPI; 1995-052004/07.  
 XX  
 DR New bombesin, gastrin releasing peptide or Neuromedin B or analogues.  
 XX - antagonists for treating conditions such as gastrointestinal  
 XX disorders, psoriasis and cancers  
 PS Claim 6; Page 34; 45pp; English.  
 XX

CC The patent discloses (1) the peptide sequence of bombesin (BBN),  
 CC gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C,  
 CC the peptide sequence having a chlorambucil group attached to the  
 CC amino terminal; (2) a BBN receptor antagonist of formula  
 CC R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
 CC antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
 CC In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
 CC Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
 CC amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His.  
 CC The compounds act as potent BBN/GRP-like peptide antagonists. They  
 CC can be used to inhibit the growth of cells that are sensitive to the  
 CC growth-promoting effects of BBN, GRP or a related peptide such as  
 CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
 CC cancerous cells or tumours. They can also be used to inhibit the  
 CC binding of BBN, GRP or a related peptide to cells capable of such  
 CC binding. They can be used for treating e.g. peptic ulcer, pancreatitis,  
 CC eating disorders, diabetes, acromegaly, enterocutaneous fistula,  
 CC psoriasis, growth retardation, gastrointestinal motility disorders or  
 CC tumours. The terminal structures of the compounds protect them from  
 CC in vivo proteolysis and provide highly potent antagonist effects that  
 CC persist for extended periods of time upon administration.

Sequence 8 AA;

Query Match 94.7%; Score 36; DB 16; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 Db 2 qwavahl 8

RESULT 11  
 AAR09335  
 ID AAR09335 standard; peptide; 9 AA.  
 XX AC AAR09335;  
 DT 30-MAR-1992 (first entry)  
 XX DE Sequence of Bombesin receptor peptide ligand with irreversible  
 DE effects.  
 XX KW Bombesin receptor; agonist; antagonist.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= H-pMel  
 FT /note= "pMel= p-bis (2-chloroethyl)  
 amino-L-phenylalanine"

Modified-site 9  
 /label= Met-NH2  
 WO9001037-A.  
 08-FEB-1990.  
 19-JUL-1989; 89WO-EP00842.  
 28-MAR-1989; 89GB-0006900.  
 21-JUL-1988; 88GB-0017379.  
 (FARM ) FARMITALIA C ERBA SPA.  
 de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciomei M;  
 Molinari I;  
 WPI; 1990-067161/09.  
 Bombesin receptor peptide ligands with irreversible effects - as  
 agonists and antagonists both weak and strong

XX Claim 2; Page 26; 32pp; English.  
 PS The inventors claim 36 peptides. Also claimed are:  
 CC (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.  
 CC of the peptides.  
 XX Sequence 9 AA;

Query Match 94.7%; Score 36; DB 11; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 Db 2 qwavahl 8

RESULT 12  
 AAR11522  
 ID AAR11522 standard; Protein; 9 AA.  
 XX AC AAR11522;  
 DT 13-JUN-1991 (first entry)  
 XX DE Example of peptide agonist of GRP, neuromedin, bombesin and litorin.  
 XX KW Non-malignant proliferative disease; cancer.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1.1  
 FT /label= OTHER  
 FT /note= "D-p-chlorophenylalanine"

PN WO9104040-A.  
 XX 04-APR-1991.  
 PD 17-SEP-1990; 90WO-US05271.  
 PF 05-MAY-1990; 90US-0520225.  
 PR 15-SEP-1989; 89US-0408125.  
 PR 21-NOV-1989; 89US-0440039.  
 XX (BIOM-) BIOMEASURE INC.  
 XX Bogden AE, Moreau J-P;  
 XX WPI; 1991-117320/16.  
 DR Treatment of non malignant proliferative disease and cancer - by  
 PT administration of natural peptide or fragment selected from  
 PT gastrin-releasing peptide, neuromedin, amphibian bombesin or  
 PT litorin  
 XX Claim 22; page 54; 73pp; English.  
 XX This is a peptide analogue of mammalian gastrin releasing peptide  
 CC (GRP), neuromedin-B or -C, amphibian bombesin and litorin.  
 CC It is an agonist of these cpds. and is used to treat smooth muscle  
 CC proliferation and cancer of the prostate, breast or lung.  
 CC Residue 6 (Ala) is D-alanine.  
 CC See also AAR11519-21 and AAR11523-30.

Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 |||| ||  
 Db 2 qwavahl 8

## RESULT 13

AAR14865  
 ID AAR14865 standard; Protein; 9 AA.

XX  
 AC

XX AAR14865;  
 14-FEB-1992 (first entry)

XX Peptide analogue #6 of litorin, GRP, neuromedin or bombesin.

XX tissue proliferation; gastrin related peptide; peptide hormone.

XX Synthetic.

Key Location/Qualifiers

Modified-site 1

FT /label= D-Phe

FT Modified-site 6

FT /label= D-Ala

XX WO9117181-A.

XX 14-NOV-1991.

XX 09-MAY-1991; 91WO-0003265.

XX 09-MAY-1990; 90US-0520226.

XX (TULA ) TULANE E FUND ADMINISTRA.

XX (BIOM-) BIOMEASURE INC.

XX Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

XX Peptide agonists of litorin, gastrin releasing peptide -

XX neuromedin B or C or bombesin, for treating cancer, preventing

XX smooth muscle proliferation and suppressing appetite and alcohol

XX craving

XX Claim 8; Page 18; 25pp; English.

XX The C-terminal residue is amidated. This peptide is one of 27  
 specific examples of a highly generic formula. The peptides are all  
 analogues of either litorin; the 10 amino acid C-terminal region of  
 mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 C-terminal region of amphibian bombesin. They act as at least partial  
 agonists of the natural peptides. The peptide analogues are made by  
 standard methods of synthesis and can be cyclised.  
 See AAR14860-R14880 and AAR15035-R15040.

XX Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 |||| ||  
 Db 2 qwavahl 8

## RESULT 14

AAR14866  
 ID AAR14866 standard; Protein; 9 AA.

XX  
 AC AAR14866;

XX 14-FEB-1992 (first entry)  
 XX Peptide analogue #7 of litorin, GRP, neuromedin or bombesin.  
 XX tissue proliferation; gastrin related peptide; peptide hormone.  
 XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= D-Phe

FT Modified-site 6

FT /label= D-Ala

XX WO9117181-A.

XX 14-NOV-1991.

XX 09-MAY-1991; 91WO-0003265.

XX 09-MAY-1990; 90US-0520226.

XX (TULA ) TULANE E FUND ADMINISTRA.

XX (BIOM-) BIOMEASURE INC.

XX Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

XX Peptide agonists of litorin, gastrin releasing peptide -

XX neuromedin B or C or bombesin, for treating cancer, preventing

XX smooth muscle proliferation and suppressing appetite and alcohol

XX craving

XX Claim 9; Page 18; 25pp; English.

XX The C-terminal residue is amidated. This peptide is one of 27  
 specific examples of a highly generic formula. The peptides are all  
 analogues of either litorin; the 10 amino acid C-terminal region of  
 mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 C-terminal region of amphibian bombesin. They act as at least partial  
 agonists of the natural peptides. The peptide analogues are made by  
 standard methods of synthesis and can be cyclised.  
 See AAR14860-R14880 and AAR15035-R15040.

XX Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 |||| ||  
 Db 2 qwavahl 8

## RESULT 15

AAR14867  
 ID AAR14867 standard; Protein; 9 AA.

XX  
 AC AAR14867;

XX 14-FEB-1992 (first entry)

XX Peptide analogue #8 of litorin, GRP, neuromedin or bombesin

XX tissue proliferation; gastrin related peptide; peptide hormone

XX Synthetic.

XX Key

XX Location/Qualifiers

FT Modified-site 1 /label= OTHER  
FT /note= "D-para-chloro-Phe"  
FT Modified-site 6  
FT /label= D-Ala  
XX  
PN W09117181-A.  
XX  
PD 14-NOV-1991.  
XX  
XX 09-MAY-1991; 91WO-0003265.  
PF  
XX 09-MAY-1990; 90US-0520226.  
PR  
XX (TULA ) TULANE E FUND ADMINISTRA.  
PA (BIOM-) BIOMEASURE INC.  
XX  
XX Coy DH, Kim SH, Moreau JP;  
PI  
XX  
XX WPI; 1991-353721/48.  
XX  
XX Peptide agonists of litorin, gastrin releasing peptide -  
XX neuromedin B or C or bombesin, for treating cancer, preventing  
PT smooth muscle proliferation and suppressing appetite and alcohol  
PT craving  
XX  
XX Claim 10; Page 18; 25pp; English.  
PS  
XX  
XX The C-terminal residue is amidated. This peptide is one of 27  
CC specific examples of a highly generic formula. The peptides are all  
CC analogues of either litorin; the 10 amino acid C-terminal region of  
CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
CC C-terminal region of amphibian bombesin. They act as at least partial  
CC agonists of the natural peptides. The peptide analogues are made by  
CC standard methods of synthesis and can be cyclised.  
CC See AARI4860-R14880 and AARI5035-R15040.  
XX  
SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
Best Local Similarity 85.7%; Pred. NO. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 2 QWAVXHL 8

Search completed: October 25, 2001, 11:22:46  
Job time: 219 sec

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:45 ; Search time 135.34 Seconds  
(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-11  
Perfect score: 38  
Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp-archaea:\*
- 2: sp-bacteria:\*
- 3: sp-fungi:\*
- 4: sp-human:\*
- 5: sp-invertebrate:\*
- 6: sp-mammal:\*
- 7: sp-mhc:\*
- 8: sp-organelle:\*
- 9: sp-phage:\*
- 10: sp-plant:\*
- 11: sp-rodent:\*
- 12: sp-unclassified:\*
- 13: sp-vertebrate:\*
- 14: sp-virus:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	86.8	517	14 Q9DSP4	Q9dsp4 saint croix
2	32	84.2	174	10 Q9M2H1	Q9m2h1 arabidopsis
3	32	84.2	328	2 Q9X5G8	Q9x5g8 streptomyce
4	32	84.2	353	5 Q21051	Q21051 caenorhabdi
5	32	84.2	806	13 Q9PDL2	Q9pdl2 brachydanio
6	31	81.6	95	2 Q911X2	Q911x2 pseudomonas
7	31	81.6	98	14 Q64981	Q64981 artichoke l
8	31	81.6	119	13 Q90253	Q90253 bombina ori
9	31	81.6	183	2 Q9RZ51	Q9rz51 deinococcus
10	31	81.6	216	11 Q9JM34	Q9jm34 mus musculus
11	31	81.6	232	3 Q9UVE4	Q9uve4 zygosacchar
12	31	81.6	236	2 Q85726	Q85726 streptomyce
13	31	81.6	256	3 Q9P6Y1	Q9p6y1 neurospora
14	31	81.6	266	5 Q9VZF7	Q9vzf7 drosophila
15	31	81.6	273	8 Q9TJQ5	Q9tjq5 prototheca
16	31	81.6	309	5 Q27106	Q27106 trichomonas
17	31	81.6	325	2 Q9PAR1	Q9par1 xylella fas
18	31	81.6	357	10 Q65366	Q65366 antirrhinum
19	31	81.6	359	10 Q9FUK9	Q9fuk9 pisum sativ

20	31	81.6	675	10 Q9S9V7	Q9s9v7 arabidopsis
21	31	81.6	696	5 Q9VCU2	Q9vcu2 drosophila
22	31	81.6	703	10 Q9LYH3	Q9lyh3 arabidopsis
23	31	81.6	1273	4 Q9NU68	Q9nu68 sapien
24	31	81.6	1275	4 Q15057	Q15057 sapien
25	30	78.9	23	13 Q9ES30	Q9es30 orthomyzom
26	30	78.9	132	2 Q9K3V3	Q9k3v3 pi
27	30	78.9	157	13 Q9I829	Q9i829 arabid
28	30	78.9	170	2 Q74711	Q74711 s.nechoysl
29	30	78.9	224	4 Q9UI28	Q9ui28 sapien
30	30	78.9	252	1 Q26248	Q26248 tuncobact
31	30	78.9	252	10 Q9FI20	Q9fi20 arabidopsis
32	30	78.9	276	2 Q9LIQ5	Q9liq5 streptomyce
33	30	78.9	283	2 Q9PCE4	Q9pc4 xylella as
34	30	78.9	291	14 Q72694	Q72694 barley mild
35	30	78.9	311	2 Q9PAE5	Q9pac5 xylella fis
36	30	78.9	318	2 Q9I066	Q9i066 p. domus
37	30	78.9	325	2 Q9K2G2	Q9k2g2 ptoyce
38	30	78.9	375	5 Q9TVW5	Q9tvw5 caenorhabdi
39	30	78.9	453	10 Q9M4A9	Q9m4a9 pisum sativ
40	30	78.9	520	10 Q65815	Q65815 h. flantius
41	30	78.9	691	2 Q55726	Q55726 syntrophost
42	30	78.9	700	2 Q07711	Q07711 streptococ
43	30	78.9	719	14 Q87541	Q87541 barley mild
44	30	78.9	721	2 Q9K7H4	Q9k7h4 h. flantius
45	30	78.9	858	5 Q17647	Q17647 caenorhabdi

ALIGNMENTS

RESULT 1	
Q9DSP4	
ID Q9DSP4	PRELIMINARY; PRT; 517 AA.
AC Q9DSP4;	
DT 01-MAR-2001 (TREMBLrel. 16, Created)	
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE NS1.	
OS Saint Croix river virus.	
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.	
OX NCBI_taxid=104581;	
RP [1]	
RN SEQUENCE FROM N.A.	
RA Attoui H., De Micco P., de Lamballerie X.;	
RT "Complete nucleotide sequence of Saint Croix river virus.;"	
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AFI45403; AAC34262.1; ..	
SQ SEQUENCE 517 AA; 58030 MW; 0104A543FB2A1B1A CRC64;	

Query Match 86.8%; Score 33; DB 14; Length 517;  
Best Local Similarity 71.4%; Pred. No. 51;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 1;

QY 2 QWAVXHL 8	
:	
Db 500 QWALHL 506	

RESULT 2	
Q9M2H1	
ID Q9M2H1	PRELIMINARY; PRT; 174 AA.
AC Q9M2H1;	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE HYPOTHETICAL 19.2 KDA PROTEIN.	
GN F14P22.40.	
OS Arabidopsis thaliana (Mouse-ear cross).	
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eur.	
OC Brassicales; Brassicaceae; Arabidopsis.	

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA E0 Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137082; CAB68183.1; -;
KW Hypothetical protein.
SQ SEQUENCE 174 AA; 19189 MW; 4C27267C5E53B4DB CRC64;

Query Match 84.2%; Score 32; DB 10; Length 174;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OV 2 QWAVXHL 8
:|||||
47 EWAVDHL 53

RESULT 3
OQX5G8 PRELIMINARY; PRT; 328 AA.
AC Q9X5G8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE DEACETYLCEPHALOSPORIN C ACETYLTRANSFERASE.
GN CVM4.
OS Streptomyces clavuligerus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1901;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 3585;
RX MEDLINE=99240369; PubMed=10223939;
RA Mosher R.H., Paradkar A.S., Anders C., Barton B., Jensen S.E.;
RA "Genes specific for the biosynthesis of clavam metabolites antipodal
RT to clavulanic acid are clustered with the gene for clavaminic
RT synthase 1 in Streptomyces clavuligerus.";
RL Antimicrob. Agents Chemother. 43:1215-1224(1999).
CC -1- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.
DR EMBL; AF124929; AAD30471.1; -.
InterPro; IPR000073; -.
pfam; PF00561; abhydrolase; 1.
Transferase; Porin.
SQ SEQUENCE 328 AA; 34642 MW; 4CBC78DAD5215034 CRC64;

Query Match 84.2%; Score 32; DB 2; Length 328;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7
|||||
DB 133 QWAVSH 138

RESULT 4
Q21051 PRELIMINARY; PRT; 353 AA.
ID Q21051;
AC Q21051;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE COSMID F59G1.
KW F59G1.4.
OS Caenorhabditis elegans.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilton R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Latreille P.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U53332; AAC71158.1; -.
SQ SEQUENCE 353 AA; 40061 MW; 7961772B498E3052 CRC64;

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Query Match 84.2%; Score 32; DB 5; Length 353;  
 Best Local Similarity 71.4%; Pred. No. 55;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 :||| ||  
 DB 201 EWAVNHL 207

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RESULT 5
O9DDL2 PRELIMINARY; PRT; 806 AA.
ID Q9DDL2;
AC Q9DDL2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARACASPASE.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11090634;
RA Uren A.G., O'Rourke K., Aravind L., Pisabarro M.T., Seshagiri S.,
RA Koonin E.V., Dixit V.M.;
RT "Identification of Paracaspases and Metacaspases. Two Ancient Famil-
RT of Caspase-like Proteins, One of which Plays a Key Role in MALT
RT Lymphoma.";
RL Mol. Cell 6:961-967(2000).
DR EMBL; AF316598; AAG38590.1; -.
SQ SEQUENCE 806 AA; 90754 MW; 589A8BC2013B0A51 CRC64;

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Query Match 84.2%; Score 32; DB 13; Length 806;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
|||||  
DB 559 QWAIHV 565

RESULT 6  
ID Q91IX2 PRELIMINARY; PRT; 95 AA.  
AC Q91IX2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL PROTEIN PA2143.  
GN PA2143.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
SEQUENCE FROM N.A.  
RX STRAIN=PA01;  
MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hufagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
RT opportunistic pathogen";  
RL Nature 406:959-964(2000).  
DR EMBL; AF004641; AAG0531.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 95 AA; 10821 MW; 5723E5D0CD08841F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 95;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
|||||  
DB 63 QWVHHL 69

RESULT 7  
ID Q64981 PRELIMINARY; PRT; 98 AA.  
AC Q64981;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
DE MRNA UNKNOWN FUNCTION (523BP) (FRAGMENT).  
OS Artichoke latent potyvirus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
OX NCBI\_TaxID=46076;  
RN [1]  
SEQUENCE FROM N.A.  
RA Grieco F.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X87255; CAA60708.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 98 AA; 11570 MW; C4A6316685E31078 CRC64;

Query Match 81.6%; Score 31; DB 14; Length 98;  
Best Local Similarity 83.3%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
DB 89 QWAVEH 94

RESULT 8  
ID Q90253 PRELIMINARY; PRT; 119 AA.  
AC Q90253;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PHE-13 BOMBESIN PREPROHORMONE.  
OS Bombina orientalis (Oriental fire-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8346;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=96205965; PubMed=8631814;  
RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.E.,  
RA Dong J.Z., Spindel E.R.;  
RT "There are three distinct forms of bombesin. Identification of  
RT [Leu13]bombesin, [Phe13]bombesin, and [Ser3,Arg10,Phe13]bombesin in  
RT the frog Bombina orientalis";  
RL J. Biol. Chem. 271:7731-7737(1996).  
DR EMBL; U49450; AAC59784.1; -.  
DR InterPro; IPR000874; -.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
FT CHAIN 45 59 PHE-13 BOMBESIN  
SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 81.6%; Score 31; DB 13; Length 119;  
Best Local Similarity 83.3%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
|||||  
DB 51 QWAVGH 56

RESULT 9  
ID Q9RZ51 PRELIMINARY; PRT; 183 AA.  
AC Q9RZ51;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 20.5 KDA PROTEIN.  
GN DRA0103.  
OS Deinococcus radiodurans.  
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.  
OX NCBI\_TaxID=1299;  
RN [1]  
SEQUENCE FROM N.A.  
RP STRAIN=R1;  
RX MEDLINE=20036896; PubMed=10567266;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.S., Lam P., McDonald L., Utterback T., Zaleski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus  
RT radiodurans R1";  
RL Science 286:1571-1577(1999).  
DR EMBL; AE001862; AAF12366.1; -.  
DR TIGR; DRA0103; -.  
KW Hypothetical protein.  
SQ SEQUENCE 183 AA; 20468 MW; 6EEAB3B483DC1BB7 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;

Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 49 QWAVFHL 55

RESULT 10  
Q9JM34 PRELIMINARY; PRT; 216 AA.  
AC Q9JM34;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OLFACTORY RECEPTOR (FRAGMENT).  
OS Mus musculus domesticus (western European house mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10092;  
[1]  
SEQUENCE FROM N.A.  
RA MEDLINE=20183981; PubMed=10706615;  
RA Rouquier S., Blancher A., Giorgi D.;  
RT "The olfactory receptor gene repertoire in primates and mouse:  
RT Evidence for reduction of the functional fraction in primates.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).  
DR EMBL; AF073967; AAD43416.1; -;  
DR InterPro; IPR000276; -;  
DR Pfam; PF00001; 7tm1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; UNKNOWN\_1.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 216 216  
SQ SEQUENCE 216 AA; 24097 MW; B2732A1870584D47 CRC64;

Query Match 81.6%; Score 31; DB 11; Length 216;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHL 8  
Db 82 WAVSHL 87

RESULT 11  
Q9UVE4 PRELIMINARY; PRT; 232 AA.  
Q9UVE4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE HYPOTHETICAL 26.4 KDA PROTEIN.  
OS Zygosaccharomyces rouxii (Candida mogii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.  
OX NCBI\_TaxID=4956;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN-CBS 732;  
RA Sychrova H., Braun V., Potier S., Souciet J.L.;  
RT "Genomic organization of Pichia sorbitophila and Zygosaccharomycetes  
RT rouxii genomes: comparison with Saccharomycetes cerevisiae.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y18560; CAB62288.1; -;  
DR InterPro; IPR001601; -;  
KW Hypothetical protein.  
SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 232;  
Best Local Similarity 71.4%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 140 QWCVGHL 146

RESULT 12  
O85726 PRELIMINARY; PRT; 236 AA.  
AC O85726;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE CEPHALOSPORIN HYDROXYLASE CMCI.  
GN CMCI.  
OS Streptomyces clavuligerus.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1901;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NRRL 3585;  
RX MEDLINE=98361893; PubMed=9696752;  
RA Alexander D.C., Jensen S.E.;  
RT "Investigation of the Streptomyces clavuligerus cephamycin C gene  
RT cluster and its regulation by the Ccar protein.";  
RL J. Bacteriol. 180:4068-4079(1998).  
DR EMBL; AF073896; AAC32491.1; -;  
SQ SEQUENCE 236 AA; 27584 MW; FD1EF1B650AF8070 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 236;  
Best Local Similarity 71.4%; Pred. No. 59;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
Db 170 QWAVDHL 176

RESULT 13  
Q9P6Y1 PRELIMINARY; PRT; 256 AA.  
AC Q9P6Y1;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE CONSERVED HYPOTHETICAL PROTEIN.  
GN 13E11.350.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
[1]  
RN SEQUENCE FROM N.A.  
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA German Neurospora genome project;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL353820; CAB88603.1; -;  
DR InterPro; IPR001601; -;  
SQ SEQUENCE 256 AA; 27789 MW; 5251FBC58B6BDD9 CRC64;

Query Match 81.6%; Score 31; DB 3; Length 256;  
Best Local Similarity 71.4%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 2 QWAVXHL 8

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Db 162 QWCVGHL 168
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RESULT 14
Q9VZF7 PRELIMINARY; PRT; 266 AA.
AC Q9VZF7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE IMPL2 PROTEIN.
GN IMPL2 OR CGI5009.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flockerzi A., Gong F., Gorrell J.H., Gu Z., Guan P., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AE003480; AAF47866.2; -.
DR HSSP; P56276; ITLK.
DR FlyBase; FBgn001257; Impl2.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 4.
SQ SEQUENCE 266 AA; 29823 MW; FC97694BDF80F33 CRC64;
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Query Match 81.6%; Score 31; DB 5; Length 266;  
Best Local Similarity 71.4%; Pred. No. 66;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 QWAVXHL 8
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Db 90 QWVVGHL 96
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RESULT 15
Q9TJQ5 PRELIMINARY; PRT; 273 AA.
AC Q9TJQ5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L2.
GN RPL2.
OS Prototheca wickerhamii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chloridiales;
OC Chlorellaceae; Prototheca.
OX NCBI_TaxID=3111;
[1]
SEQUENCE FROM N.A.
RP STRAIN=263-11;
RC Knauf U., Hachtel W.;
RT "A 22 kb fragment of the 53 kb plastid genome of the colourless, alga
RT Prototheca wickerhamii containing atp-, rpl-, rps-, rrn-, and trn-
RT genes.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245645; CAB53116.1; -.
DR HSSP; P04257; IRL2.
DR InterPro; IPR001412; -.
DR InterPro; IPR002171; -.
DR InterPro; IPR002222; -.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR ProDom; PD001012; -.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Ribosomal protein; Chloroplast.
SQ SEQUENCE 273 AA; 29952 MW; EE05656E77830BD4 CRC64;
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Query Match 81.6%; Score 31; DB 8; Length 273;  
Best Local Similarity 71.4%; Pred. No. 68;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
|||  
Db 170 QWATLHL 176  
|||

Search completed: October 25, 2001, 11:27:45  
Job time: 448 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:28:30 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-11

Perfect score: 38

Sequence: 1 XQAVXHL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	35	92.1	14	1 ALYT_ALYOB
2	35	92.1	107	1 BOMB_BOMVA
3	35	92.1	119	1 BOMB_BOMOR
4	31	81.6	9	1 LITO_LITAU
5	31	81.6	13	1 BOML_PSEGU
6	31	81.6	82	1 RANA_RANPI
7	31	81.6	232	1 YB9H_YEAST
8	31	81.6	263	1 IML2_DROME
9	31	81.6	265	1 IHA_SHEEP
10	31	81.6	360	1 IHA_BOVIN
11	31	81.6	364	1 IHA_PIG
12	31	81.6	366	1 IHA_MOUSE
13	31	81.6	366	1 IHA_RAT
14	31	81.6	769	1 SWI6_KLULA
15	30	78.9	10	1 GRP_RANRI
16	30	78.9	25	1 GRP_SCVCA
17	30	78.9	27	1 GRP_CANFA
18	30	78.9	27	1 GRP_CHICK
19	30	78.9	27	1 GRP_PIG
20	30	78.9	28	1 GRP_ALIMI
21	30	78.9	120	1 NEUB_XENLA
22	30	78.9	134	1 GRP_SHEEP
23	30	78.9	147	1 GRP_RAT
24	30	78.9	148	1 GRP_HUMAN
25	30	78.9	155	1 GRP_BOMOR
26	30	78.9	250	1 AGL8_SOLCO
27	30	78.9	361	1 IHA_TRIVU
28	30	78.9	366	1 IHA_HUMAN
29	30	78.9	367	1 IHA_HORSE
30	30	78.9	458	1 GYF6_YEAST
31	29	76.3	219	1 YDRE_SCHPO
32	29	76.3	227	1 PGSA_MYCPN
33	29	76.3	301	1 GCVA_HAEIN

```

34 29 76.3 384 1 AAPM_RHILV Q52814 Rhizobium l
35 29 76.3 510 1 ACHG_XENLA P05376 Xenopus lae
36 28 73.7 197 1 YCB7_PSEDE P29940 pseudomus
37 28 73.7 239 1 CYSH_THIRO P52672 Trichostema r
38 28 73.7 244 1 CYSH_BUCAL P57501 Trichostema ap
39 28 73.7 308 1 ACPI_ENTHI P36184 Trichostema h
40 28 73.7 353 1 COA2_POVBO P24849 Trichostema h
41 28 73.7 362 1 LDOX_VITVI P51093 Trichostema v
42 28 73.7 406 1 UL43_VZVD P09273 Trichostema v
43 28 73.7 430 1 LDOX_PETHY P51092 Trichostema v
44 28 73.7 496 1 C7B1_THLAR P49264 Trichostema
45 28 73.7 543 1 CP1B_HUMAN Q16678 Homo s

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## ALIGNMENTS

```

RESULT 1
ALYT_ALYOB
ID ALYT_ALYOB STANDARD; PRT; 14 AA.
AC P08944;

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DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ALYTESIN.
OS Alytes obstetricans (Midwife toad).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.
OX NCBI_TaxID=8443;
RN [1]

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RP MEDLINE=84131098; PubMed=6141890;
RA Ersamer V., Ersamer G.F., Mazzanti G., Endean R.;
RT "Active peptides in the skins of one hundred amphibian species from
RT Australia and Papua New Guinea.";
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR InterPro: IPR000874;
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

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Query Match 92.1%; Score 35; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 0.17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

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QY 2 QWAVXHL 8
DB 7 QWAVGHL 13

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RESULT 2
BOMB_BOMVA
ID BOMB_BOMVA STANDARD; PRT; 107 AA.
AC P01296;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE BOMBESIN PRECURSOR.
OS Bombina variegata (Yellow-bellied toad), and
OS Bombina variegata (Fire-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348, 8345;
RN [1]

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RP SEQUENCE FROM N.A.
RC SPECIES=B.variegata; TISSUE=Skin;
RX MEDLINE=90242964; PubMed=2335218;

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RA Richter K., Egger R., Kreil G.;  
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
 of Bombina variegata.";  
 RL FEBS Lett. 262:353-355(1990).  
 RN [2]  
 RP SEQUENCE OF 42-55.  
 RC SPECIES=B.variegata, and B.bombina;  
 RX MEDLINE=72163516; PubMed=4537042;  
 RA Anastasi A., Erspamer V., Buccì M.;  
 RT "Isolation and amino acid sequences of altytesin and bombesin, two  
 analogous active tetradecapeptides from the skin of European  
 discoglossid frogs";  
 RL Arch. Biochem. Biophys. 148:443-446(1972).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
 GASTROINTESTINAL HORMONES.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
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 CC -----  
 DR EMBL; X52447; CAA36686.1; -;  
 DR PIR; A01564; BSTD.  
 DR PIR; B01564; BSTDY.  
 DR PIR; S09095; S09095.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT PEPTIDE 42 55 BOMBESIN.  
 FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 107 AA; 12341 MW; 9692B50600FAF618 CRC64;  
 Query Match 92.18; Score 35; DB 1; Length 107;  
 Best Local Similarity 85.78; Pred. No. 1.2;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 DQ |||||  
 DB 48 QWAVGHL 54  
 RESULT 3  
 ID BOMB\_BOMOR STANDARD; PRT; 119 AA.  
 AC P21591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE BOMBESIN PRECURSOR.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088602; PubMed=2263631;  
 RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;  
 RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
 relationship between bombesin and gastrin-releasing peptide.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
 CC -!- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
 CC -!- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULAR CELLS IN  
 THE SKIN AND THE BRAIN.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M55255; AAA48551.1; -;  
 DR PIR; A39261; A39261.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 ?  
 FT PEPTIDE 45 58 BOMBESIN.  
 FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROU.  
 SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2445A44A CRC64;  
 Query Match 92.18; Score 35; DB 1; Length 119;  
 Best Local Similarity 85.78; Pred. No. 1.3;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 DQ |||||  
 DB 51 QWAVGHL 57  
 RESULT 4  
 ID LITO\_LITAU STANDARD; PRT; 9 AA.  
 AC P08945;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LITORIN.  
 OS Litoria aurea (Australian frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75187011; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Amino acid composition and sequence of litorin, a bombesin-like  
 nonapeptide from the skin of the Australian leptodactylid frog  
 Litoria aurea.";  
 RL Experientia 31:510-511(1975).  
 RN [2]  
 RP SEQUENCE (METHYLATED VARIANT).  
 RX MEDLINE=78003546; PubMed=908397;  
 RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;  
 RT "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in  
 methanol extracts of the skin of the Australian frog Litoria aurea.";  
 RL Experientia 33:1289-1289(1977).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
 CC -----  
 DR PIR; S07204; S07204.  
 DR PIR; S07205; S07205.  
 DR InterPro; IPR000874; -;  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Methylation.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 2 2 METHYLATION (IN A VARIANT).  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1103 MW; D7CCCL1E862CDC366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+04;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 |||||  
 Db 2 QWAVGH 7

RESULT 5  
 BOML\_PSEGU STANDARD; PRT; 13 AA.  
 AC P42991; 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE BOMBESIN-LIKE PEPTIDE L (PG-L).  
 OS Pseudophryne guentheri (Frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OX Pseudophryne.  
 NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304 (1990).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
 DR PIR; A60409; A60409.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 13;  
 Best Local Similarity 83.3%; Pred. No. 1;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
 |||||  
 Db 6 QWAVGH 11

RESULT 6  
 RANA\_RANPI STANDARD; PRT; 82 AA.  
 AC P08950;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DE 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE RANATENSIN PRECURSOR.  
 OS Rana pipiens (Northern leopard frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88330837; PubMed=2458345;  
 RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;

RT "Molecular cloning of cDNAs encoding the human bombesin-like peptide  
 neuromedin B. Chromosomal localization and comparison to cDNAs  
 encoding its amphibian homolog ranatensin.";  
 RL J. Biol. Chem. 263:13317-13323 (1988).  
 RN [2]  
 RP SEQUENCE OF 48-58.  
 RA Nakajima T., Tanimura T., Pisano J.J.;  
 RT "Isolation and structure of a new vasoactive polypeptide.";  
 Fed. Proc. 29:282-282 (1970).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 FAMILY.  
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 CC -----

EMBL; M21552; AAA49533.1; -  
 DR PIR; B28945; B28945.  
 DR InterPro; IPR000874; -.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residue.  
 KQ Signal.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT PROPEP 28 47  
 FT PEPTIDE 48 58 RANATENSIN.  
 FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE ...)  
 SQ SEQUENCE 82 AA; 9159 MW; 09194FFD0E7436DE CRC64;

Query Match 81.6%; Score 31; DB 1; Length 82;  
 Best Local Similarity 83.3%; Pred. No. 6.1;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 2 QWAVXH 7  
 |||||  
 Db 51 QWAVGH 56

RESULT 7  
 YB9H\_YEAST STANDARD; PRT; 232 AA.  
 AC P38340;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DE 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE HYPOTHETICAL 26.1 KDA PROTEIN IN POP4-SHM1 INTERGENIC REGION.  
 GN YBR261C OR YBR1729.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=93220397; PubMed=8465606;  
 RA Daignon F., Biteau N., Crouzet M., Aigle M.;  
 RT "The complete sequence of a 19,482 bp segment located on the right  
 arm of chromosome II from Saccharomyces cerevisiae.";  
 RL Yeast 9:189-199 (1993).  
 CC -!- SIMILARITY: TO S.POMBE SPAC16E8.14C.

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 CC -----

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CC -----
DR EMBL; X70529; CAA49926.1; -.
DR EMBL; Z36130; CAA85224.1; -.
DR PTR; S32963; S32963.
DR SGD; S0000465; YBR261C.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 232;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
   ||| ||
Db 139 QMCVGH 145

RESULT 8
2-DROME
IML2_DROME STANDARD; PRT; 263 AA.
Q09024;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2 PRECURSOR.
GN IML2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CANTON-S; TISSUE=Embryo;
RA MEDLINE=941139565; PubMed=8306886;
RA Garbe J.C., Yang E., Fristrom J.W.;
RT "IMP-L2: an essential secreted immunoglobulin family member
RL implicated in neural and ectodermal development in Drosophila.";
RL Development 119:1237-1250(1993).
CC -1- FUNCTION: ESSENTIAL DEVELOPMENTAL ROLE DURING EMBRYOGENESIS, IN
CC PARTICULAR THE NORMAL DEVELOPMENT OF THE NERVOUS SYSTEM. MAY BE
CC INVOLVED IN SOME ASPECT OF CELL ADHESION.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: DETECTED IN SEVERAL SITES INCLUDING THE
CC VENTRAL NEUROECTODERM, THE TRACHEAL PITS, THE PHARYNX AND
CC ORSOPHAGUS, AND SPECIFIC NEURONAL CELL BODIES, WHERE IT IS
CC PRIMARILY EXPRESSED.
CC -1- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT THE CELLULAR BLASTODERM
CC STAGE AND CONTINUES TO BE EXPRESSED THROUGH SUBSEQUENT
CC DEVELOPMENT.
CC -1- INDUCTION: BY 20-HYDROXYECDSONE.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC EMBL; L23066; AAB59251.1; -.
CC HSP; P56276; ITLK.
CC FlyBase; FBgn001257; Imlp2.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 2.
KW Immunoglobulin domain; Cell adhesion; Signal.
FT SIGNAL 1 23
FT CHAIN 24 263
FT DOMAIN 69 142
FT DOMAIN 184 247
FT IG-LIKE C2-TYPE DOMAIN.
FT IG-LIKE C2-TYPE DOMAIN.
```

```
FT DISULFID 76 135 BY SIMILARITY.
FT DISULFID 191 240 BY SIMILARITY.
FT VARIANT 173 173 V -> I.
SQ SEQUENCE 263 AA; 29421 MW; 44AADB1B22DD1804 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 263;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
   ||| ||
Db 87 QWVVGHL 93

RESULT 9
IHA_SHEEP
ID IHA_SHEEP STANDARD; PRT; 265 AA.
AC P38440;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INHIBIN ALPHA CHAIN (FRAGMENT).
GN INHA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Sadanandan S.L., Jeyaseelan K.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBIN IS A CONADAL GLYCOPETIDE THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L28815; AAA31553.1; -.
CC InterPro; IPR001839; -.
CC Pfam; PF00019; TGF-beta; 1.
CC PROSITE; PS00250; TGF-BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein.
FT NON_TER 1 227 BY SIMILARITY.
FT DISULFID 161 227 BY SIMILARITY.
FT DISULFID 190 262 BY SIMILARITY.
FT DISULFID 194 264 BY SIMILARITY.
FT DISULFID 226 226 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 265 AA; 28754 MW; D80E9AB156B656 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 265;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8
   ||| ||
Db 74 RWAVLHL 80
```

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RESULT 10
IHA_BOVIN STANDARD; PRT; 360 AA.
ID IHA_BOVIN AC P07994;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
GN INHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicular fluid;
RX MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
"Cloning and sequence analysis of cDNA species coding for the two
subunits of inhibin from bovine follicular fluid.";
Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
RN [2]
RP SEQUENCE OF 1-87 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
"Genomic cloning and sequence analyses of the bovine alpha-, beta A-
and beta B-inhibin/activin genes. Identification of transcription
factor AP-2-binding sites in the 5'-flanking regions by DNase I
footprinting.";
Eur. J. Biochem. 226:751-764(1994).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYPEPTIDE THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL; M13273; AAA97414.1; -.
DR EMBL; A14416; CAA01156.1; -.
DR EMBL; U16237; AAB60262.1; -.
DR PIR; A25732; A25732.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR FOLLITROPIN INHIBITOR; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 226
FT CHAIN 227 360
FT DISULFID 256 322
FT DISULFID 285 357
FT DISULFID 289 359
FT DISULFID 321 321
FT CARBOHYD 140 140
FT CARBOHYD 262 262
FT SEQUENCE 360 AA; 38809 MW; FBF385DD1EEFE46 CRC64;
SQ
Query Match 81.6%; Score 31; DB 1; Length 360;
Best Local Similarity 71.4%; Pred. No. 25;

Matches 5; Conservative 1; Mismatches 1; Indels 0.

QY 2 QWAVXHL 8
DB 169 RWAVLHL 175

RESULT 11
IHA_PIG STANDARD; PRT; 364 AA.
ID IHA_PIG AC P04087;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
GN INHA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86287350; PubMed=3016724;
RA Mayo K.E., Cerelli G.M., Spiess J., Rivier J., Rosenfeld M.,
Evans R.M., Vale W.;
"INHIBIN A-subunit cDNAs from porcine ovary and human placenta.";
Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 231-256.
RC TISSUE=Ovarian follicular fluid;
RX MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying Y.,
Guillemin R., Niall H., Seeburg P.H.;
"Complementary DNA sequences of ovarian follicular fluid inhibin show
precursor structure and homology with transforming growth
factor-beta.";
Nature 318:659-663(1985).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYPEPTIDE THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL; M13980; AAA31057.1; -.
DR EMBL; X03285; CAA27019.1; -.
DR PIR; A01392; WFPGA.
DR PIR; A25947; A25947.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR FOLLITROPIN INHIBITOR; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 230
FT CHAIN 231 364
FT DISULFID 260 326
FT DISULFID 289 361
FT DISULFID 293 363
FT DISULFID 325 325
FT CARBOHYD 144 144
FT CARBOHYD 266 266
FT CONFLICT 120 120
FT CONFLICT 125 125
FT INHIBIN ALPHA CHAIN.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT INTERCHAIN (BY SIMILARITY).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT R -> H (IN REF. 2).
FT A -> T (IN REF. 2).

```

SO SEQUENCE 364 AA; 39160 MW; BB595B9B7958A168 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 364;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 :||| ||  
 Db 173 RWAHL 179

RESULT 12

ID IHA\_MOUSE STANDARD; PRT; 366 AA.

AC 004997; 1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DT INHIBIN ALPHA CHAIN PRECURSOR.

INHA.

Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-93321614; PubMed-8330535;

RA Albano P.M., Groome N., Smith J.C.;

RT "Activins are expressed in preimplantation mouse embryos and in ES

and EC cells and are regulated on their differentiation.";

RL Development 117:711-723(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-92337610; PubMed-1632772;

RA Su J.G.W., Hsueh A.J.W.;

RT "Characterization of mouse inhibin alpha gene and its promoter.";

RL Biochem. Biophys. Res. Commun. 186:293-300(1992).

RN [3]

RP SEQUENCE OF 49-366 FROM N.A.

RX STRAIN-SWISS WEBSTER;

RX MEDLINE-91071531; PubMed-2253839;

RA Tone S., Katoh Y., Fujimoto H., Togashi S., Yanazawa M., Kato Y.,

RA Higashinakagawa T.;

RT "Expression of inhibin alpha-subunit gene during mouse

gametogenesis.";

RL Differentiation 44:62-68(1990).

CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE

ACTIVATION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND

ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN.

CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; X69618; CAA49324.1; -

DR EMBL; M95525; AAA39314.1; -

DR EMBL; M95526; AAA39314.1; JOINED.

DR EMBL; X55957; CAA39424.1; -

DR PIR; S31439;

DR PIR; JCI106; JCI106.

DR MGD; MGI:96569; Inha.

DR InterPro; IPR001839; -

DR InterPro; IPR002405; -

DR Pfam; PF000019; TGF-beta; 1.

DR PRINTS; PR00669; INHIBINA.  
 KW PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT PROPEP 21 233  
 FT CHAIN 234 366 INHIBIN ALPHA CHAIN.  
 FT DISULFID 263 328 BY SIMILARITY.  
 FT DISULFID 292 363 BY SIMILARITY.  
 FT DISULFID 296 365 BY SIMILARITY.  
 FT DISULFID 327 327 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 269 269 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 165 165 A -> R (IN REF. 2).  
 FT CONFLICT 171 171 V -> G (IN REF. 2 AND 3).  
 FT CONFLICT 336 336 T -> R (IN REF. 2 AND 3).  
 SQ SEQUENCE 366 AA; 39536 MW; 8F3951B722FE0011 CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8

Db 176 RWAHL 182

RESULT 13

ID IHA\_RAT

AC P17490; STANDARD; PRT; 366 AA.

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE INHIBIN ALPHA CHAIN PRECURSOR.

GN INHA.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE-90190649; PubMed-2628729;

RA Feng Z.-M., Li Y.-P., Chen C.-L.C.;

RT "Analysis of the 5'-flanking regions of rat inhibin alpha- and

beta-B-subunit genes suggests two different regulatory mechanisms.";

RL Mol. Endocrinol. 3:1914-1925(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-91042598; PubMed-3153478;

RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;

RT "Rat inhibin: molecular cloning of alpha- and beta-subunit

complementary deoxyribonucleic acids and expression in the ovary

RL Mol. Endocrinol. 1:561-568(1987).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE-90331931; PubMed-2484214;

RA Esch F.S., Shimasaki S., Cooksey K., Mercado M., Mason A.J.,

RA Ying S.Y., Ueno N., Ling N.;

RT "Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence

analysis of rat ovarian inhibitors.";

RL Mol. Endocrinol. 1:388-396(1987).

CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE

SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND

ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN.

CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

CC -1- TISSUE SPECIFICITY: ALPHA- AND BETA-B-SUBUNITS ARE THE

PREDOMINANT FORMS FOUND IN RAT TESTIS.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC -----

DR EMBL; M32755; AAA41437.1; -;  
DR EMBL; M32754; AAA41437.1; JOINED.  
DR EMBL; M36453; AAA41435.1; -;  
DR PIR; A40905; A40905.  
DR PIR; A41398; A41398.  
DR PIR; A40056; A40056.  
DR InterPro; IPR001839; -;  
DR Pfam; PF00019; TGF-beta; 1.  
DR PRINTS; PR00669; INHIBINA.  
DR PROSITE; PS00250; TGF-BETA\_1; 1.  
CC Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.  
CC SIGNAL 1 20  
CC PROPEP 21 233  
CC CHAIN 234 366  
CC BY SIMILARITY.  
CC DISULFID 263 328  
CC DISULFID 292 363  
CC DISULFID 296 365  
CC DISULFID 327 327  
CC INTERCHAIN (BY SIMILARITY).  
CC CARBOHYD 147 147  
CC N-LINKED (GLCNAC. .) (POTENTIAL).  
CC N-LINKED (GLCNAC. .) (POTENTIAL).  
CC SEQUENCE 366 AA; 39496 MW; 327A233B9FEDFCDC CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
Best Local Similarity 71.4%; Pred. No. 25;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNAVXHL 8  
DB 176 RWAVLHL 182

RESULT 14  
SWI6\_KLULA  
ID SWI6\_KLULA STANDARD; PRT; 769 AA.  
AC P40418;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
CC REGULATORY PROTEIN SWI6 (CELL-CYCLE BOX FACTOR, CHAIN SWI6) (TRANS-  
CC ACTING ACTIVATOR OF HO ENDONUCLEASE GENE) (MBF SUBUNIT P90).  
GN SWI6.  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93383264; PubMed=8372350;  
RA Koch C., Moll T., Neuberg M., Ahorn H., Nasmyth K.;  
RT "A role for the transcription factors Mbp1 and Swi4 in progression  
RT from G1 to S phase.";  
RL Science 261:1551-1557(1993).  
CC -!- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT  
CC TRANSCRIPTION. SWI4 AND SWI6 ARE REQUIRED FOR FORMATION OF THE  
CC CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE  
CC UPSTREAM REGION OF HO (5'-CACGAAA-3') IS CALLED THE CELL CYCLE  
CC BOX (CCB).  
CC -!- SUBUNIT: MBF CONTAINS SWI6 AND MBP1; SBF CONTAINS SWI6 AND SWI4.  
CC -!- SIMILARITY: STRONG, TO S.POMBE CDC10.  
CC -!- SIMILARITY: CONTAINS 2 ANK REPEATS.  
CC -----

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CC -----

DR EMBL; X74292; CAA52345.1; -;  
DR PIR; S36657; S36657.  
DR InterPro; IPR002110; -;  
DR Pfam; PF00023; ank; 2.  
DR PROSITE; PS50088; ANK\_REPEAT\_2.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 2.  
KW Transcription regulation; DNA-binding; ANK repeat; Repeat.  
FT REPEAT 286 315 ANK 1.  
FT REPEAT 422 451 ANK 2.  
SQ SEQUENCE 769 AA; 86669 MW; E3A5328B4DA084FB CRC64;

Query Match 81.6%; Score 31; DB 1; Length 769;  
Best Local Similarity 57.1%; Pred. No. 51;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNAVXHL 8  
DB 409 QWVITHL 415

RESULT 15  
GRP\_RANRI  
ID GRP\_RANRI STANDARD; PRT; 10 AA.  
AC P23260;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-APR-1993 (Rel. 25, Last annotation update)  
DE NEUROMEDIN C.  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; F...  
OX NCBI\_TaxID=8406;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=91315477; PubMed=1859413;  
RA Conlon J.M., O'Harte F., Vaudry H.;  
RT "Primary structures of the bombesin-like neuropeptides in frog brain  
RT show that bombesin is not the amphibian gastrin-releasing peptide.";  
RL Biochem. Biophys. Res. Commun. 178:526-530(1991).  
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
CC FAMILY.  
CC PIR; PQ0177; PQ0177.  
CC InterPro; IPR000874; -;  
CC Pfam; PF02044; Bombesin; 1.  
CC PROSITE; PS00257; BOMBESIN; 1.  
KW Bombesin family; Amidation.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.3;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WAVXHL 8  
DB 4 WAVGHL 9

Search completed: October 25, 2001, 11:28:30  
Job time: 478 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:22 ; Search time 76.25 Seconds  
(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-11  
Perfect score: 38  
Sequence: 1 QWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_58:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	92.1	14	1 BSTDY	bombesin - fire-be
2	35	92.1	107	1 BSTDY	bombesin precursor
3	35	92.1	119	2 A39261	bombesin precursor
4	32	84.2	174	2 T45665	hypothetical prote
5	32	84.2	353	2 T34312	hypothetical prote
6	31	81.6	9	2 S07204	litorin I - Austr
7	31	81.6	13	2 A60409	bombesin-like pept
8	31	81.6	82	2 B28945	ranatensin precurs
9	31	81.6	95	2 H83378	hypothetical prote
10	31	81.6	183	2 A75605	hypothetical prote
11	31	81.6	232	2 S32963	hypothetical prote
12	31	81.6	256	2 T48787	hypothetical prote
13	31	81.6	309	2 S41427	cysteine proteins
14	31	81.6	325	2 F82558	lipopolysaccharide
15	31	81.6	357	2 T17027	MYB-related transc
16	31	81.6	360	1 A25732	inhibin alpha chai
17	31	81.6	364	1 WFPGA	inhibin alpha chai
18	31	81.6	366	1 JCL106	inhibin alpha chai
19	31	81.6	366	1 A40056	inhibin alpha chai
20	31	81.6	703	2 T48559	probable receptor-
21	31	81.6	769	2 S36657	SWf6 protein - yea
22	30	78.9	10	2 PQ0177	neuromedin C - lau
23	30	78.9	10	2 A60647	gastrin-releasing
24	30	78.9	25	2 S06263	gastrin-releasing
25	30	78.9	27	1 RHGPGA	gastrin-releasing
26	30	78.9	27	1 RHGPGA	gastrin-releasing
27	30	78.9	27	1 RHGCHA	gastrin-releasing
28	30	78.9	120	2 A47201	bombesin-like pepti
29	30	78.9	134	2 I47010	gastrin-releasing

30	30	78.9	138	2 A26182	gastrin-releasing
31	30	78.9	147	1 A40922	gastrin-releasing
32	30	78.9	148	1 B26182	gastrin-releasing
33	30	78.9	155	2 A2437	gastrin-releasing
34	30	78.9	170	2 S76918	hypothetical prote
35	30	78.9	250	2 T07902	MADS box protein -
36	30	78.9	252	2 A69060	conserved hypoxan
37	30	78.9	283	2 B82631	hypothetical prote
38	30	78.9	311	2 H82541	conserved hypoxan
39	30	78.9	318	2 H83298	conserved hypoxan
40	30	78.9	366	1 A24248	inhibin - pha chai
41	30	78.9	375	2 T43049	hypothetical prote
42	30	78.9	453	2 T50645	glucan endo-1,3-br
43	30	78.9	458	2 S58816	GTPase activating
44	30	78.9	505	2 T10896	cytochrome P450 (E
45	30	78.9	691	1 S76521	hypothetical prote

ALIGNMENTS

RESULT 1  
BSTDY  
bombesin - fire-bellied toad  
C:Species: Bombina bombina (fire-bellied toad)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 0  
C:Accession: A01564  
R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin. Two analogues a  
A:Reference number: A01564; MUID:72163516  
A:Accession: A01564  
A:Molecule type: protein  
A:Residues: 1-14 <ANA>  
C:Superfamily: gastrin-releasing peptide  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyroglutam  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 92.1%; Score 35; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QWAVXHL 8  
|||||  
Db 7 QWAVGHL 13  
RESULT 2  
BSTDY  
bombesin precursor - yellow-bellied toad  
C:Species: Bombina variegata (yellow-bellied toad)  
C:Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 0  
C:Accession: S09095; B01564; A01564  
R:Richter, K.; Egger, R.; Kreil, G.  
FEBS Lett. 262, 353-355, 1990  
A:Title: Molecular cloning of a cDNA encoding the bombesin precursor in su  
A:Reference number: S09095; MUID:90242964  
A:Accession: S09095  
A:Molecule type: mRNA  
A:Residues: 1-107 <RIC>  
R:Anastasi, A.; Erspamer, V.; Bucci, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin. Two analogues a  
A:Reference number: A01564; MUID:72163516  
A:Accession: B01564  
A:Molecule type: protein  
A:Residues: 42-55 <ANA>  
C:Superfamily: ranatensin  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyro  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-41/Domain: amino-terminal propeptide #status predicted <PRO>

F:42-55/Product: bombesin #status experimental <MAT>  
 F:56-107/Domain: carboxyl-terminal propeptide #status predicted <CPT>  
 F:42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F:55/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 92.1%; Score 35; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 2.5;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 ||||| ||  
 Db 48 QWAVGHL 54

RESULT 3  
 A39261  
 bombesin precursor - Bombina orientalis  
 C:Species: Bombina orientalis  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999  
 C:Accession: A39261  
 R:Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990  
 A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship between  
 A:Reference number: A39261; MUID:91088602  
 A:Accession: A39261  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <SPI>  
 A:Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017  
 C:Superfamily: ranatensin  
 C:Keywords: neuropeptide

Query Match 92.1%; Score 35; DB 2; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 2.8;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 ||||| ||  
 Db 51 QWAVGHL 57

RESULT 4  
 T45665  
 hypothetical protein F14P22.40 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C:Accession: T45665  
 M:Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z23011  
 A:Accession: T45665  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-174 <DAN>  
 A:Cross-references: EMBL:AL137082  
 A:Experimental source: cultivar Columbia; BAC clone F14P22  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 90/1; 126/3; 166/2  
 A:Note: F14P22.40

Query Match 84.2%; Score 32; DB 2; Length 174;  
 Best Local Similarity 71.4%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 :||| ||  
 Db 47 BWAVDHL 53

RESULT 5  
 T34312  
 hypothetical protein F59G1.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jun-2000  
 C:Accession: T34312  
 R:Latreille, P.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid F59G1.  
 A:Reference number: Z21504  
 A:Accession: T34312  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-353 <LAT>  
 A:Cross-references: EMBL:U53332; PIDN:AAC71158.1; GSPDB:GN00020; CESP:F59G1;  
 A:Experimental source: strain Bristol N2; clone F59G1  
 C:Genetics:  
 A:Gene: CESP:F59G1.4  
 A:Map position: 2  
 A:Introns: 23/1; 47/2; 83/3; 114/3; 151/1; 187/2; 229/3; 257/3; 316/1  
 C:Superfamily: Caenorhabditis elegans hypothetical protein F59G1.4

Query Match 84.2%; Score 32; DB 2; Length 353;  
 Best Local Similarity 71.4%; Pred. No. 33;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
 :||| ||  
 Db 201 EWAVNHL 207

RESULT 6  
 S07204  
 litorin I - Australian tree frog (Litoria aurea)  
 C:Species: Litoria aurea  
 C:Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
 C:Accession: S07204  
 R:Anastasi, A.; Erspamer, V.; Endean, R.  
 Experientia 31, 510-511, 1975  
 A:Title: Amino acid composition and sequence of litorin, a bombesin-like nonapeptide f  
 A:Reference number: S07204; MUID:75187011  
 A:Accession: S07204  
 A:Molecule type: protein  
 A:Residues: 1-9 <ANA>  
 C:Superfamily: gastrin-releasing peptide  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 7  
 |||||  
 Db 2 QWAVGH 7

RESULT 7  
 A60409  
 bombesin-like peptide L - frog (Pseudophryne guentheri)  
 C:Species: Pseudophryne guentheri  
 C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
 C:Accession: A60409  
 R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melch  
 Peptides 11, 299-304, 1990  
 A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aus  
 A:Reference number: A60409; MUID:90287814  
 A:Accession: A60409  
 A:Molecule type: protein  
 A:Residues: 1-13 <SIM>

C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
||| |  
Db 6 QWAVGH 11

RESULT 8  
B28945  
ranatensin precursor - northern leopard frog  
C:Species: Rana pipiens (northern leopard frog)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
C:Accession: B28945  
C:Author: Crane, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.  
J. Biol. Chem. 263, 13317-13323, 1988  
A:Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromedin  
A:Reference number: A92667; MUID:88330837  
A:Accession: B28945  
A:Molecule type: mRNA  
A:Residues: 1-82 <KRA>  
A:Cross-references: GB:M21552; GB:J03948; NID:g213693; PIDN:AAA49533.1; PID:g213694  
C:Superfamily: ranatensin  
C:Keywords: neuropeptide

Query Match 81.6%; Score 31; DB 2; Length 82;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 QWAVXH 7  
||| |  
Db 51 QWAVGH 56

RESULT 9  
H83378  
hypothetical protein PA2143 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83378  
C:Author: Fowler, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brogan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: H83378  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-95 <STO>  
A:Cross-references: GB:AE004641; GB:AE004091; NID:g9948150; PIDN:AAG05531.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2143

Query Match 81.6%; Score 31; DB 2; Length 95;  
Best Local Similarity 71.4%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXH 8  
||| |  
Db 63 QWVHH 69

RESULT 10  
A75605  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
C:Accession: A75605  
C:Author: R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, L.D.; Dodson, J.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, L.; Zeleny, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896  
A:Accession: A75605  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-183 <WHI>  
A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AA11366.1; PID:g646  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRA0103  
A:Map position: 2  
C:Superfamily: Deinococcus radiodurans hypothetical protein DRA0103

Query Match 81.6%; Score 31; DB 2; Length 183;  
Best Local Similarity 71.4%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| |  
Db 49 RWAVFHL 55

RESULT 11  
S32963  
hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YBR1729  
C:Species: Saccharomyces cerevisiae  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
C:Accession: S32963; S46142  
C:Author: Dolignon, F.; Biteau, N.; Crouzet, M.; Aigle, M.  
Yeast 9, 189-199, 1993  
A:Title: The complete sequence of a 19,482 bp segment located on the right arm of chr  
A:Reference number: S29348; MUID:93220397  
A:Accession: S32963  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-232 <DOI>  
A:Cross-references: EMBL:X70529; NID:gl907246; PIDN:CAA49926.1; F:1; 296560  
R:Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Dolignon, F.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45940  
A:Accession: S46142  
A:Molecule type: DNA  
A:Residues: 1-232 <AIG>  
A:Cross-references: EMBL:X36130; NID:g536688; PIDN:CAA5224.1; PID:g536688; MIPS:YBR2  
C:Genetics:  
A:Map position: 2R  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 232;  
Best Local Similarity 71.4%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| |  
Db 139 QWCVGHL 145

RESULT 12  
T48787  
hypothetical protein 13E11.350 [imported] - Neurospora crassa

C:Species: Neurospora crassa  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 28-Jul-2000  
C:Accession: T48787  
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000  
A:Reference number: 224541  
A:Accession: T48787  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-256 <SCH>  
A:Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.350  
A:Experimental source: cosmid contig 13E11; strain 74  
C:Genetics:  
A:Gene: NCSP:13E11.350  
A:Map position: 2  
A:Introns: 213/2  
C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 256;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| ||  
Db 162 QWCVGHL 168

RESULT 13  
S41427  
cysteine proteinase (PC 3.4.22.-) CP1 precursor - Trichomonas vaginalis  
C:Species: Trichomonas vaginalis  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 04-Feb-2000  
C:Accession: S41427  
R:Mallinson, D.J.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41425  
A:Accession: S41427  
A:Molecule type: mRNA  
A:Residues: 1-309 <MAL>  
A:Cross-references: EMBL:X77218; NID:g452291; PIDN:CAA54435.1; PID:g452292  
A:Experimental source: G3  
C:Genetics:  
A:Gene: CP1  
C:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase  
F:1-89/Domain: signal sequence #status predicted <SIG>  
P:0-309/Product: cysteine proteinase CP1 #status predicted <MAT>  
4,254,274/Active site: Cys, His, Asn #status predicted

Query Match 81.6%; Score 31; DB 2; Length 309;  
Best Local Similarity 83.3%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXH 7  
||| |  
Db 126 QWAVKH 131

RESULT 14  
F82558  
lipopolysaccharide core biosynthesis protein XF2434 [imported] - Xylella fastidiosa (str  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: F82558  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: F82558  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-325 <SIM>  
A:Cross-references: GB:AF004052; GB:AF003849; NID:g9107617; PIDN:AF85233.1; GS148:GN  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, K  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carri  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Ju  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramaci, E.; Ma  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF2434

Query Match 81.6%; Score 31; DB 2; Length 325;  
Best Local Similarity 71.4%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| ||  
Db 6 QWVVLHL 12

## RESULT 15

T17027

MYB-related transcription factor - garden snapdragon

C:Species: Antirrhinum majus (garden snapdragon)

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000

C:Accession: T17027

R:Waites, R.; Selvadurai, H.R.; Oliver, I.R.; Hudson, A.

Cell 93, 779-789, 1998

A:Title: The PHANTASTICA gene encodes a MYB transcription factor involved in growth a

A:Reference number: Z18662; MUID:98292176

A:Accession: T17027

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-357 &lt;WAI&gt;

A:Cross-references: EMBL:AJ005586; NID:g3183616; PIDN:CAA06612.1; PID:g3183617

A:Experimental source: cultivar JI.98; inflorescence

C:Genetics:

A:Gene: phan

C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat hom  
C:Keywords: transcription factor

Query Match 81.6%; Score 31; DB 2; Length 357;  
Best Local Similarity 71.4%; Pred. No. 54;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
||| ||  
Db 330 QWAAKHL 336

Search completed: October 25, 2001, 11:25:22  
Job time: 335 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:57 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-11  
Perfect score: 38  
Sequence: 1 XQWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	8	1 US-08-168-390-12	Sequence 12, Appl
2	36	94.7	8	6 5217955-35	Patent No. 5217955
3	36	94.7	8	6 5217955-36	Patent No. 5217955
4	36	94.7	9	6 5217955-13	Patent No. 5217955
5	36	94.7	9	6 5217955-14	Patent No. 5217955
6	36	94.7	9	6 5217955-15	Patent No. 5217955
7	36	94.7	9	6 5217955-22	Patent No. 5217955
8	35	92.1	8	1 US-08-168-390-11	Sequence 11, Appl
9	35	92.1	8	2 US-08-337-127-9	Sequence 9, Appl
10	35	92.1	8	6 5217955-32	Patent No. 5217955
11	35	92.1	8	6 5217955-34	Patent No. 5217955
12	35	92.1	9	1 US-07-619-747B-1	Sequence 1, Appl
13	35	92.1	9	1 US-07-619-747B-2	Sequence 2, Appl
14	35	92.1	9	1 US-07-619-747B-4	Sequence 4, Appl
15	35	92.1	9	1 US-07-619-747B-5	Sequence 5, Appl
16	35	92.1	9	1 US-07-619-747B-9	Sequence 9, Appl
17	35	92.1	9	1 US-07-619-747B-10	Sequence 10, Appl
18	35	92.1	9	1 US-07-619-747B-12	Sequence 12, Appl
19	35	92.1	9	1 US-07-619-747B-14	Sequence 14, Appl
20	35	92.1	9	1 US-07-619-747B-15	Sequence 15, Appl
21	35	92.1	9	1 US-07-619-747B-17	Sequence 17, Appl
22	35	92.1	9	1 US-07-619-747B-18	Sequence 18, Appl
23	35	92.1	9	1 US-07-619-747B-22	Sequence 22, Appl
24	35	92.1	9	1 US-07-619-747B-23	Sequence 23, Appl
25	35	92.1	9	1 US-07-619-747B-24	Sequence 24, Appl
26	35	92.1	9	1 US-07-619-747B-25	Sequence 25, Appl
27	35	92.1	9	1 US-07-619-747B-26	Sequence 26, Appl

28	35	92.1	9	1 US-07-619-747B-27	Sequence 27, Appl
29	35	92.1	9	1 US-07-619-747B-28	Sequence 28, Appl
30	35	92.1	9	1 US-07-619-747B-29	Sequence 29, Appl
31	35	92.1	9	1 US-07-619-747B-30	Sequence 30, Appl
32	35	92.1	9	1 US-07-619-747B-31	Sequence 31, Appl
33	35	92.1	9	1 US-07-619-747B-32	Sequence 32, Appl
34	35	92.1	9	1 US-07-619-747B-33	Sequence 33, Appl
35	35	92.1	9	1 US-07-619-747B-34	Sequence 34, Appl
36	35	92.1	9	1 US-07-619-747B-35	Sequence 35, Appl
37	35	92.1	9	1 US-07-619-747B-36	Sequence 36, Appl
38	35	92.1	9	1 US-07-619-747B-37	Sequence 37, Appl
39	35	92.1	9	1 US-07-619-747B-38	Sequence 38, Appl
40	35	92.1	9	1 US-07-619-747B-39	Sequence 39, Appl
41	35	92.1	9	1 US-07-619-747B-40	Sequence 40, Appl
42	35	92.1	9	1 US-08-031-325A-37	Sequence 41, Appl
43	35	92.1	9	1 US-08-263-905-4	Sequence 42, Appl
44	35	92.1	9	1 US-08-263-905-5	Sequence 43, Appl
45	35	92.1	9	1 US-08-263-905-6	Sequence 44, Appl

ALIGNMENTS

RESULT 1  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SKS  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "The alanine at position 6  
; OTHER INFORMATION: is dextrorotatory alanine."  
; FEATURE:

NAME/KEY: Modified-site  
 LOCATION: 8  
 OTHER INFORMATION: /note= "The carboxy-terminal  
 OTHER INFORMATION: residue comprises an ethyl ester."  
 US-08-168-390-12

Query Match 94.7%; Score 36; DB 1; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||| ||  
 Db 2 QWAVAHL 8

RESULT 2  
 5217955-35  
 ;Patent No. 5217955  
 ; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
 ; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
 ; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
 ; NUMBER OF SEQUENCES: 42  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 440.039  
 ; FILING DATE: 21-NOV-1989  
 ; APPLICATION NUMBER: 408.125  
 ; FILING DATE: 15-SEP-1989  
 ;SEQ ID NO:35:  
 ; LENGTH: 8  
 5217955-35

Query Match 94.7%; Score 36; DB 6; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||| ||  
 Db 2 QWAVAHL 8

RESULT 3  
 5217955-36  
 ;Patent No. 5217955  
 ; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
 ; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
 ; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
 ; NUMBER OF SEQUENCES: 42  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 440.039  
 ; FILING DATE: 21-NOV-1989  
 ; APPLICATION NUMBER: 408.125  
 ; FILING DATE: 15-SEP-1989  
 ;SEQ ID NO:36:  
 ; LENGTH: 8  
 5217955-36

Query Match 94.7%; Score 36; DB 6; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||| ||  
 Db 2 QWAVAHL 8

RESULT 4  
 5217955-13  
 ;Patent No. 5217955  
 ; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
 ; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
 ; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
 ; NUMBER OF SEQUENCES: 42  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 440.039  
 ; FILING DATE: 21-NOV-1989  
 ; APPLICATION NUMBER: 408.125  
 ; FILING DATE: 15-SEP-1989  
 ;SEQ ID NO:13:  
 ; LENGTH: 9  
 5217955-13

Query Match 94.7%; Score 36; DB 6; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||| ||  
 Db 2 QWAVAHL 8

RESULT 5  
 5217955-14  
 ;Patent No. 5217955  
 ; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
 ; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
 ; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
 ; NUMBER OF SEQUENCES: 42  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 440.039  
 ; FILING DATE: 21-NOV-1989  
 ; APPLICATION NUMBER: 408.125  
 ; FILING DATE: 15-SEP-1989  
 ;SEQ ID NO:14:  
 ; LENGTH: 9  
 5217955-14

Query Match 94.7%; Score 36; DB 6; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
 |||| ||  
 Db 2 QWAVAHL 8

RESULT 6  
 5217955-15  
 ;Patent No. 5217955  
 ; APPLICANT: aBOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE  
 ; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
 ; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
 ; NUMBER OF SEQUENCES: 42  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: 440.039  
 ; FILING DATE: 21-NOV-1989  
 ; APPLICATION NUMBER: 408.125  
 ; FILING DATE: 15-SEP-1989  
 ;SEQ ID NO:15:  
 ; LENGTH: 9  
 5217955-15

; FILING DATE: 15-SEP-1989  
; SEQ ID NO:15:  
; LENGTH: 9  
5217955-15

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
IIIIII  
DB 2 QWAVHL 8

## RESULT 7

5217955-22  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:22:  
; LENGTH: 9  
5217955-22

Query Match 94.7%; Score 36; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
IIIIII  
DB 2 QWAVHL 8

## RESULT 8

US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazayuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "the amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "the carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-11

Query Match 92.1%; Score 35; DB 1; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QWAVXHL 8  
IIIIII  
DB 2 QWAVHL 8

## RESULT 9

US-08-337-127-9  
; Sequence 9, Application US/08337127  
; Patent No. 5877277  
; GENERAL INFORMATION:  
; APPLICANT: COY, David H.  
; APPLICANT: Moreau, Jacques-Pierre  
; APPLICANT: Kim, Sun H.  
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,127  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/779,039  
; FILING DATE: 10/18/91  
; APPLICATION NUMBER: 07/502,438  
; FILING DATE: 03/30/90  
; APPLICATION NUMBER: 07/397,169  
; FILING DATE: 08/21/89  
; APPLICATION NUMBER: 07/376,555  
; FILING DATE: 07/07/89  
; APPLICATION NUMBER: 07/317,941  
; FILING DATE: 03/02/89  
; APPLICATION NUMBER: 07/282,328  
; FILING DATE: 12/09/88  
; APPLICATION NUMBER: 07/257,998

; FILING DATE: 10/14/88  
; APPLICATION NUMBER: 07/248,771  
; FILING DATE: 09/23/88  
; APPLICATION NUMBER: 07/207,759  
; FILING DATE: 06/16/88  
; APPLICATION NUMBER: 07/204,171  
; FILING DATE: 06/08/88  
; APPLICATION NUMBER: 07/173,311  
; FILING DATE: 03/25/88  
; APPLICATION NUMBER: 07/100,571  
; FILING DATE: 09/24/87  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00537/00900D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The sequence contains at  
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,  
; OTHER INFORMATION: and has an methylester C-terminus (i.e., CO<sub>2</sub>CH<sub>3</sub>),  
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., CO<sub>2</sub>H).

US-08-337-127-9

Query Match 92.1%; Score 35; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVGHL 8

RESULT 10  
5217955-32  
; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:32:  
; LENGTH: 8  
5217955-32

Query Match 92.1%; Score 35; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVGHL 8

RESULT 11  
5217955-34

; Patent No. 5217955  
; APPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440,039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:34:  
; LENGTH: 8  
5217955-34

Query Match 92.1%; Score 35; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QWAVXHL 8  
| | | | |  
Db 2 QWAVGHL 8

RESULT 12  
US-07-619-747B-1  
; Sequence 1, Application US/07619747B  
; Patent No. 5244883  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Ren Zhi  
; APPLICANT: Schally, Andrew V.,  
; TITLE OF INVENTION: No. 5244883apeptide Bombesin  
; TITLE OF INVENTION: Antagonists  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Andrew V. Schally  
; STREET: 5025 Kawanne Avenue  
; CITY: Metairie  
; STATE: Louisiana  
; COUNTRY: USA  
; ZIP: 70002

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 360K Diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: WP 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/619,747B  
; FILING DATE: 19901129  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: No. 5244883e  
; FILING DATE: N/A  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Behr, Omri M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908)494-5240  
; TELEFAX: 1-908-494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: peptide

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Db      2 QWAVGHL 8
||||||
RESULT 14
US-07-619-747B-4
; Sequence 4, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; APPLICANT: Schally, Andrew V.,
; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-434-0428
; TELEX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: Position 1 is 5F-D-Trip
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: Isostere of named aminoacid
; US-07-619-747B-4

Query Match 92.1%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels

Qy      2 QWAVXHL 8
||||||
Db      2 QWAVGHL 8

RESULT 15
US-07-619-747B-5
; Sequence 5, Application US/07619747B
; Patent No. 5244883
; GENERAL INFORMATION:
; APPLICANT: Cai, Ren zhi
; APPLICANT: Schally, Andrew V.,

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; TITLE OF INVENTION: No. 5244883apeptide Bombesin
; TITLE OF INVENTION: Antagonists
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Andrew V. Schally
; STREET: 5025 Kawanne Avenue
; CITY: Metairie
; STATE: Louisiana
; COUNTRY: USA
; ZIP: 70002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 360K Diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/619,747B
; FILING DATE: 19901129
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5244883e
; FILING DATE: N/A
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Behr, Omri M.
; REGISTRATION NUMBER: 22,940
; REFERENCE/DOCKET NUMBER: SHAL3.0-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)494-5240
; TELEFAX: 1-908-494-0428
; TELEX: 511642 BEPATEDIN
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION: Position 1 is D-Tpi
; OTHER INFORMATION: Position 8 is a reduced
; OTHER INFORMATION: isostere of named aminoacid
US-07-619-747B-5

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Query Match 92.1%; Score 35; DB 1; Length 9;
St Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 2 QWAVXHL 8
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Db 2 QWAVGHL 8

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Search completed: October 25, 2001, 11:23:57  
Job time: 270 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-11  
Perfect score: 38  
Sequence: 1 XQWAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	94.7	7	10 AAP91147	Sequence of new ne
2	36	94.7	7	13 AAR20585	Antagonist of bomb
3	36	94.7	7	13 AAR32998	[D-Ala1]-bombesin
4	36	94.7	7	20 AAW94610	Bombesin/gastrin r
5	36	94.7	8	3 AAP20294	Bombesin analog pe
6	36	94.7	8	12 AAR11241	Linear litorin ana
7	36	94.7	8	12 AAR11242	Linear litorin ana
8	36	94.7	8	13 AAR29155	Bombesin analogue
9	36	94.7	8	13 AAR29157	Bombesin analogue
10	36	94.7	8	16 AAW64911	Bombesin receptor
11	36	94.7	9	11 AAR09335	Sequence of Bombes

12	36	94.7	9	12 AAR11522	Example of peptide
13	36	94.7	9	12 AAR14865	Peptide analogue #
14	36	94.7	9	12 AAR14866	Peptide analogue #
15	36	94.7	9	12 AAR14867	Peptide analogue #
16	36	94.7	9	12 AAR14873	Peptide analogue #
17	36	94.7	9	14 AAR40903	Bombesin analogue
18	36	94.7	9	19 AAW51195	Peptide derived fr
19	36	94.7	9	19 AAW51201	Peptide derived fr
20	36	94.7	10	10 AAP96113	Sequence of new ne
21	35	92.1	7	22 AAB48341	Bombesin/gastrin r
22	35	92.1	8	11 AAR04531	Non-cyclic analog
23	35	92.1	8	12 AAR11224	Linear litorin ana
24	35	92.1	8	12 AAR11240	Linear litorin ana
25	35	92.1	8	12 AAR14877	Peptide analogue #
26	35	92.1	8	13 AAR28456	Bombesin antagonist
27	35	92.1	8	13 AAR28459	Bombesin antagonist
28	35	92.1	8	16 AAW64910	Bombesin receptor
29	35	92.1	8	19 AAW50941	Bombesin receptor
30	35	92.1	8	20 AAW92740	Bombesin peptide a
31	35	92.1	8	21 AAB08302	Amino acid sequenc
32	35	92.1	8	21 AAB08308	Amino acid sequenc
33	35	92.1	8	22 AAB72406	Bombesin analogue
34	35	92.1	9	11 AAR04526	Non-cyclic analog
35	35	92.1	9	11 AAR04527	Non-cyclic analog
36	35	92.1	9	11 AAR04529	Non-cyclic analog
37	35	92.1	9	11 AAR04528	Non-cyclic analog
38	35	92.1	9	11 AAR04530	Non-cyclic analog
39	35	92.1	9	11 AAR08345	Peptide bombesin
40	35	92.1	9	12 AAR11520	Example of peptide
41	35	92.1	9	12 AAR11521	Example of peptide
42	35	92.1	9	12 AAR11525	Example of peptide
43	35	92.1	9	12 AAR11529	Example of peptide
44	35	92.1	9	12 AAR12033	Bombesin antagonist
45	35	92.1	9	12 AAR14860	Peptide analogue #

ALIGNMENTS

RESULT 1  
AAP91147  
ID AAP91147 standard; protein; 7 AA.  
XX AAP91147:  
XX  
DT 13-MAY-1990 (first entry)  
DT 22-DEC-1990 (corrected)  
XX  
DE Sequence of new neuromedin C deriv.  
XX  
KW Bombesin antagonist; malignant disease; therapy; gastric acid secretion  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /label=OTHER  
FT /note="Ac-D-Gln"  
FT Misc-difference 5 /label=OTHER  
FT /note="D-Ala"  
FT Misc-difference 7 /label=OTHER  
FT /note="Leu-OMe"

XX  
XX EP315367-A.  
XX  
PD 10-MAY-1989.  
XX  
PF 27-OCT-1988; 88EP-0310094.  
XX  
PR 06-JUN-1988; 88GB-0013355.  
XX  
PA (ICIL ) IMPERIAL CHEM INDS PLC.  
XX

PI Camble R, Cotton R, Dutta AS, Hayward CF;  
 XX WPI; 1989-139341/19.  
 XX  
 XX New Neuromedin C polypeptide derivs. -  
 PT are potent bombesin antagonist used for treating malignant  
 PT disease and conditions associated with gastrin or gastric acid  
 PT secretion  
 XX  
 XX Disclosure; Page 929; 49pp; English.  
 XX  
 XX It is a potent bombesin antagonist. It may be used for the treatment of  
 CC e.g. malignant disease, conditions associated with the over-prodn. of  
 CC bombesin and conditions associated with failure of normal physiological  
 CC control of the regulation of gastric acid secretion.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 94.7%; Score 36; DB 10; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 Db 1 qwavahl 7

RESULT 2  
 AAR20585  
 ID AAR20585 standard; Peptide; 7 AA.  
 XX  
 AC AAR20585;  
 XX  
 DT 07-MAY-1992 (first entry)  
 XX  
 DE Antagonist of bombesin/GRP.  
 XX  
 KW Antitumour agent; leukaemia.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 5 /note= "D-Ala"  
 FT  
 XX EP468497-A.  
 XX 29-JAN-1992.  
 XX  
 PF 25-JUL-1991; 91EP-0112504.  
 XX  
 PR 26-JUL-1990; 90US-0558031.  
 XX  
 PA (RICH ) MERRELL DOW PHARM INC.  
 XX  
 PI Krstenansky JL;  
 XX  
 DR WPI; 1992-034251/05.  
 XX  
 XX New peptide bombesin-GRP antagonists - used as antitumour agents  
 PT to treat e.g. leukaemia, small cell lung and prostatic carcinoma  
 PT and to inhibit gastric acid secretion.  
 XX  
 XX Claim 7; Page 12; 14pp; English.  
 XX  
 XX The peptide is modified at the N-terminal with a lauryl, palmitoyl  
 CC or esp. an octanoyl gp. The Leu at position 7 may be absent. The  
 CC C-terminal (Leu or His) is amidated. The peptides and derived  
 CC salts can be used to treat small cell lung carcinoma, prostatic  
 CC carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-  
 CC ciated conditions, and to effect antagonism of bombesin/gastrin  
 CC releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at

CC 5-200 mg/dose.  
 XX Sequence 7 AA;  
 SQ

Query Match 94.7%; Score 36; DB 13; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 Db 1 qwavahl 7

RESULT 3  
 AAR32998  
 ID AAR32998 standard; peptide; 7 AA.  
 XX  
 AC AAR32998;  
 XX  
 DT 13-APR-1993 (first entry)  
 XX  
 DE [D-Ala11]-bombesin(7-13)amide derivs.  
 XX  
 KW Intracellular signal; inhibition; gastrointestinal tract;  
 KW litorin; Gastrin Releasing Peptide; GRP.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /label= OTHER  
 FT /note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,  
 FT N-alpha-lauryl-Gln or N-alpha-palmityl-Gln"  
 FT Misc-difference 5 /note= "D-Ala"  
 FT Modified-site 7 /note= "amidated"  
 FT  
 XX WO9220707-A.  
 XX  
 PN 26-NOV-1992.  
 XX  
 PD 21-APR-1992; 92WO-US03287.  
 XX  
 PF 23-MAY-1991; 91US-0704863.  
 XX  
 PR (RICH ) MERRELL DOW PHARM INC.  
 XX  
 PA Edwards JV, Fanger BO;  
 XX  
 PI WPI; 1992-415707/50.  
 XX  
 DR New bombesin peptide agonists and antagonists - stimulate or  
 PT inhibit digestion, increase susceptibility of tumours to  
 PT chemotherapeutic agents, treat gastric ulcers and tumours etc.  
 XX  
 XX Example; Page 40; 64pp; English.  
 XX  
 XX The peptides in this example are bombesin analogues. The peptides  
 CC were tested in a competitive binding assay and a Phosphatidyl Inositol  
 CC (PI)-turnover assay in mouse pancreas. None of the peptides  
 CC demonstrated agonist activity but all inhibited PI-turnover (c.f.  
 CC stimulation produced by 100nM GRP). Analogues of bombesin are  
 CC potentially useful for growth therapy and the treatment of digestive  
 CC disorders, e.g. for stimulating digestion, stimulating growth of  
 CC tissue in the lung, pancreas and intestine, stimulating NK cell  
 CC activity against tumour cells and stimulating growth of tumours to  
 CC increase susceptibility to chemotherapeutic agents.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 94.7%; Score 36; DB 13; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QMAVXHL 8  
Db 1 qwavahl 7

RESULT 4  
ID AAW94610 standard; peptide; 7 AA.  
AC AAW94610;  
DT 27-APR-1999 (first entry)  
XX Bombesin/gastrin releasing peptide type inhibitor peptide #2.  
DE Bombesin: gastrin releasing peptide; GRP; inhibitor; antagonist;  
XX small cell lung carcinoma; tumour; frog; antimitotic; antisecretory;  
XX peptic ulcer.  
OS Synthetic.  
OS Bombina bombina.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 1 /note- "optionally modified by octanoyl, lauroyl or  
FT Modified-site 7 palmitoyl"  
FT Modified-site 7 /note- "amidated"  
XX  
XX US5834433-A.  
XX  
XX 10-NOV-1998.  
XX  
XX 23-FEB-1996; 96US-0960130.  
XX  
XX 24-JUL-1991; 91US-0735402.  
XX 26-JUL-1990; 90US-0558031.  
XX 21-JUL-1994; 94US-0278692.  
XX 23-MAY-1995; 95US-0447528.  
XX 23-FEB-1996; 96US-0960130.  
XX  
XX (RICH ) MERRELL PHARM INC.  
XX  
XX Kristenansky JL;  
XX WPI; 1999-141255/12.  
XX  
XX New peptide antagonists of bombesin or gastrin releasing peptide -  
XX are useful as antimitotic and antisecretory agents in treating,  
XX e.g., small cell lung carcinoma or peptic ulcers  
XX  
XX Claim 5; Column 14; 9pp; English.  
XX  
XX The present sequence represents a bombesin/gastrin releasing peptide  
XX type inhibitor peptide. The peptide may be used as an antimitotic and  
XX antisecretory peptide. It can control growth of small cell lung and  
XX prostatic carcinomas, and it can also inhibit gastric secretions which  
XX are causative and symptomatic of peptic ulcers. Administration may be  
XX oral but is preferably subcutaneous, intravenous, intramuscular or  
XX intraperitoneal, by depot injection, by implant preparation or by  
XX application to the mucous membranes (e.g. of the nose or bronchial  
XX tubes) by aerosol.  
XX  
XX Sequence 7 AA:

Query Match 94.7%; Score 36; DB 20; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QMAVXHL 8  
Db 1 qwavahl 7

RESULT 5  
ID AAP20294 standard; peptide; 8 AA.  
AC AAP20294;  
DT 09-DEC-1992 (first entry)  
XX Bombesin analog peptide.  
XX Bombesin; hypothermic; analgesic.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 1 /label= D-Glu  
FT Misc-difference 5 /label= D-Ala  
XX  
XX US4331661-A.  
XX  
XX 25-MAY-1982.  
XX  
XX 03-OCT-1980; 80US-0193621.  
XX  
XX 03-OCT-1980; 80US-0193621.  
XX  
XX (SALK-) SALK INST BIOLOGICA.  
XX  
XX Markl WE, Brown MR, Rivier JEF;  
XX WPI; 1982-48049E/23 (48049E).  
XX  
XX Octa-peptide bombesin analogues - having hypothermic and  
XX analgesic props.  
XX  
XX Claim 8; Column 8; 5pp; English.  
XX  
XX The peptide may be preceded by a formyl, acetyl, propionyl, acetyl  
XX or benzoyl group at its C-terminal. The peptide may be used : r  
XX reducing the body temp. of a mammal, as well as for inducing  
XX analgesia. It produces hypothermia when injected i.c., but not  
XX when given i.v. or s.c. See also AAP20291-3.  
XX  
XX Sequence 8 AA:

Query Match 94.7%; Score 36; DB 3; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0.  
QY 2 QMAVXHL 8  
Db 1 qwavahl 7

RESULT 6  
ID AAR11241 standard; Protein; 8 AA.  
AC AAR11241;  
XX  
XX 17-MAY-1991 (first entry)  
DT  
XX  
XX Linear litorin analogue (III).  
DE  
XX

KW Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 KW diabetes.  
 XX Synthetic.  
 OS  
 XX  
 FT Key Location/Qualifiers  
 FT Modified-site 1..1  
 FT /label= D-p-chloro-phenylalanine  
 XX  
 XX MO9102746-A.  
 XX  
 XX PD 07-MAR-1991.  
 XX  
 XX PF 17-AUG-1990; 90WO-US04646.  
 XX  
 XX PR 21-AUG-1989; 89US-0397169.  
 XX PR 30-MAR-1990; 90US-0502438.  
 XX  
 PA (TULA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.  
 PI  
 PI COY DH, Moreau JP, Kim SH;  
 DR WPI; 1991-087241/12.  
 XX  
 PT New linear peptide analogues of bombesin - modified to eliminate  
 PT biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.  
 XX  
 XX PS Claim 18; Page 54; 58pp; English.  
 XX  
 CC This peptide is a specifically claimed example of a generic  
 CC formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to an amide and Phe 8 has been replaced  
 CC by beta-leu. Gly 6 has also been replaced by D-Ala.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, arteriosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological  
 CC activity.  
 CC The analogue may also be of a naturally occurring peptide  
 CC terminating at the C-terminus with a Met residue, such as the  
 CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
 CC bombesin.  
 CC See also AAR11239-242.  
 CC  
 XX  
 XX SQ Sequence 8 AA;  
 SQ

Query Match 94.7%; Score 36; DB 12; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 2 gwavahl 8

RESULT 7  
 AAR11242  
 ID AAR11242 standard; Protein; 8 AA.  
 XX  
 AC AAR11242;  
 XX  
 XX DT 17-MAY-1991 (first entry)  
 XX  
 XX DE Linear litorin analogue (IV).  
 XX  
 KW Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 KW diabetes.  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Modified-site 1..1  
 FT /label=D-Phe, pentafuoro-Phe  
 FT Modified-site 6..6  
 FT /label= N-methyl-D-Ala  
 XX  
 XX MO9102746-A.  
 XX  
 XX PD 07-MAR-1991.  
 XX  
 XX PF 17-AUG-1990; 90WO-US04646.  
 XX  
 XX PR 21-AUG-1989; 89US-0397169.  
 XX PR 30-MAR-1990; 90US-0502438.  
 XX  
 PA (TULA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.  
 PI  
 PI COY DH, Moreau JP, Kim SH;  
 DR WPI; 1991-087241/12.  
 XX  
 PT New linear peptide analogues of bombesin - modified to eliminate  
 PT biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.  
 XX  
 XX PS Claim 20+21; Page 54; 58pp; English.  
 XX  
 CC These peptides are specifically claimed examples of a generic  
 CC formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to a methyl ester.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, arteriosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological  
 CC activity.  
 CC The analogue may also be of a naturally occurring peptide  
 CC terminating at the C-terminus with a Met residue, such as the  
 CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
 CC bombesin.  
 CC See also AAR11239-242.  
 CC  
 XX  
 XX SQ Sequence 8 AA;  
 SQ

Query Match 94.7%; Score 36; DB 12; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 2 gwavahl 8

RESULT 8  
 AAR29155  
 ID AAR29155 standard; peptide; 8 AA.  
 XX  
 AC AAR29155;  
 XX  
 XX DT 16-APR-1993 (first entry)  
 XX  
 XX DE Bombesin analogue (5).  
 XX  
 KW Hepatoma; liver cancer; antagonist.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1  
 FH /note= "D-form residue"  
 FT Modified-site 6  
 FT /note= "NMe-D-Ala"

PI	Bodgen AE, Coy DH, Kim SH, Moreau J;
XX	
DR	WPI; 1992-415466/50.
XX	
PT	Treatment of hepatoma - by admin. of admixed bombesin analog
PT	with carrier
XX	
PS	Claim 15; Page 48; 54pp; English.
CC	
CC	The peptide is an example of a highly generic formula. It is
CC	in a medicament for treating hepatoma. The cpd. acts as ant
CC	to bombesin, which has been detected in a number of human cai
CC	lines.
XX	
SQ	Sequence 8 AA;
XX	
Query Match	94.7%; Score 36; DB 13; Length 8;
Best Local Similarity	85.7%; Pred. No. 3.4e+05;
Matches 6; Conservative	0; Mismatches 1; Indels
OY	2 QMAVXHL 8
Db	2 qwavahl 8
RESULT	10
AAW64911	
AAW64911	standard; peptide; 8 AA.

XX		RESULT 10
XX	AAM64911	
ID	AAM64911 standard; peptide; 8 AA.	
AC	AAM64911;	
DT	06-JUL-1999 (first entry)	
DE	Bombesin receptor antagonist.	
KM	Bombesin; antagonist; chlorambucil; peptic ulcer; pancreaticitis; eating disorder; diabetes; acromegaly; enterocutaneous fistula; psoriasis; growth retardation; gastrointestinal motility disorders antitumour.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Modified-site	1
FT	/note= "The amino terminal is acylated with acetamido- bromacetyl, chloroacetyl, [bis(2-chloroethyl) amide], L-phenylalanine or a chlorambucil group"	
FT	Modified-site	8
FT	/note= "The carboxy terminal is in the form of ethyl ester"	
PN	WO9500542-A1.	
PD	05-JAN-1995.	
PE	15-JUN-1994; 94MO-US06757.	
PR	17-DEC-1993; 93US-0168390.	
PR	18-JUN-1993; 93US-0078062.	
PA	(PEPT-) PEPTIDE TECHNOLOGIES CORP.	
PI	Chandrasekhar B, Knight M, Takahashi K;	
DR	WPI; 1995-052004/07.	
PT	New bombesin, gastrin releasing peptide or Neuromedin B or C derivatives disorders, psoriasis and cancers	
PS	Claim 6; Page 34; 45pp; English.	

CC The patent discloses (1) the peptide sequence of bombesin (BBN),  
 CC gastrin releasing peptide (GRP), Neurexmedin B or Neurexmedin C,  
 CC the peptide sequence having a chlorambutil group attached to the  
 CC amino terminal; (2) a BBN receptor antagonist of formula  
 CC R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
 CC antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
 CC In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
 CC Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
 CC amino]-L-phenylalanine or a chlorambutil group; and R5 = Gln or His.  
 CC The compounds act as potent BBN/GRP-like peptide antagonists. They  
 CC can be used to inhibit the growth of cells that are sensitive to the  
 CC growth-promoting effects of BBN, GRP or a related peptide such as  
 CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
 CC cancerous cells or tumours. They can also be used to inhibit the  
 CC binding of BBN, GRP or a related peptide to cells capable of such  
 CC binding. They can be used for treating e.g. peptic ulcer, pancreatitis,  
 CC eating disorders, diabetes, acromegaly, enterocutaneous fistula,  
 CC psoriasis, growth retardation, gastrointestinal motility disorders or  
 CC tumours. The terminal structures of the compounds protect them from  
 CC in vivo proteolysis and provide highly potent antagonist effects that  
 CC persist for extended periods of time upon administration.

SQ Sequence 8 AA;

Query Match 94.7%; Score 36; DB 16; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 2 qwavahl 8

RESULT 11

AAR09335 AAR09335 standard; peptide; 9 AA.

AC AAR09335;

DT 30-MAR-1992 (first entry)

DE Sequence of Bombesin receptor peptide ligand with irreversible  
 DE effects.

KW Bombesin receptor; agonist; antagonist.

Key Location/Qualifiers

Modified-site 1  
 /label= H-pMel  
 /note= "pMel= p-bls (2-chloroethyl)  
 amino-L-phenylalanine"

Modified-site 9  
 /label= Met-NH2

WO9001037-A.

08-FEB-1990.

19-JUL-1989; 89WO-EP00842.

28-MAR-1989; 89GB-0006900.

21-JUL-1988; 88GB-0017379.

(FARM) FARMITALIA C ERBA SPA.

de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciomel M,  
 Molinari I;

WPI: 1990-067161/09.

Bombesin receptor peptide ligands with irreversible effects - as  
 agonists and antagonists both weak and strong

XX Claim 2; Page 26; 32pp; English.

CC The inventors claim 36 peptides. Also claimed are:  
 CC (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.  
 CC of the peptides.

SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 11; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 2 qwavahl 8

RESULT 12

AAR11522 AAR11522 standard; Protein; 9 AA.

AC AAR11522;

DT 13-JUN-1991 (first entry)

DE Example of peptide agonist of GRP, neuromedin, bombesin and 1,1'-in.

KW Non-malignant proliferative disease; cancer.

Key Location/Qualifiers

Modified-site 1.1  
 /label= OTHER  
 /note= "D-p-chlorophenylalanine"

WO9104040-A.

04-APR-1991.

17-SEP-1990; 90WO-US05271.

05-MAY-1990; 90US-0520225.

15-SEP-1989; 89US-0408125.

21-NOV-1989; 89US-0440039.

(BIOM-) BIOMEASURE INC.

Bogden AE, Moreau J-P;

WPI: 1991-117320/16.

Treatment of non malignant proliferative disease and cancer, by  
 administration of natural peptide or fragment selected from  
 gastrin-releasing peptide, neuromedin, amphibian bombesin or  
 litorin

Claim 22; page 54; 73pp; English.

This is a peptide analogue of mammalian gastrin releasing peptide  
 (GRP), neuromedin-B or -C, amphibian bombesin and litorin.  
 It is an agonist of these cpds. and is used to treat smooth muscle  
 proliferation and cancer of the prostate, breast or lung.  
 Residue 6 (Ala) is D-alanine.  
 See also AAR11519-21 and AAR11523-30.

SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 ||||| 11  
 Db 2 qwavahl 8

RESULT 13  
 AARI4865  
 ID AARI4865 standard; Protein; 9 AA.

AC AARI4865;

DT 14-FEB-1992 (first entry)

DE Peptide analogue #6 of litorin, GRP, neuromedin or bombesin.

KW tissue proliferation; gastrin related peptide; peptide hormone.

OS Synthetic.

Key Modified-site 1 Location/Qualifiers

FT Modified-site 6 /label= D-Phe

FT Modified-site 6 /label= D-Ala

PN MO9117181-A.

PD 14-NOV-1991.

PF 09-MAY-1991; 91WO-0003265.

PR 09-MAY-1990; 90US-0520226.

PA (TULANE ) TULANE E FUND ADMINISTRATOR.

PI (BIOM-) BIOMEASURE INC.

PI Coy DH, Kim SH, Moreau JP;

DR WPI; 1991-353721/48.

PT Peptide agonists of litorin, gastrin releasing peptide -

PT neuromedin B or C or bombesin, for treating cancer, preventing

PT smooth muscle proliferation and suppressing appetite and alcohol

PS Claim 8; Page 18; 25pp; English.

XX The C-terminal residue is amidated. This peptide is one of 27

CC Specific examples of a highly generic formula. The peptides are all

CC analogues of either litorin; the 10 amino acid C-terminal region of

CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid

CC C-terminal region of amphibian bombesin. They act as at least partial

CC agonists of the natural peptides. The peptide analogues are made by

CC standard methods of synthesis and can be cyclised.

CC See AARI4860-R14880 and AARI5035-R15040.

XX SQ Sequence 9 AA;

OY 2 QWAVXHL 8

||||| 11

Db 2 qwavahl 8

RESULT 14

AARI4866

ID AARI4866 standard; Protein; 9 AA.

XX AC AARI4866;

XX 14-FEB-1992 (first entry)

DE Peptide analogue #7 of litorin, GRP, neuromedin or bombesin

KW tissue proliferation; gastrin related peptide; peptide hormone;

OS Synthetic.

Key Modified-site 1 Location/Qualifiers

FT Modified-site 6 /label= D-Phe

FT Modified-site 6 /label= D-Ala

PN MO9117181-A.

PD 14-NOV-1991.

PF 09-MAY-1991; 91WO-0003265.

PR 09-MAY-1990; 90US-0520226.

PA (TULANE ) TULANE E FUND ADMINISTRATOR.

PI (BIOM-) BIOMEASURE INC.

PI Coy DH, Kim SH, Moreau JP;

DR WPI; 1991-353721/48.

PT Peptide agonists of litorin, gastrin releasing peptide -

PT neuromedin B or C or bombesin, for treating cancer, preventing

PT smooth muscle proliferation and suppressing appetite and alcohol

PS Claim 9; Page 18; 25pp; English.

XX The C-terminal residue is amidated. This peptide is one of 27

CC Specific examples of a highly generic formula. The peptides are all

CC analogues of either litorin; the 10 amino acid C-terminal region of

CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid

CC C-terminal region of amphibian bombesin. They act as at least partial

CC agonists of the natural peptides. The peptide analogues are made by

CC standard methods of synthesis and can be cyclised.

CC See AARI4860-R14880 and AARI5035-R15040.

XX SQ Sequence 9 AA;

OY 2 QWAVXHL 8

||||| 11

Db 2 qwavahl 8

RESULT 15

AARI4867

ID AARI4867 standard; Protein; 9 AA.

XX AC AARI4867;

DT 14-FEB-1992 (first entry)

DE Peptide analogue #8 of litorin, GRP, neuromedin or bombesin

KW tissue proliferation; gastrin related peptide; peptide hormone

OS Synthetic.

XX Key

XX Location/Qualifiers

FT Modified-site 1  
 FT /label= OTHER  
 FT /note= "D-para-chloro-Phe"  
 FT Modified-site 6  
 FT /label= D-Ala  
 XX  
 PN WO9117181-A.  
 XX  
 PD 14-NOV-1991.  
 XX  
 PF 09-MAY-1991; 91MO-0003265.  
 XX  
 PR 09-MAY-1990; 90US-0520226.  
 XX  
 PA (TULANE ) TULANE E FUND ADMINISTRA.  
 PA (BIOM- ) BIOMEASURE INC.  
 XX  
 PI Coy DH, Kim SH, Moreau JP;  
 XX  
 WI: 1991-353721/48.  
 PT Peptide agonists of litorin, gastrin releasing peptide -  
 PT neuromedin B or C or bombesin, for treating cancer, preventing  
 PT smooth muscle proliferation and suppressing appetite and alcohol  
 PT craving  
 XX  
 PS Claim 10; Page 18; 25pp; English.  
 XX  
 CC The C-terminal residue is amidated. This peptide is one of 27  
 CC specific examples of a highly generic formula. The peptides are all  
 CC analogues of either litorin; the 10 amino acid C-terminal region of  
 CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid  
 CC C-terminal region of amphibian bombesin. They act as at least partial  
 CC agonists of the natural peptides. The peptide analogues are made by  
 CC standard methods of synthesis and can be cyclised.  
 CC See AARI4860-R14880 and AARI5035-R15040.  
 XX  
 SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QNAAVXHL 8  
 IIII II  
 DB 2 gwavahl 8

Search completed: October 25, 2001, 11:22:46  
 Job time: 219 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:27:45 ; Search time 135.34 Seconds

(without alignments)  
7.821 Million cell updates/sec

Title: US-09-630-333-12

Perfect score: 38

Sequence: 1 XQNAVXHL 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 425026

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP-archaea:\*
- 2: SP-bacteria:\*
- 3: SP-fungi:\*
- 4: SP-human:\*
- 5: SP-invertebrate:\*
- 6: SP-mammal:\*
- 7: SP-mhc:\*
- 8: SP-organelle:\*
- 9: SP-phage:\*
- 10: SP-plant:\*
- 11: SP-rodent:\*
- 12: SP-unclassified:\*
- 13: SP-vertebrate:\*
- 14: SP-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	86.8	517	14	Q9DSP4	Q9dsp4 saint croix
2	32	84.2	174	10	Q9M2H1	Q9m2h1 arabidopsis
3	32	84.2	328	2	Q9X5G8	Q9x5g8 streptomyces
4	32	84.2	353	5	Q21051	Q21051 caenorhabditis
5	32	84.2	806	13	Q9DDI2	Q9ddi2 brachydanio
6	31	81.6	95	2	Q911X2	Q911x2 pseudomonas
7	31	81.6	98	14	Q64981	Q64981 artichoke 1
8	31	81.6	119	13	Q90253	Q90253 bombina ori
9	31	81.6	183	2	Q9R251	Q9r251 delinococcus
10	31	81.6	216	11	Q9JW34	Q9jw34 mus musculus
11	31	81.6	232	3	Q9GVE4	Q9gve4 zygosacchar
12	31	81.6	236	2	Q85726	Q85726 streptomyces
13	31	81.6	256	3	Q9P6Y1	Q9p6y1 neosporea
14	31	81.6	266	5	Q9VZF7	Q9vzf7 drosophila
15	31	81.6	273	8	Q9TJ05	Q9tj05 prototheca
16	31	81.6	309	5	Q27106	Q27106 trichomonas
17	31	81.6	325	2	Q9PAR1	Q9par1 xylella fast
18	31	81.6	357	10	Q65366	Q65366 antirrhinum
19	31	81.6	359	10	Q9FUK9	Q9fuk9 pisum sativ

20	31	81.6	675	10	Q9S9V7	Q9s9v7 arabidopsis
21	31	81.6	696	5	Q9VCU2	Q9vcu2 drosophila
22	31	81.6	703	10	Q9LYH3	Q9lyh3 arabidopsis
23	31	81.6	1273	4	Q9ND68	Q9nd68 homo sapien
24	31	81.6	1275	4	Q15057	Q15057 homo sapien
25	30	78.9	23	13	Q9PS30	Q9ps30 oncorhynchus
26	30	78.9	132	2	Q9K3V3	Q9k3v3 streptomyces
27	30	78.9	157	13	Q918Z9	Q918z9 carassius auratus
28	30	78.9	170	2	P74711	P74711 synecocyst
29	30	78.9	224	4	Q9U1Z8	Q9u1z8 homo sapien
30	30	78.9	252	4	Q26248	Q26248 metanact
31	30	78.9	252	10	Q9F120	Q9f120 arabidopsis
32	30	78.9	276	2	Q9L105	Q9l105 streptomyces
33	30	78.9	283	2	Q9PCE4	Q9pce4 xylella fast
34	30	78.9	291	14	Q72694	Q72694 leishmania
35	30	78.9	311	2	Q9PAE5	Q9pae5 xylella fast
36	30	78.9	318	2	Q91066	Q91066 pseudomonas
37	30	78.9	325	2	Q9K6G2	Q9k6g2 streptomyces
38	30	78.9	375	5	Q9TVM5	Q9tvm5 carnotaurus
39	30	78.9	453	10	Q9MAA9	Q9maa9 pisum sativ
40	30	78.9	520	10	Q65815	Q65815 leishmania
41	30	78.9	691	2	Q55726	Q55726 synechocyst
42	30	78.9	700	2	Q07711	Q07711 staphylococcus
43	30	78.9	719	14	P87541	P87541 bailey milled
44	30	78.9	721	2	Q9K7H4	Q9k7h4 bacillus subtilis
45	30	78.9	858	5	Q17647	Q17647 caenorhabditis

## ALIGNMENTS

RESULT	ID	Q9DSP4	PRELIMINARY	PRT	517 AA
AC	Q9DSP4	Q9DSP4	Q9DSP4	Q9DSP4	Q9DSP4
DT	01-MAR-2001	(TREMBLrel. 16, Created)			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)			
DE	NSI.	Saint Croix river virus.			
OS	NSI.	Saint Croix river virus.			
OC	Viruses; dsRNA viruses; Reoviridae; Orbivirus.				
OX	NCBI_Taxid=104581;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Attoui H., De Micco P., de Lamballerie X.;				
RT	*Complete nucleotide sequence of Saint Croix river virus.*				
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF145403; AAC34262.1; -				
SO	SEQUENCE	517 AA; 58030 MW; 0104A543FB2A1B1A CRC64;			

Query Match	86.8%	Score 33	DB 14	Length 517
Best Local Similarity	71.4%	Pred. No. 51		
Matches	5	Conservative	1	Mismatches 0, Indels 0, Gaps 0
QY	2 QNAVXHL 8			
	:			
DB	500 QMALAHL 506			
RESULT	2			
Q9M2H1				
ID	Q9M2H1	PRELIMINARY	PRT	174 AA.
AC	Q9M2H1			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	HYPOHETICAL 19.2 KDA PROTEIN.			
GN	F14P22.40.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustatus II;			
OC	Brassicales; Brassicaceae; Arabidopsis.			

OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,  
 RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL137082; CAB68183.1; -  
 KW Hypothetical protein  
 SQ SEQUENCE 174 AA; 19189 MW; 4C27267C5E53B4DB CRC64;

QY 2 QMAVXHL 8  
 :|||||  
 47 EMAYVDHL 53

Query Match 84.2%; Score 32; DB 10; Length 174;  
 Best Local Similarity 71.4%; Pred. No. 27;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3  
 ID Q9X5G8 PRELIMINARY; PRT; 328 AA.  
 AC Q9X5G8;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE PUTATIVE DEACETYLCEPHALOSPORIN C ACETYLTRANSFERASE.  
 GN CVM4.  
 OS Streptomyces clavuligerus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRRL 3585;  
 RC MEDLINE=99240369; PubMed=10223939;  
 RA Mosher R.H., Paradkar A.S., Anders C., Barton B., Jensen S.E.;  
 RT "Genes specific for the biosynthesis of clavam metabolites antipodal  
 to clavulanic acid are clustered with the gene for clavaminic  
 synthase 1 in Streptomyces clavuligerus.";  
 RL Antimicrob. Agents Chemother. 43:1215-1224(1999).  
 CC -1- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.  
 DR EMBL: AF124929; AAD30471.1; -  
 DR InterPro: IPR000073; -  
 DR Pfam: PR00561; abhydrolase; 1.  
 DR Transferrase; Forin.  
 SQ SEQUENCE 328 AA; 34642 MW; 4CB78DAD5215034 CRC64;

QY 2 QMAVXHL 7  
 :|||||  
 DB 133 QMAVSH 138

Query Match 84.2%; Score 32; DB 2; Length 326;  
 Best Local Similarity 83.3%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4  
 ID Q21051 PRELIMINARY; PRT; 353 AA.  
 AC Q21051;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE COSMID F59G1.  
 DE F59G1.4.  
 GN Caenorhabditis elegans.  
 OS

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderiinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Latreille P.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U53352; AAC71158.1; -  
 SQ SEQUENCE 353 AA; 40061 MW; 7961772B498E3052 CRC64;

QY 2 QMAVXHL 8  
 :|||||  
 DB 201 EMAYVHLL 207

Query Match 84.2%; Score 32; DB 5; Length 353;  
 Best Local Similarity 71.4%; Pred. No. 55;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 5  
 ID Q9DDL2 PRELIMINARY; PRT; 806 AA.  
 AC Q9DDL2;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE PARACASPASE.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11090634;  
 RA Uren A.G., O'Rourke K., Aravind L., Pisabarro M.T., Seshagiri S.,  
 RA Koonin E.V., Dixit V.M.;  
 RT "Identification of Paracaspases and Metacaspases. Two Ancient Families  
 of Caspase-Like Proteins, One of which Plays a Key Role in MALT  
 Lymphoma.";  
 RL Mol. Cell 6:961-967(2000).  
 DR EMBL: AF316598; AAG38590.1; -  
 SQ SEQUENCE 806 AA; 90754 MW; 589A8BC2013B0A51 CRC64;

Query Match 84.2%; Score 32; DB 13; Length 806;  
 Best Local Similarity 57.1%; Pred. No. 1,36+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||: ||:  
 DB 559 QMAIAHV 565

RESULT 6  
 ID Q911X2 PRELIMINARY: PRT: 95 AA.  
 AC Q911X2:  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE HYPOTHETICAL PROTEIN PA2143.  
 GN PA2143.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 CC Pseudomonas.  
 NCBI\_TaxID=287;  
 [1]  
 [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lartig K., Llm R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reiter J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL: AE004641; AAC05531.1; -.  
 KW Hypothetical protein  
 SQ SEQUENCE 95 AA; 10821 MW; 57335D0CD0841F CRC64;

Query Match 81.6%; Score 31; DB 2; Length 95;  
 Best Local Similarity 71.4%; Pred. No. 23;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 7  
 ID Q64981 PRELIMINARY: PRT: 98 AA.  
 AC Q64981:  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)  
 DE MRNA UNKNOWN FUNCTION (523BP).  
 OS Arlichoke latent polyvirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;  
 OC Polyvirus.  
 NCBI\_TaxID=46076;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Grieco F.;  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: X87255; CAA60708.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 98 AA; 11570 MW; C4A6316685E31078 CRC64;

Query Match 81.6%; Score 31; DB 14; Length 98;  
 Best Local Similarity 83.3%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8  
 ID Q90253 PRELIMINARY: PRT: 119 AA.  
 AC Q90253:  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE PHE-13 BOMBESIN PREPROHORMONE.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina  
 NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96205965; PubMed=8631814;  
 RA Nagalla S.R., Barry B.J., Fallick A.M., Gibson B.W., Taylor J.,  
 RA Dong J.Z., Spindel E.R.;  
 RT "There are three distinct forms of bombesin. Identification of  
 RT [Leu13]bombesin, [Phe13]bombesin, and [Ser3,Arg10,Phe13]bombe... in  
 RT the frog Bombina orientalis.";  
 RL J. Biol. Chem. 271:7731-7737(1996).  
 DR EMBL: U49450; AAC59784.1; -.  
 DR InterPro: IPR000874; -.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 FT CHAIN 45  
 SQ SEQUENCE 119 AA; 13888 MW; 3C9BDF367441E99A CRC64;

Query Match 81.6%; Score 31; DB 13; Length 119;  
 Best Local Similarity 83.3%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9  
 ID Q9R251 PRELIMINARY: PRT: 183 AA.  
 AC Q9R251:  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE HYPOTHETICAL 20.5 KDA PROTEIN.  
 GN DRA0103.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.  
 OC NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RI;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski J.,  
 RA Makarova K.S., Aravind L., Daly M.J., Miron K.W., Fleischmann W.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RT radiodurans RI.";  
 RL Science 286:1571-1577(1999).  
 DR EMBL: AE001862; AAF12366.1; -.  
 DR TIGR: DRA0103; -.  
 KW Hypothetical protein  
 SQ SEQUENCE 183 AA; 20468 MW; 6EEAB3B483DC1BB7 CRC64;

Query Match 81.6%; Score 31; DB 2; Length 183;

Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 2 QWAVXHL 8  
DB 49 KMAVPHL 55

RESULT 10  
O9JMJ34 PRELIMINARY; PRT; 216 AA.  
AC O9JMJ34:  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE OLFACTORY RECEPTOR (FRAGMENT).  
OS Mus musculus domesticus (western European house mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
NCBI\_TaxID=10092;  
OX NCBI\_TaxID=10092;  
RN [1]  
SEQUENCE FROM N.A.  
MEDLINE-20183981; PubMed-10706615;  
Rouquier S., Blancher A., Giorzi D.;  
"The olfactory receptor gene repertoire in primates and mouse:  
Evidence for reduction of the functional fraction in primates.";  
Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).  
DR EMBL; AF073967; AAD43416.1; -  
DR InterPro; IPR000276; -  
DR Pfam; PR00001; 7tm\_1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEPTOR; UNKNOWN\_1.  
KM Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 216 216  
SQ SEQUENCE 216 AA; 24097 MW; B2732A1870584D47 CRC64;

Query Match  
Best Local Similarity 81.6%; Score 31; DB 11; Length 216;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WAVXHL 8  
DB 82 WAVSHL 87  
RESULT 11  
O9UYE4 PRELIMINARY; PRT; 232 AA.  
AC O9UYE4:  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, last annotation update)  
DE HYPOTHEICAL 26.4 KDA PROTEIN.  
OS Zygosaccharomyces rouxi (Candida mogii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
NCBI\_TaxID=4956;  
OX NCBI\_TaxID=4956;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN-CBS 732;  
RA Sychrova H., Braun V., Potler S., Souciet J.L.;  
"Genomic organization of Pichia sorbitophila and Zygosaccharomyces  
rouxi genomes: comparison with Saccharomyces cerevisiae.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y18560; CAB62288.1; -  
DR InterPro; IPR001601; -  
KW Hypothetical protein.  
SQ SEQUENCE 232 AA; 26369 MW; 43CD832A6ED7F6B4 CRC64;

Query Match  
Best Local Similarity 81.6%; Score 31; DB 3; Length 232;  
Matches 5; Conservative 71.4%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2 QWAVXHL 8  
DB 140 QMCVGH 146

RESULT 12  
O85726 PRELIMINARY; PRT; 236 AA.  
AC O85726:  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)  
DE CEPHALOSPORIN HYDROXYLASE CMCT.  
GN CMCT.  
OS Streptomyces clavuligerus.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxID=1901;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=NRRL 3585;  
RX MEDLINE=98361893; PubMed=9696752;  
RA Alexander D.C., Jensen S.E.;  
"Investigation of the Streptomyces clavuligerus cephamycin C gene  
cluster and its regulation by the Ccar protein.";  
J. Bacteriol. 180:4068-4079(1998).  
DR EMBL; AF073896; AAC32491.1; -  
SQ SEQUENCE 236 AA; 27584 MW; FD1EFLB650AF8070 CRC64;

Query Match  
Best Local Similarity 81.6%; Score 31; DB 2; Length 236;  
Matches 5; Conservative 71.4%; Pred. No. 59;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

OY 2 QWAVXHL 8  
DB 170 KWAVDHL 176  
RESULT 13  
O9P6Y1 PRELIMINARY; PRT; 256 AA.  
AC O9P6Y1:  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE CONSERVED HYPOTHEICAL PROTEIN.  
GN 13E11.350.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
NCBI\_TaxID=5141;  
OX NCBI\_TaxID=5141;  
RN [1]  
SEQUENCE FROM N.A.  
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
Wakamura G., Mewes H.W., Mannhaupt G.;  
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
SEQUENCE FROM N.A.  
RA German Neurospora genome project;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL533820; CAB88603.1; -  
DR InterPro; IPR001601; -  
SQ SEQUENCE 256 AA; 27789 MW; 5251PBC58B6BDD9 CRC64;

Query Match  
Best Local Similarity 81.6%; Score 31; DB 3; Length 256;  
Matches 5; Conservative 71.4%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 2; Indels 2; Gaps 0;



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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:28:30 ; Search time 40.36 Seconds  
(without alignments)  
6.790 Million cell updates/sec

Title: US-09-630-333-12  
Perfect score: 38  
Sequence: 1 XQWAVXHL 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Minimum number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	14	ALYT_ALYOB	P08944 alytes obst
2	35	92.1	107	BOMB_BOMVA	P01296 bomblina var
3	35	92.1	119	BOMB_BOMOR	P21596 bomblina ori
4	31	81.6	9	LITO_LITAU	P08945 litorea aur
5	31	81.6	13	BOWL_PSEGU	P42891 pseudophryn
6	31	81.6	82	RANA_RANPI	P08950 rana pipien
7	31	81.6	232	YB9H_YEAST	P38340 saccharomyc
8	31	81.6	263	IML2_DROME	Q09024 drosophila
9	31	81.6	265	IHA_SHEEP	P38440 ovis aries
10	31	81.6	360	IHA_BOVIN	P07994 bos taurus
11	31	81.6	364	IHA_PIG	P04087 sus scrofa
12	31	81.6	366	IHA_MOOSE	Q04997 mus muscula
13	31	81.6	366	IHA_RAT	P17490 rattus norv
14	31	81.6	769	SWI6_KIULA	P40418 kluyveromyc
15	30	78.9	10	GRP_RANRI	P23260 rana ridibu
16	30	78.9	25	GRP_SCYCA	P09472 scyliorhinu
17	30	78.9	27	GRP_CANFA	P08986 canis famill
18	30	78.9	27	GRP_CANFA	P01295 gallus gall
19	30	78.9	27	GRP_PIG	P01295 gallus gall
20	30	78.9	28	GRP_ALIMI	P31886 alligator m
21	30	78.9	120	NEUB_XENLA	P43443 xenopus lae
22	30	78.9	134	GRP_SHEEP	P47851 ovis aries
23	30	78.9	147	GRP_RAT	P24393 rattus norv
24	30	78.9	148	GRP_HUMAN	P07492 homo sapien
25	30	78.9	155	GRP_BOMOR	P29007 bomblina ori
26	30	78.9	250	AGL8_SOLCO	O22328 solanum com
27	30	78.9	361	IHA_TRIIVU	O77755 trichosurus
28	30	78.9	366	IHA_HUMAN	P05111 homo sapien
29	30	78.9	367	IHA_HORSE	P55101 equus cabal
30	30	78.9	458	GRP_YEAST	P32806 saccharomyc
31	29	76.3	219	YDRE_SCHPO	O13748 schizosacch
32	29	76.3	227	PGSA_WYCPN	P75520 mycoplasma
33	29	76.3	301	GCVA_HAEIN	P45099 haemophilus

34	29	76.3	384	1	AAPM_RHIIV	O52814 rhinobius
35	29	76.3	510	1	ACHG_XENLA	P05376 xenopus lae
36	28	73.7	197	1	YCB7_PSEDE	P29940 pseudomorus
37	28	73.7	239	1	CYSH_THIRO	P52672 thiodapsa
38	28	73.7	244	1	CYSH_BUCAT	P57501 bucinera ap
39	28	73.7	308	1	ACPL_ENTHI	P36184 entamoeba h
40	28	73.7	353	1	COA2_POVBO	P24849 bovine polio
41	28	73.7	362	1	LDOX_VITVI	P51093 vitis vitifol
42	28	73.7	406	1	UL43_VZVD	P09273 varicele
43	28	73.7	430	1	LDOX_PETHY	P51092 petunia hybr
44	28	73.7	496	1	C7B1_THIAR	P49264 thlaspi riv
45	28	73.7	543	1	CP1B_HUMAN	O16678 homo sapien

## ALIGNMENTS

RESULT	ID	ALYT_ALYOB	STANDARD:	PRT:	14 AA.
AC	P08944;				
DT	01-NOV-1988	(Rel. 09, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	ALYTESIN.				
OS	Alytes obstetricans (Midwife toad).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.				
OC	Amphibia; Batrachia; Anura; Archaeobatrachia; Discoglossidae; Alytes.				
OX	NCBI_TaxID=8443;				
RN	[1]				
RP	SEQUENCE:				
RX	MEDLINE=84131098; PubMed=6141890;				
RA	Erspermer V., Erspermer G.F., Mazzanti G., Endean R.;				
RT	*Active peptides in the skins of one hundred amphibian species from				
RT	Australia and Papua New Guinea.*;				
RL	Comp. Biochem. Physiol. 77C:99-108(1984).				
CC	-1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUREMEDIN B/RANATENSIN				
CC	FAMILY				
DR	InterPro: IPR000874; -				
DR	Pfam: PF02044; Bombesin; 1.				
DR	PROSITE: PS00257; BOMBESIN; 1.				
KW	Bombesin family; Amidation.				
FT	MOD_RES 1 1				
FT	MOD_RES 14 14				
SQ	SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;				
Query Match 92.1%; Score 35; DB 1; Length 14;					
Best local Similarity 85.7%; Pred. No. 0.17;					
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps					
QY	2 QWAVXHL 8				
Db	7 QWAVGHL 13				
RESULT 2					
ID	BOMB_BOMVA	STANDARD:	PRT:	107 AA.	
AC	P01296;				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	01-FEB-1993	(Rel. 31, Last annotation update)			
DE	BOMBESIN PRECURSOR.				
OS	Bombina variegata (Yellow-bellied toad), and				
OS	Bombina bombina (Fire-bellied toad).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.				
OX	NCBI_TaxID=8345; 8345;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=B. variegata; TISSUE=Skin;				
RX	MEDLINE=90242964; PubMed=2335218;				

RA Richter K., Egger R., Kreil G.;  
 RT "Molecular cloning of a cDNA encoding the bombesin precursor in skin  
 of Bombina variegata.";  
 RL FEBS Lett. 262:353-355(1990).  
 RP SEQUENCE OF 42-55.  
 RC SPECIES=B.variegata, and B.bombina;  
 RX MEDLINE=72163516; PubMed=4537042;  
 RA Anastasi A., Erspamer V., Buccì M.;  
 RT Isolation and amino acid sequences of alytesin and bombesin, two  
 analogous active tetradecapeptides from the skin of European  
 arch. Biochem. Biophys. 148:443-446(1972).  
 CC -1- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY  
 GASTROINTESTINAL HORMONES.  
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
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 CC -----  
 CC EMBL: X52447; CAA36686.1; -  
 DR PIR: A01564; BSTD.  
 DR PIR: B01564; BSTDY.  
 DR PIR: S09095; S09095.  
 DR InterPro: IPR000874; -  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 DR Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 24 POTENTIAL..  
 FT PEPTIDE 42 55 BOMBESIN..  
 FT MOD\_RES 42 42 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 55 55 AMIDATION (G-56 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 107 AA; 12341 MW; 9692B5060FAP618 CRC64;  
 Query Match Best Local Similarity 92.1%; Score 35; DB 1; Length 107;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 2 QMAVXHL 8  
 111111  
 48 QMAVGH 54  
 RESULT 3  
 BOMB\_BOMOR STANDARD; PRT; 119 AA.  
 AC P21591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE BOMBESIN PRECURSOR.  
 OS Bombina orientalis (Oriental fire-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 CC NCBI\_TaxID=8346;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088602; PubMed=2263631;  
 RA Spindel E.R., Gibson B.W., Reeve J.R. Jr., Kelly M.;  
 RT "Cloning of cDNAs encoding amphibian bombesin: evidence for the  
 relationship between bombesin and gastrin-releasing peptide.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9813-9817(1990).  
 CC -1- FUNCTION: STIMULATES SMOOTH MUSCLE CONTRACTION. ROLE IN INDUCTION  
 OF HYPOTHERMIA, STIMULATION OF DNA REPLICATION AND RELEASE OF MANY

CC GASTROINTESTINAL HORMONES.  
 CC -1- TISSUE SPECIFICITY: LOCALIZED TO THE CUTANEOUS GRANULOUS GLANDS IN  
 CC THE SKIN AND THE BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
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 CC -----  
 CC EMBL: M55255; AAA48551.1; -  
 DR PIR: A39261; A39261.  
 DR InterPro: IPR000874; -  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 2  
 FT PEPTIDE 45 58 BOMBESIN..  
 FT MOD\_RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 119 AA; 13863 MW; 3A3D84EA2445A44A CRC64;  
 Query Match Best Local Similarity 92.1%; Score 35; DB 1; Length 119;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 2 QMAVXHL 8  
 111111  
 51 QMAVGH 57  
 Db 51 QMAVGH 57  
 RESULT 4  
 LITO\_LITAU STANDARD; PRT; 9 AA.  
 ID LITO\_LITAU  
 AC P08945;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE LITORIN.  
 OS Litoria aurea (Australian frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyliidae;  
 CC Litoria.  
 CC NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75187011; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Amino acid composition and sequence of litorin, a bombesin-like  
 nonapeptide from the skin of the Australian leptodactylid frog  
 Litoria aurea.";  
 RL Experientia 31:510-511(1975).  
 RN [2]  
 RP SEQUENCE (METHYLATED VARIANT).  
 RX MEDLINE=78005546; PubMed=908397;  
 RA Anastasi A., Montecuccchi P.C., Angelucci F., Erspamer V., Buccì M.;  
 RT "Glu(OMe)-litorin, the second bombesin-like peptide occurring in  
 the skin of the Australian frog Litoria aurea.";  
 RL Experientia 33:1289-1289(1977).  
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 CC PIR: S07204; S07204.  
 CC PIR: S07205; S07205.  
 DR InterPro: IPR000874; -  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation; Methylation.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD.RES 2 2 METHYLATION (IN A VARIANT).  
 FT MOD.RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1103 MW; DTCCIB86ZC366 CRC64;

## Query Match

Best Local Similarity 81.6%; Score 31; DB 1; Length 9;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXH 7  
 |||||  
 Db 2 QWAVGH 7

## RESULT 5

BOML\_PSECU STANDARD; PRT; 13 AA.

ID BOML\_PSECU STANDARD; PRT; 13 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

OS BOMBESIN-LIKE PEPTIDE L (PG-L).

OC Pseudophryne guentheri (Frog).

OC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;

OC Pseudophryne

NCBI\_TaxID=30349;

RN NCBI\_TaxID=30349;

RP SEQUENCE.

RC TISSUE=Skin;

RA MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

Roberts J.D., Melchiorri P., Espamer V.,

"Six novel tachykinin- and bombesin-related peptides from the skin of

the Australian frog Pseudophryne guentheri.";

CC Peptides 11:299-304(1990).

CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN

CC FAMILY.

DR PIR: A60409; A60409.

DR InterPro: IPR000874; -

DR Pfam: PF02044; Bombesin; 1.

DR PROSITE: PS00257; BOMBESIN; 1.

KW Bombesin family; Amidation.

FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD.RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1372 MW; DEDDD24BD98C366 CRC64;

## Query Match

Best Local Similarity 81.6%; Score 31; DB 1; Length 13;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXH 7  
 |||||  
 Db 6 QWAVGH 11

## RESULT 6

RANA\_RANPI STANDARD; PRT; 82 AA.

ID RANA\_RANPI STANDARD; PRT; 82 AA.

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE RANATENSIN PRECURSOR.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

NCBI\_TaxID=8404;

RN NCBI\_TaxID=8404;

RP SEQUENCE FROM N.A.

RA MEDLINE=88330837; PubMed=2458345;

RA Krane I.M., Naylor S.L., Helin-Davis D., Chin W.W., Spindel E.R.;

RT "Molecular cloning of cDNAs encoding the human bombesin-like peptide  
 RT neuromedin B. Chromosomal localization and comparison to cDNA."  
 RT encoding its amphibian homolog ranatensin.";  
 RL J. Biol. Chem. 263:13317-13323(1988).

RN (2)

RP SEQUENCE OF 48-58.

RA Nakajima T., Tanimura T., Pisano J.J.;

"Isolation and structure of a new vasoactive polypeptide.";

RL Fed. Proc. 29:282-282(1970).

CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN

CC FAMILY.

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CC EMBL: M21552; AAA49533.1; -

DR PIR: B28945; B28945.

DR InterPro: IPR000874; -

DR Pfam: PF02044; Bombesin; 1.

DR PROSITE: PS00257; BOMBESIN; 1.

KW Bombesin family; Amidation; Cleavage on pair of basic residues

KW Signal.

FT SIGNAL 1 27 POTENTIAL.

FT PROPEP 28 47

FT PEPTIDE 48 58 RANATENSIN.

FT MOD.RES 58 58 AMIDATION (G-59 PROVIDE AMIDE GROUP).

SQ SEQUENCE 82 AA; 9159 MW; 09194FFDDE7436DE CRC64;

Query Match 81.6%; Score 31; DB 1; Length 82;  
 Best Local Similarity 83.3%; Pred. No. 6.1;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXH 7  
 |||||  
 Db 51 QWAVGH 56

## RESULT 7

YB9H\_YEAST STANDARD; PRT; 232 AA.

ID YB9H\_YEAST STANDARD; PRT; 232 AA.

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE HYPOHETICAL 26.1 KDA PROTEIN IN POP4-SH1 INTERGENIC REGION

GN YBR261C OR YBR1729.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyc

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI\_TaxID=4932;

RN NCBI\_TaxID=4932;

RP SEQUENCE FROM N.A.

RC STRAIN=S288C;

RA MEDLINE=93220397; PubMed=8465606;

RA Dolignon F., Bileau N., Grouzet M., Aigle M.;

"The complete sequence of a 19,482 bp segment located on the right

arm of chromosome II from Saccharomyces cerevisiae.";

RL Yeast 9:189-199(1993).

CC -1- SIMILARITY: TO S.POMBE SPAC168.14C.

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PROTEIN	CHAIN	24	263	NEURAL/ECTODERMAL DEVELOPMENT FACTOR IMP-L2.
CTP	DOMAIN	69	142	IG-LIKE C2-TYPE DOMAIN.
CTP	DOMAIN	184	247	IG-LIKE C2-TYPE DOMAIN.

QY	2	QMAVXHL	8
	:		
Db	74	RMAVLEHL	80

```

RESULT 10
IHA_BOVIN          STANDARD:      PRT:      360 AA.
AC P07994;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
GN INHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBL_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicular fluid;
RX MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
  Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
  Wettenhall R.E.H., Burger H.G., de Kretser D.M.,
  "Cloning and sequence analysis of cDNA species coding for the two
  subunits of inhibin from bovine follicular fluid."
RT Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
RL [2]
RN SEQUENCE OF 1-87 FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
  "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
  and beta B-inhibin/activin genes. Identification of transcription
  factor AP-2-binding sites in the 5'-flanking regions by DNase I
  footprinting."
RT Eur. J. Biochem. 226:751-764(1994).
RL CC
-1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
  SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC CC
-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC CC
  INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC CC
  INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC CC
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC CC
-----
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EMBL: M13273; AAA97414.1; -
DR EMBL: A14416; CAA01156.1; -
DR EMBL: U16237; AAB60262.1; -
DR PIR: A25732; A25732.
DR InterPro: IPR001839; -
DR InterPro: IPR002405; -
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PRO0669; INHIBIN.
DR PROSITE: PS00250; TGF-BETA_1; 1.
DR Follitropin inhibitor; Contrareceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 226
FT CHAIN 227 360
FT DISULFID 227 360
FT DISULFID 256 322
FT DISULFID 285 357
FT DISULFID 289 359
FT DISULFID 321 321
FT CARBOHYD 140 140
FT CARBOHYD 262 262
SQ SEQUENCE 360 AA; 38809 MW; FBBF385DDIEFEF46 CRC64;

Query Match      81.6%; Score 31; DB 1; Length 360;
Best Local Similarity 71.4%; Pred. No. 25;

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Matches 5; Conservative 1; Mismatches 1; Indels 1; 0;
QY 2 QNAVXHL 8
   :||| 11
Db 169 RWAYLHL 175

RESULT 11
IHA_PIG          STANDARD:      PRT:      364 AA.
AC P04087;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE INHIBIN ALPHA CHAIN PRECURSOR.
GN INHA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBL_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86287350; PubMed=3016724;
RA Mayo K.E., Cerelli G.M., Spless J., Ravlier J., Rosenfeld M.G.,
  Evans R.M., Vale W.;
  "Inhibin A-subunit cDNAs from porcine ovary and human placenta."
RT Proc. Natl. Acad. Sci. U.S.A. 83:5849-5853(1986).
RL [2]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 231-256.
RP TISSUE=Ovarian follicular fluid;
RX MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying
  Guillemin R., Niall H., Seeburg P.H.;
  "Complementary DNA sequences of ovarian follicular fluid inhibin show
  precursor structure and homology with transforming growth
  factor-beta."
RT Nature 318:659-663(1985).
RL CC
-1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS
  SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC CC
-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC CC
  INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC CC
  INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC CC
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC CC
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-----
EMBL: M13980; AAA31057.1; -
DR EMBL: X03265; CAA27019.1; -
DR PIR: A01392; WREGA.
DR PIR: A25947; A25947.
DR InterPro: IPR001839; -
DR InterPro: IPR002405; -
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PRO0669; INHIBIN.
DR PROSITE: PS00250; TGF-BETA_1; 1.
DR Follitropin inhibitor; Contrareceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 17
FT PROPEP 18 230
FT CHAIN 231 364
FT DISULFID 260 326
FT DISULFID 289 361
FT DISULFID 293 363
FT DISULFID 325 325
FT CARBOHYD 144 144
FT CARBOHYD 266 266
FT CONFLICT 120 120
FT CONFLICT 125 125
A -> T (IN REF. 2).

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 CC -----  
 DR EMBL: M32755; AAAA1437.1; -  
 DR EMBL: M32754; AAAA1437.1; JOINED.  
 DR EMBL: M36453; AAAA1435.1; -  
 DR PIR: A40905; A40905.  
 DR PIR: A41398; A41398.  
 DR PIR: A40056; A40056.  
 DR InterPro: IPR001839; -  
 DR InterPro: IPR002405; -  
 DR Pfam: PF00019; TGF-Beta\_1.  
 DR PRINTS: PR00669; INHIBIN.  
 DR PROSITE: PS00250; TGF-BETA\_1; 1.  
 DR Follitropin Inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.  
 DR SIGNAL: 1 20 POTENTIAL.  
 DR PROPEP 21 23  
 FT CHAIN 234 366 INHIBIN ALPHA CHAIN.  
 FT DISULFID 263 328 BY SIMILARITY.  
 FT DISULFID 292 363 BY SIMILARITY.  
 FT DISULFID 296 365 BY SIMILARITY.  
 FT DISULFID 327 327 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 366 AA; 39496 MW; 327A233B9FEDECDC CRC64;

Query Match 81.6%; Score 31; DB 1; Length 366;  
 Best Local Similarity 71.4%; Pred. No. 25;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 Db 176 RAAVHL 182

RESULT 14  
 ID SW16\_KLU1A STANDARD; PRT; 769 AA.  
 AC P40418;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 FT REGULATORY PROTEIN SW16 (CELL-CYCLE BOX FACTOR, CHAIN SW16) (TRANS-  
 ACTING ACTIVATOR OF HO ENDONUCLEASE GENE) (MBF SUBUNIT P90).  
 GN SW16.  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93383264; PubMed=8372350;  
 RA Koch C., Moll T., Neuberg M., Ahorn H., Nasmyth K.;  
 RT "A role for the transcription factors Mbp1 and Swi4 in progression  
 from G1 to S phase."  
 RL Science 261:1551-1557 (1993).  
 CC -!- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT  
 TRANSCRIPTION. SW14 AND SW16 ARE REQUIRED FOR FORMATION OF THE  
 CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE  
 UPSTREAM REGION OF HO (5'-CACGAAA-3') IS CALLED THE CELL CYCLE  
 BOX (CCB).  
 CC -!- SUBUNIT: MBF CONTAINS SW16 AND MBP1. SBF CONTAINS SW16 AND SW14.  
 CC -!- SIMILARITY: STRONG, TO S. POMBE CDC10.  
 CC -!- SIMILARITY: CONTAINS 2 ANK REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: X74292; CAA52345.1; -  
 DR PIR: S36657; S36657.  
 DR InterPro: IPR002110; -  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50088; ANK\_REPEAT; 2.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 2.  
 KW Transcription regulation; DNA-binding; ANK repeat; Repeat.  
 FT REPEAT 246 315 ANK 1.  
 FT REPEAT 422 451 ANK 2.  
 SQ SEQUENCE 769 AA; 86669 MW; E3A5328B4DA084FB CRC64;

Query Match 81.6%; Score 31; DB 1; Length 769;  
 Best Local Similarity 57.1%; Pred. No. 51;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 QWAVXHL 8  
 Db 409 QWVTHL 415

RESULT 15  
 ID GRP\_RANR1 STANDARD; PRT; 10 AA.  
 AC P23260;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE NEURUMEDIN C.  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=8406;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91315477; PubMed=1859413;  
 RA Conlon J.M., O'Harte F., Vaudry H.;  
 RT Primary structures of the bombesin-like neuropeptides in the  
 RT show that bombesin is not the amphibian gastrin-releasing peptide.  
 RL Biochem. Biophys. Res. Commun. 178:526-530 (1991).  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEURUMEDIN B/RANATENSIN  
 FAMILY.  
 CC PIR: PQ0177; PQ0177.  
 DR InterPro: IPR000874; -  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD.RES 10 10  
 SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0.  
 QY 3 WAVXHL 8  
 Db 4 WAVGHL 9

Search completed: October 25, 2001, 11:28:30  
 Job time: 478 sec

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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:25:22 ; Search time 76.25 Seconds

(without alignments)  
7.992 Million cell updates/sec

Title: US-09-630-333-12

Perfect score: 38

Sequence: 1 XQNAVXHL 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	14	1	BSTD
2	35	92.1	107	1	BSTDY
3	35	92.1	119	2	A39261
4	32	84.2	174	2	T45665
5	32	84.2	353	2	T34312
6	31	81.6	9	2	S07204
7	31	81.6	13	2	A60409
8	31	81.6	82	2	B28945
9	31	81.6	95	2	H83378
10	31	81.6	183	2	A75605
11	31	81.6	232	2	S32963
12	31	81.6	256	2	T48787
13	31	81.6	309	2	S41427
14	31	81.6	325	2	T17027
15	31	81.6	357	2	T17027
16	31	81.6	360	1	A25732
17	31	81.6	364	1	WERGA
18	31	81.6	366	1	JC1106
19	31	81.6	366	1	A40056
20	31	81.6	703	2	T48559
21	31	81.6	769	2	S36657
22	30	78.9	10	2	PC0177
23	30	78.9	10	2	A60647
24	30	78.9	25	2	S06263
25	30	78.9	27	1	RHPGA
26	30	78.9	27	1	RHPGA
27	30	78.9	27	1	RHPGA
28	30	78.9	120	2	A47201
29	30	78.9	134	2	I47010

30	30	78.9	138	2	A26182
31	30	78.9	147	2	A40922
32	30	78.9	148	1	B26182
33	30	78.9	155	2	A42437
34	30	78.9	170	2	S76918
35	30	78.9	250	2	T07902
36	30	78.9	252	2	A69060
37	30	78.9	283	2	B82631
38	30	78.9	311	2	H82941
39	30	78.9	318	2	H83298
40	30	78.9	366	1	A24248
41	30	78.9	375	2	T43049
42	30	78.9	453	2	T50645
43	30	78.9	458	2	S56816
44	30	78.9	505	2	T10896
45	30	78.9	691	1	S76521

#### ALIGNMENTS

RESULT 1  
BSTD  
bombesin - fire-bellied toad  
C:Species: Bombina bombina (fire-bellied toad)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998  
C:Accession: A01564  
R:Anastasi, A.; Erspamer, V.; Buccil, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin.  
A:Reference number: A01564; MWID:72163516  
A:Accession: A01564  
A:Molecule type: protein  
A:Residues: 1-14 <ANA>  
C:Superfamily: gastrin-releasing peptide  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuromodulator  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 92.1%; Score 35; DB 1; Length 14;  
Best local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gap 0.

QY 2 QNAVXHL 8  
DB 7 QNAVXHL 13

RESULT 2  
BSTDY  
bombesin precursor - yellow-bellied toad  
C:Species: Bombina variegata (yellow-bellied toad)  
C:Date: 31-Dec-1991 #sequence\_revision 01-Dec-2000 #text\_change 08-Mar-2001  
C:Accession: S09095; B01564; A01564  
R:Richter, K.; Egger, R.; Krell, G.  
FEBS Lett. 262, 353-355, 1990  
A:Title: Molecular cloning of a cDNA encoding the bombesin precursor.  
A:Reference number: S09095; MWID:90242964  
A:Accession: S09095  
A:Molecule type: mRNA  
A:Residues: 1-107 <RIC>  
R:Anastasi, A.; Erspamer, V.; Buccil, M.  
Arch. Biochem. Biophys. 148, 443-446, 1972  
A:Title: Isolation and amino acid sequences of alytesin and bombesin.  
A:Reference number: A01564; MWID:72163516  
A:Accession: B01564  
A:Molecule type: protein  
A:Residues: 42-55 <ANA>  
C:Superfamily: ranatensin  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; neuromodulator  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-41/Domain: amino-terminal propeptide #status predicted <PRO>

F:42-55/Product: bombesin #status experimental <MAT>  
 F:56-107/Domains: carboxyl-terminal propeptide #status predicted <CPN>  
 F:42/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment  
 F:55/Modified site: amidated carboxyl end (Met) (amide in mature form from following g1y

Query Match 92.1%; Score 35; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 2.5;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 ||| |  
 Db 48 QWAVGHL 54

RESULT 3  
 A39261  
 bombesin precursor - Bombina orientalis

C:Species: Bombina orientalis  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 24-Sep-1999

Accession: A39261  
 R:Latreille, P.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990

A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet

A:Reference number: A39261; MUID:91088602  
 A:Accession: A39261  
 A:Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 1-119 <SP1>

A:Cross-references: GB:M55255; NID:g211016; PIDN:AAA48551.1; PID:g211017

C:Superfamily: ranatensin  
 C:Keywords: neuropeptide

Query Match 92.1%; Score 35; DB 2; Length 119;  
 Best Local Similarity 85.7%; Pred. No. 2.8;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 ||| |  
 Db 51 QWAVGHL 57

RESULT 4

T45665  
 hypothetical protein F14P22.40 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000

Accession: T45665  
 R:Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23011  
 A:Accession: T45665

A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-174 <DAN>

A:Cross-references: EMBL:AL137082

A:Experimental source: cultivar Columbia; BAC clone F14P22

C:Genetics:  
 A:Map position: 3  
 A:Introns: 90/1; 126/3; 166/2  
 A:Note: F14P22.40

Query Match 84.2%; Score 32; DB 2; Length 174;  
 Best Local Similarity 71.4%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 ||| |  
 Db 47 EWAVDHL 53

RESULT 5  
 T34312  
 hypothetical protein F59G1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jan-2000

Accession: T34312  
 R:Latreille, P.

submitted to the EMBL Data Library, April 1996

A:Description: The sequence of C. elegans cosmid F59G1.

A:Reference number: Z21504  
 A:Accession: T34312

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA  
 A:Residues: 1-353 <LAT>

A:Cross-references: EMBL:U53332; PIDN:AACT1158.1; GSPDB:GN00020; TSP:F59G1.4

A:Experimental source: strain Bristol N2; clone F59G1

C:Genetics:  
 A:Gene: CESP:F59G1.4

A:Map position: 2  
 A:Introns: 23/1; 47/2; 83/3; 114/3; 151/1; 187/2; 229/3; 257/3; 310/1

C:Superfamily: Caenorhabditis elegans hypothetical protein F59G1.4

Query Match 84.2%; Score 32; DB 2; Length 353;  
 Best Local Similarity 71.4%; Pred. No. 33;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 ||| |  
 Db 201 EWAVNHL 207

RESULT 6  
 S07204  
 Iltorin I - Australian tree frog (Litoria aurea)

C:Species: Litoria aurea

C:Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 14-Feb-2000

Accession: S07204  
 R:Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 510-511, 1975

A:Title: Amino acid composition and sequence of Iltorin, a bombesin-like nonapeptide F

A:Reference number: S07204; MUID:75187011

A:Accession: S07204  
 A:Molecule type: protein

A:Residues: 1-9 <ANA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+05;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXHL 7  
 ||| |  
 Db 2 QWAVGH 7

RESULT 7

A60409  
 bombesin-like peptide L - frog (Pseudophryne guentheri)

C:Species: Pseudophryne guentheri

C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

Accession: A60409  
 R:Simmaco, M.; Severini, C.; De Bisse, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Mich

Peptides 11, 299-304, 1990

A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aves

A:Reference number: A60409; MUID:90287814

A:Accession: A60409  
 A:Molecule type: protein

A:Residues: 1-13 <SIM>

C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 81.6%; Score 31; DB 2; Length 13;  
 Best Local Similarity 83.3%; Pred. No. 2;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 OMVAVXH 7  
 |||||  
 DB 6 OMVAVGH 11

RESULT 8  
 B28945  
 ranatensin precursor - northern leopard frog  
 C:Species: Rana pipiens (northern leopard frog)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
 C:Accession: B28945  
 A:Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromedin  
 A:Reference number: A92667; MUID:88330837  
 A:Accession: B28945  
 A:Molecule type: mRNA  
 A:Residues: 1-82 <KRA>  
 A:Cross-references: GB:J03948; NID:g213693; PIDN:AAAA9533.1; PID:g213694  
 C:Superfamily: ranatensin  
 C:Keywords: neuropeptide

Query Match 81.6%; Score 31; DB 2; Length 82;  
 Best Local Similarity 83.3%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 OMVAVXH 7  
 |||||  
 DB 51 OMVAVGH 56

RESULT 9  
 H83378  
 hypothetical protein PA2143 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: H83378  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337  
 A:Accession: H83378  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-95 <STO>  
 A:Cross-references: GB:AE004641; GB:AE004091; NID:g9948150; PIDN:AAG0531.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA2143

Query Match 81.6%; Score 31; DB 2; Length 95;  
 Best Local Similarity 71.4%; Pred. No. 15;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 OMVAVXHL 8  
 |||||  
 DB 63 OMVAVHHL 69

RESULT 10  
 A75605  
 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
 C:Accession: A75605

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dougan, G.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans  
 A:Reference number: A75250; MUID:20036896  
 A:Accession: A75605  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-183 <WHI>  
 A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:A75605  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DRA0103  
 A:Map position: 2  
 C:Superfamily: Deinococcus radiodurans hypothetical protein DRA010

Query Match 81.6%; Score 31; DB 2; Length 183;  
 Best Local Similarity 71.4%; Pred. No. 28;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 OMVAVXHL 8  
 |||||  
 DB 49 RMVAVFHL 55

RESULT 11  
 S32963  
 hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein YBR1729  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Sep-2000  
 C:Accession: S32963; S46142  
 R:Dolignon, F.; Bileau, N.; Crouzet, M.; Aigle, M.  
 Yeast 9, 189-199, 1993  
 A:Title: The complete sequence of a 19,482 bp segment located on the right arm of  
 A:Reference number: S29348; MUID:93220397  
 A:Accession: S32963  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-232 <DOI>  
 A:Cross-references: EMBL:X70529; NID:g1907246; PIDN:CAA49926.1; PID:g29656  
 R:Aigle, M.; Bacle, M.C.; Barthe, C.; Bileau, N.; Crouzet, M.; Dolignon, F.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45940  
 A:Accession: S46142  
 A:Molecule type: DNA  
 A:Residues: 1-232 <AIG>  
 A:Cross-references: EMBL:D36130; NID:g536688; PIDN:CAA85224.1; PID:g536689; M  
 C:Genetics:  
 A:Map position: 2R  
 C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 232;  
 Best Local Similarity 71.4%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 OMVAVXHL 8  
 |||||  
 DB 139 QMCVGH 145

RESULT 12  
 T48787  
 hypothetical protein 13E11.350 [imported] - Neurospora crassa

C:Species: Neurospora crassa  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 28-Jul-2000  
 C:Accession: T48787  
 R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fairmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000  
 A:Reference number: 224541  
 A:Accession: T48787  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-256 <SCH>  
 A:Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.350  
 C:Genetics:  
 A:Gene: NCSP:13E11.350  
 A:Map position: 2  
 A:Introns: 213/2  
 C:Superfamily: Neurospora crassa hypothetical protein 13E11.350

Query Match 81.6%; Score 31; DB 2; Length 256;  
 Best Local Similarity 71.4%; Pred. No. 39;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 |||||  
 DB 162 QWCVGHL 168

RESULT 13  
 S41427  
 Cysteine proteinase (EC 3.4.22.-) Cpl precursor - Trichomonas vaginalis  
 C:Species: Trichomonas vaginalis  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 04-Feb-2000  
 C:Accession: S41427  
 R:Malinson, D.J.  
 submitted to the EMBL Data Library, January 1994  
 A:Reference number: S41425  
 A:Accession: S41427  
 A:Molecule type: mRNA  
 A:Residues: 1-309 <MAL>  
 A:Cross-references: EMBL:X77218; NID:q452291; PIDN:CAA54435.1; PID:q452292  
 A:Experimental source: 3  
 C:Genetics:  
 A:Gene: Cpl  
 C:Superfamily: papain  
 C:Keywords: cysteine proteinase; hydrolase  
 F:1-89/Domain: signal sequence #status predicted <SIG>  
 F:90-309/Product: cysteine proteinase Cpl #status predicted <MAT>  
 M:4,254,274/Active site: Cys, His, Asn #status predicted

Query Match 81.6%; Score 31; DB 2; Length 309;  
 Best Local Similarity 83.3%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QWAVXH 7  
 |||||  
 DB 126 QWAVKH 131

RESULT 14  
 F82558  
 11popolysaccharide core biosynthesis protein XF2434 [Imported] - Xylella fastidiosa (str  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: F82558  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: F82558  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-325 <SIB>  
 A:Cross-references: GB:AE004052; GB:AE003849; NID:g9107617; PIDN:AA 233  
 A:Experimental source: strain 995c  
 R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Azeiteiro, M.; Almeida, B.  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.T.; Currie  
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincaant, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marqu, S.M.V.; Martins  
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Vertovski-Almeida, S.; Vettore, A.L.  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF2434

Query Match 81.6%; Score 31; DB 2; Length 325;  
 Best Local Similarity 71.4%; Pred. No. 49;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 |||||  
 DB 6 QWVVLHL 12

RESULT 15  
 T17027  
 MYB-related transcription factor - garden snapdragon  
 C:Species: Antirrhinum majus (garden snapdragon)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T17027  
 R:Walters, R.; Selvadurai, H.R.; Oliver, I.R.; Hudson, A.  
 Cell 93, 779-789, 1998  
 A:Title: The PHANTASTICA gene encodes a MYB transcription factor involved in gr...  
 A:Reference number: Z18662; MUID:98292176  
 A:Accession: T17027  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-357 <MAI>  
 A:Cross-references: EMBL:AJ005586; NID:g3183616; PIDN:CAA06612.1; PID:g3183617  
 A:Experimental source: cultivar JI.98; Inflorescence  
 C:Genetics:  
 A:Gene: phan  
 C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat  
 C:Keywords: transcription factor

Query Match 81.6%; Score 31; DB 2; Length 357;  
 Best Local Similarity 71.4%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QWAVXHL 8  
 |||||  
 DB 330 QWAAKHL 336

Search completed: October 25, 2001, 11:25:22  
 Job time: 335 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 25, 2001, 11:23:57 ; Search time 64.17 Seconds  
(without alignments)  
2.567 Million cell updates/sec

Title: US-09-630-333-12

Perfect score: 38

Sequence: 1 XQNAVXHL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

al number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents,AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	8	1	US-08-168-390-12
2	36	94.7	8	6	5217955-35
3	36	94.7	8	6	5217955-36
4	36	94.7	9	6	5217955-13
5	36	94.7	9	6	5217955-14
6	36	94.7	9	6	5217955-15
7	36	94.7	9	6	5217955-22
8	35	92.1	8	1	US-08-168-390-11
9	35	92.1	8	2	US-08-337-127-9
10	35	92.1	8	6	5217955-32
11	35	92.1	8	6	5217955-34
12	35	92.1	9	1	US-07-619-747B-1
13	35	92.1	9	1	US-07-619-747B-2
14	35	92.1	9	1	US-07-619-747B-4
15	35	92.1	9	1	US-07-619-747B-5
16	35	92.1	9	1	US-07-619-747B-9
17	35	92.1	9	1	US-07-619-747B-10
18	35	92.1	9	1	US-07-619-747B-12
19	35	92.1	9	1	US-07-619-747B-14
20	35	92.1	9	1	US-07-619-747B-15
21	35	92.1	9	1	US-07-619-747B-17
22	35	92.1	9	1	US-07-619-747B-18
23	35	92.1	9	1	US-07-619-747B-22
24	35	92.1	9	1	US-07-619-747B-23
25	35	92.1	9	1	US-07-619-747B-24
26	35	92.1	9	1	US-07-619-747B-25
27	35	92.1	9	1	US-07-619-747B-26

28	35	92.1	9	1	US-07-619-747B-27	Sequence 17, Appl.
29	35	92.1	9	1	US-07-619-747B-28	Sequence 18, Appl
30	35	92.1	9	1	US-07-619-747B-29	Sequence 19, Appl
31	35	92.1	9	1	US-07-619-747B-30	Sequence 20, Appl
32	35	92.1	9	1	US-07-619-747B-31	Sequence 21, Appl
33	35	92.1	9	1	US-07-619-747B-32	Sequence 22, Appl
34	35	92.1	9	1	US-07-619-747B-33	Sequence 23, Appl
35	35	92.1	9	1	US-07-619-747B-34	Sequence 24, Appl
36	35	92.1	9	1	US-07-619-747B-35	Sequence 25, Appl
37	35	92.1	9	1	US-07-619-747B-36	Sequence 26, Appl
38	35	92.1	9	1	US-07-619-747B-37	Sequence 27, Appl
39	35	92.1	9	1	US-07-619-747B-38	Sequence 28, Appl
40	35	92.1	9	1	US-07-619-747B-39	Sequence 29, Appl
41	35	92.1	9	1	US-07-619-747B-40	Sequence 30, Appl
42	35	92.1	9	1	US-08-031-325A-37	Sequence 31, Appl
43	35	92.1	9	1	US-08-263-905-4	Sequence 32, Appl
44	35	92.1	9	1	US-08-263-905-5	Sequence 33, Appl
45	35	92.1	9	1	US-08-263-905-6	Sequence 34, Appl

#### ALIGNMENTS

RESULT 1  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OR INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note="The amino-terminal residue  
; comprises one of several chemical end caps."  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note="The alanine at position 6  
; is dextrorotatory alanine."  
; FEATURE:

```
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note="The carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-12
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Query Match          94.7%; Score 36; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 QMAVXHL 8
    |||||
DB 2 QMAVAHL 8
```

```
RESULT 2
5217955-35
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:35:
; LENGTH: 8
5217955-35
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```
Query Match          94.7%; Score 36; DB 6; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 QMAVXHL 8
    |||||
DB 2 QMAVAHL 8
```

```
RESULT 3
5217955-36
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:36:
; LENGTH: 8
5217955-36
```

```
Query Match          94.7%; Score 36; DB 6; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 QMAVXHL 8
    |||||
DB 2 QMAVAHL 8
```

```
RESULT 4
5217955-13
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:13:
; LENGTH: 9
5217955-13
```

```
Query Match          94.7%; Score 36; DB 6; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 2 QMAVXHL 8
    |||||
DB 2 QMAVAHL 8
```

```
RESULT 5
5217955-14
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:14:
; LENGTH: 9
5217955-14
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Query Match          94.7%; Score 36; DB 6; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 2 QMAVXHL 8
    |||||
DB 2 QMAVAHL 8
```

```
RESULT 6
5217955-15
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
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```
; FILING DATE: 15-SEP-1989
; SEQ ID NO:15
; LENGTH: 9
5217955-15

Query Match          94.7%; Score 36; DB 6; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QMAVXHL 8
        ||| |
        2 QMAVAHL 8

RESULT 7
5217955-22
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:22
; LENGTH: 9
5217955-22

Query Match          94.7%; Score 36; DB 6; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QMAVXHL 8
        ||| |
        2 QMAVAHL 8

Db

RESULT 8
US-08-168-390-11
; Sequence 11, Application US/08168390
; Patent No. 5620955
; GENERAL INFORMATION:
; APPLICANT: Knight, Martha
; APPLICANT: Takahashi, Kazayuki
; APPLICANT: Chandrasekhar, Bhaskar
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,390
; FILING DATE: Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
```

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; REFERENCE/DOCKET NUMBER: 0871.0040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note="the amino-terminal residue
; OTHER INFORMATION: comprises one of several chemical end
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note="the carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-11

Query Match          92.1%; Score 35; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QMAVXHL 8
        ||| |
        2 QMAVAHL 8

Db

RESULT 9
US-08-337-127-9
; Sequence 9, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
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FILING DATE: 10/14/88  
APPLICATION NUMBER: 07/248,771  
FILING DATE: 09/23/88  
APPLICATION NUMBER: 07/207,759  
FILING DATE: 06/16/88  
APPLICATION NUMBER: 07/204,171  
FILING DATE: 06/08/88  
APPLICATION NUMBER: 07/173,311  
FILING DATE: 03/25/88  
APPLICATION NUMBER: 07/100,571  
FILING DATE: 09/24/87  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00537/00900D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The sequence contains at  
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,  
OTHER INFORMATION: and has an methylster C-terminus (i.e., COYCH3),  
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COYOH).  
US-08-337-127-9

Query Match 92.1%; Score 35; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QWAVXHL 8  
Db 2 QWAVGHL 8  
RESULT 10  
5217955-32  
Patent No. 5217955  
APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO: 32;  
LENGTH: 8  
5217955-32

Query Match 92.1%; Score 35; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QWAVXHL 8  
Db 2 QWAVGHL 8

RESULT 11  
5217955-34

Patent No. 5217955  
APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO: 34;  
LENGTH: 8  
5217955-34  
Query Match 92.1%; Score 35; DB 6; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QWAVXHL 8  
Db 2 QWAVGHL 8  
RESULT 12  
US-07-619-747B-1  
Sequence 1, Application US/07619747B  
Patent No. 5244883  
GENERAL INFORMATION:  
APPLICANT: Cai, Ren zhi  
TITLE OF INVENTION: No. 524483apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanee Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omri M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide

FEATURE:  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: Isostere of named aminoacid  
US-07-619-747B-1

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
Db 2 QMAVGHL 8

RESULT 13  
US-07-619-747B-2  
Sequence 2, Application US/07619747B  
Patent No. 5244883

## GENERAL INFORMATION:

APPLICANT: Cal, Ren Zhi  
APPLICANT: Schally, Andrew V.,  
TITLE OF INVENTION: No. 5244883apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002

COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 5244883e  
FILING DATE: N/A

## APPLICATION NUMBER:

## FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Behr, Omri M.

REGISTRATION NUMBER: 22,940

REFERENCE/DOCKET NUMBER: SHAL3.0-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)494-5240

TELEFAX: 1-908-494-0428

TELEX: 511642 BEPATEDIN

INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: AMINO

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: Position 1 is D-Tip

OTHER INFORMATION: Position 8 is a reduced

OTHER INFORMATION: Isostere of named aminoacid

US-07-619-747B-2

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8

Db 2 QMAVGHL 8

RESULT 14  
US-07-619-747B-4

Sequence 4, Application US/07619747B  
Patent No. 5244883

## GENERAL INFORMATION:

APPLICANT: Cal, Ren Zhi

APPLICANT: Schally, Andrew V.,

TITLE OF INVENTION: No. 5244883apeptide Bombesin

TITLE OF INVENTION: Antagonists

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dr. Andrew V. Schally

STREET: 5025 Kawanne Avenue

CITY: Metairie

STATE: Louisiana

COUNTRY: USA

ZIP: 70002

COMPUTER READABLE FORM:

MEDIUM TYPE: 360K Diskette

COMPUTER: IBM PC

OPERATING SYSTEM: DOS 5.0

SOFTWARE: WP 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/619,747B

FILING DATE: 19901129

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: No. 5244883e

FILING DATE: N/A

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Behr, Omri M.

REGISTRATION NUMBER: 22,940

REFERENCE/DOCKET NUMBER: SHAL3.0-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)494-5240

TELEFAX: 1-908-494-0428

TELEX: 511642 BEPATEDIN

INFORMATION FOR SEQ ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: AMINO

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: Position 1 is 5F-D-Tip

OTHER INFORMATION: Position 8 is a reduced

OTHER INFORMATION: Isostere of named aminoacid

US-07-619-747B-4

Query Match 92.1%; Score 35; DB 1; Length 9;  
Best Local Similarity 85.7%; Pred. No. 1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
Db 2 QMAVGHL 8

RESULT 15  
US-07-619-747B-5

Sequence 5, Application US/07619747B  
Patent No. 5244883

## GENERAL INFORMATION:

APPLICANT: Cal, Ren Zhi

APPLICANT: Schally, Andrew V.,

TITLE OF INVENTION: No. 524483apeptide Bombesin  
TITLE OF INVENTION: Antagonists  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Andrew V. Schally  
STREET: 5025 Kawanne Avenue  
CITY: Metairie  
STATE: Louisiana  
COUNTRY: USA  
ZIP: 70002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 360K Diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/619,747B  
FILING DATE: 19901129  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 524483e  
FILING DATE: N/A  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Behr, Omti M.  
REGISTRATION NUMBER: 22,940  
REFERENCE/DOCKET NUMBER: SHAL3.0-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)494-5240  
TELEFAX: 1-908-494-0428  
TELEX: 511642 BEPATEDIN  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: Position 1 is D-Trp  
OTHER INFORMATION: Position 8 is a reduced  
OTHER INFORMATION: isostere of named aminoacid  
US-07-619-747B-5

Query Match 92.1%; Score 35; DB 1; Length 9;  
1st Local Similarity 85.7%; Pred.No.1.5e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

OY 2 QWAVYHL 8  
111111  
Db 2 QWAVGHL 8

Search completed: October 25, 2001, 11:23:57  
Job time: 270 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 25, 2001, 11:22:46 ; Search time 129.78 Seconds  
(without alignments)  
3.737 Million cell updates/sec

Title: US-09-630-333-12

Perfect score: 38

Sequence: 1 XQNAVXHL 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

al number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: A.Geneseq.0601.\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
5: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
6: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
15: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
16: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
23: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	7	10	AA191147
2	36	94.7	7	13	AA120585
3	36	94.7	7	13	AA132998
4	36	94.7	7	20	AA194610
5	36	94.7	8	3	AA120294
6	36	94.7	8	12	AA11241
7	36	94.7	8	12	AA11242
8	36	94.7	8	13	AA129155
9	36	94.7	8	13	AA129157
10	36	94.7	8	16	AA164911
11	36	94.7	9	11	AA109335

12	36	94.7	9	12	AA11522	Example of peptide
13	36	94.7	9	12	AA114865	Peptide analogue #
14	36	94.7	9	12	AA114866	Peptide analogue #
15	36	94.7	9	12	AA114867	Peptide analogue #
16	36	94.7	9	12	AA114873	Peptide analogue #
17	36	94.7	9	14	AA140903	Peptide analogue #
18	36	94.7	9	19	AA151195	Peptide analogue #
19	36	94.7	9	19	AA151201	Peptide analogue #
20	36	94.7	10	10	AA196113	Sequence of new ne
21	35	92.1	7	22	AA148341	Bombesin/gastrin-1
22	35	92.1	8	11	AA1404531	Non-cyclic analogue
23	35	92.1	8	12	AA111224	Linear litorin ana
24	35	92.1	8	12	AA111240	Linear litorin ana
25	35	92.1	8	12	AA114877	Peptide analogue #
26	35	92.1	8	13	AA128456	Bombesin analogue
27	35	92.1	8	13	AA128459	Bombesin analogue
28	35	92.1	8	16	AA164910	Bombesin receptor
29	35	92.1	8	19	AA150941	Bombesin antagonist
30	35	92.1	8	20	AA192740	Bombesin peptide a
31	35	92.1	8	21	AA108302	Amino acid sequenc
32	35	92.1	8	21	AA108308	Amino acid sequenc
33	35	92.1	8	22	AA172406	Bombesin analogue
34	35	92.1	9	11	AA104526	Non-cyclic analogue
35	35	92.1	9	11	AA104527	Non-cyclic analogue
36	35	92.1	9	11	AA104529	Non-cyclic analogue
37	35	92.1	9	11	AA104528	Non-cyclic analogue
38	35	92.1	9	11	AA104530	Non-cyclic analogue
39	35	92.1	9	11	AA108345	Peptide analogue
40	35	92.1	9	12	AA11520	Example of peptide
41	35	92.1	9	12	AA11521	Example of peptide
42	35	92.1	9	12	AA11525	Example of peptide
43	35	92.1	9	12	AA11529	Example of peptide
44	35	92.1	9	12	AA112033	Bombesin analogue
45	35	92.1	9	12	AA114860	Peptide analogue #

## ALIGNMENTS

RESULT 1	
ID	AA191147 standard; protein; 7 AA.
XX	
AC	AA191147;
XX	
DT	13-MAY-1990 (first entry)
DT	22-DEC-1990 (corrected)
XX	
DE	Sequence of new neuromedin C deriv.
XX	
KW	Bombesin antagonist; malignant disease; therapy; gastric
XX	
FT	Key
FT	Misc-difference 1
FT	Location/Qualifiers
FT	/label=OTHER
FT	/note="Ac-D-Gln"
FT	
FT	Misc-difference 5
FT	/label=OTHER
FT	/note="D-Ala"
FT	
FT	Misc-difference 7
FT	/label=OTHER
FT	/note="Leu-Ome"
XX	
XX	EP15367-A.
PN	
XX	
PD	10-MAY-1989.
XX	
PF	27-OCT-1988; 88EP-0310094.
XX	
PR	06-JUN-1988; 88GB-0013355.
XX	
PA	(ICIL ) IMPERIAL CHEM INDS PLC.
XX	

PI Camble R, Cotton R, Dutta AS, Hayward CF;  
 XX  
 DR WPI; 1989-139341/19.  
 XX  
 PT New Neuromedin C polypeptide derivs. -  
 PT are potent bombesin antagonist used for treating malignant  
 PT disease and conditions associated with gastrin or gastric acid  
 PT secretion  
 XX  
 PS Disclosure; Page 929; 49pp; English.  
 XX  
 CC It is a potent bombesin antagonist. It may be used for the treatment of  
 CC e.g. malignant disease, conditions associated with the over-prodn. of  
 CC bombesin and conditions associated with failure of normal physiological  
 CC control of the regulation of gastric acid secretion.  
 CC  
 CC Sequence 7 AA;  
 SQ  
 Query Match 94.7%; Score 36; DB 10; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 QMAVXHL 8  
 |||||  
 Db 1 qwavahl 7  
 RESULT 2  
 AAR20585  
 ID AAR20585 standard; Peptide; 7 AA.  
 AC AAR20585;  
 XX  
 DT 07-MAY-1992 (first entry)  
 XX  
 DE Antagonist of bombesin/GRP.  
 XX  
 KW Antitumour agent; leukaemia.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 5 /note= "D-Ala"  
 FT  
 XX EP468497-A.  
 PN  
 29-JAN-1992.  
 PF 25-JUL-1991; 91EP-0112504.  
 XX  
 PR 26-JUL-1990; 90US-0558031.  
 PA  
 XX (RICH ) MERRELL DOW PHARM INC.  
 PI Kristenansky JL;  
 XX  
 XX WPI; 1992-034251/05.  
 DR  
 XX  
 XX New peptide bombesin-GRP antagonists - used as antitumour agents  
 PT to treat e.g. leukaemia, small cell lung and prostatic carcinoma  
 PT and to inhibit gastric acid secretion.  
 PT  
 XX Claim 7; Page 12; 14pp; English.  
 PS  
 XX The peptide is modified at the N-terminal with a lauryl, palmitoyl  
 CC or esp. an octanoyl gp. The leu at position 7 may be absent. The  
 CC C-terminal (leu or his) is amidated. The peptides and derived  
 CC salts can be used to treat small cell lung carcinoma, prostatic  
 CC carcinoma, tumour tissue growth, peptide ulcers, cancer and asso-  
 CC ciated conditions, and to effect antagonism of bombesin/gastrin  
 CC releasing peptide. Dosage is 0.2-250 mg/kg daily in 1-4 doses, at

CC 5-200 mg/dose.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 94.7%; Score 36; DB 13; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0.  
 OY 2 QMAVXHL 8  
 |||||  
 Db 1 qwavahl 7  
 RESULT 3  
 AAR32998  
 ID AAR32998 standard; peptide; 7 AA.  
 AC AAR32998;  
 XX  
 DT 13-APR-1993 (first entry)  
 XX  
 DE [D-Ala1]-bombesin(7-13)amide derivs.  
 XX  
 KW Intracellular signal; inhibition; gastrointestinal tract;  
 KW litorin; Gastrin Releasing Peptide; GRP.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /label= OTHER  
 FT /note= "N-alpha-acetyl-Gln, N-alpha-octyl-Gln,  
 FT N-alpha-lauryl-Gln or N-alpha-palmityl-Gln"  
 FT Misc-difference 5 /note= "D-Ala"  
 FT Modified-site 7 /note= "amidated"  
 FT  
 XX WO9220707-A.  
 PN  
 XX 26-NOV-1992.  
 PD  
 XX 21-APR-1992; 92WO-US03287.  
 PF  
 XX 23-MAY-1991; 91US-0704863.  
 PR  
 XX (RICH ) MERRELL DOW PHARM INC.  
 PA  
 XX Edwards JV, Fanger BO;  
 PI  
 XX WPI; 1992-415707/50.  
 DR  
 XX  
 XX New bombesin peptide agonists and antagonists - stimulate or  
 PT inhibit digestion, increase susceptibility of tumours to  
 PT chemotherapeutic agents, treat gastric ulcers and tumours etc.  
 PT  
 XX Example; Page 40; 64pp; English.  
 PS  
 XX The peptides in this example are bombesin analogues. The peptides  
 CC were tested in a competitive binding assay and a Phosphatidyl Inositl.  
 CC (PI)-turnover assay in mouse pancreas. None of the peptides  
 CC demonstrated agonist activity but all inhibited PI-turnover (c.f.  
 CC stimulation produced by 100nM GRP). Analogues of bombesin are  
 CC potentially useful for growth therapy and the treatment of digestive  
 CC disorders, e.g. for stimulating digestion, stimulating growth of  
 CC tissue in the lung, pancreas and intestine, stimulating NK cell  
 CC activity against tumour cells and stimulating growth of tumours to  
 CC increase susceptibility to chemotherapeutic agents.  
 CC  
 CC Sequence 7 AA;

Query Match 94.7%; Score 36; DB 13; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 1 qwavahl 7

## RESULT 4

AAW94610  
 ID AAW94610 standard; peptide; 7 AA.

AC AAW94610;

DT 27-APR-1999 (first entry)

XX Bombesin/gastrin releasing peptide type inhibitor peptide #2.

DE Bombesin; gastrin releasing peptide; GRP; inhibitor; antagonist;  
 XX small cell lung carcinoma; tumour; frog; antimitotic; antisecretory;  
 XX peptic ulcer.

OS Synthetic.

OS Bombina bombina.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "optionally modified by octanoyl, lauroyl or  
 FT palmitoyl"

FT Modified-site 7 /note= "amidated"

XX US5834433-A.

PN 10-NOV-1998.

XX 23-FEB-1996; 96US-0960130.

XX 24-JUL-1991; 91US-0735402.

PR 26-JUL-1990; 90US-0558031.

PR 21-JUL-1994; 94US-0278692.

PR 23-MAY-1995; 95US-0447528.

PR 23-FEB-1996; 96US-0960130.

XX (RICH ) MERRELL PHARM INC.

XX Krstenansky JL;

XX WPI; 1999-141255/12.

XX New peptide antagonists of bombesin or gastrin releasing peptide -  
 PT are useful as antimitotic and antisecretory agents in treating,  
 PT e.g., small cell lung carcinoma or peptic ulcers

XX Claim 5; Column 14; 9pp; English.

XX The present sequence represents a bombesin/gastrin releasing peptide  
 CC type inhibitor peptide. The peptide may be used as an antimitotic and  
 CC antisecretory peptide. It can control growth of small cell lung and  
 CC prostatic carcinomas, and it can also inhibit gastric secretions which  
 CC are causative and symptomatic of peptic ulcers. Administration may be  
 CC oral but is preferably subcutaneous, intravenous, intramuscular or  
 CC intraperitoneal, by depot injection, by implant preparation or by  
 CC application to the mucous membranes (e.g. of the nose or bronchial  
 CC tubes) by aerosol.

XX Sequence 7 AA;

Query Match 94.7%; Score 36; DB 20; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 1 qwavahl 7

## RESULT 5

AAW94610  
 ID AAP20294 standard; peptide; 8 AA.

AC AAP20294;

DT 09-DEC-1992 (first entry)

XX Bombesin analog peptide.

XX Bombesin; hypothermic; analgesic.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= D-Glu

FT Misc-difference 5 /label= D-Ala

XX US4331661-A.

XX 25-MAY-1982.

PF 03-OCT-1980; 80US-0193621.

PR 03-OCT-1980; 80US-0193621.

XX (SALK-) SALK INST BIOLOGICA.

XX Marki WE, Brown MR, Rivier JEF;

XX WPI; 1982-48049E/23 (48049E).

XX Octa-peptide bombesin analogues - having hypothermic and  
 PT analgesic props.

XX Claim 8; Column 8; 5pp; English.

XX The peptide may be preceded by a formyl, acetyl, propionyl, acetyl  
 CC or benzoyl group at its C-terminal. The peptide may be used for  
 CC reducing the body temp. of a mammal, as well as for inducing  
 CC analgesia. It produces hypothermia when injected i.c., but not  
 CC when given i.v. or s.c. See also AAP20291-3.

XX Sequence 8 AA;

Query Match 94.7%; Score 36; DB 3; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 1 qwavahl 7

## RESULT 6

AAW94610  
 ID AAR11241 standard; Protein; 8 AA.

AC AAR11241;

DT 17-MAY-1991 (first entry)

XX Linear litorin analogue (III).

XX

KW Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 XX diabetes.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1..1  
 FT /label= D-p-chloro-phenylalanine  
 PN MO9102746-A.  
 XX  
 PD 07-MAR-1991.  
 XX  
 PF 17-AUG-1990; 90WO-US04646.  
 XX  
 PR 21-AUG-1989; 89US-0397169.  
 PR 30-MAR-1990; 90US-0502438.  
 XX  
 PA (TULSA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.  
 PI Coy DH, Moreau JP, Kim SH;  
 DR WPI; 1991-087241/12.  
 XX  
 PT New linear peptide analogues of bombesin - modified to eliminate  
 PT biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.  
 XX  
 PS Claim 18; Page 54; 58pp; English.  
 XX  
 CC This peptide is a specifically claimed example of a generic  
 CC formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to an amide and Phe 8 has been replaced  
 CC by beta-Ileu. Gly 6 has also been replaced by D-Ala.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, arteriosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological  
 CC activity.  
 CC The analogue may also be of a naturally occurring peptide  
 CC terminating at the C-terminus with a Met residue, such as the  
 CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
 CC bombesin.  
 CC See also AAR11239-242.  
 CC  
 CC Sequence 8 AA;  
 XX  
 SQ  
 Query Match 94.7%; Score 36; DB 12; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 QWAVXHL 8  
 DB 2 gwavahl 8  
 RESULT 7  
 AAR11242  
 ID AAR11242 standard; Protein; 8 AA.  
 XX  
 AC AAR11242;  
 XX  
 DT 17-MAY-1991 (first entry)  
 XX  
 DE Linear litorin analogue (IV).  
 XX  
 KW Bombesin; litorin analogue; linear; receptor affinity; cancer;  
 KW diabetes.  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Modified-site 1..1  
 FT /label=D-Phe, pentafluoro-Phe  
 FT Modified-site 6..6  
 FT /label= N-methyl-D-Ala  
 PN MO9102746-A.  
 XX  
 PD 07-MAR-1991.  
 XX  
 PF 17-AUG-1990; 90WO-US04646.  
 XX  
 PR 21-AUG-1989; 89US-0397169.  
 PR 30-MAR-1990; 90US-0502438.  
 XX  
 PA (TULSA ) ADMIN TULANE EDUCATIONAL.  
 PA (BIOM-) BIOMEASURE INC.  
 PI Coy DH, Moreau JP, Kim SH;  
 DR WPI; 1991-087241/12.  
 XX  
 PT New linear peptide analogues of bombesin - modified to eliminate  
 PT biological activity while retaining receptor affinity, for treating  
 PT cancer, diabetes, etc.  
 XX  
 PS Claim 20+21; Page 54; 58pp; English.  
 XX  
 CC These peptides are specifically claimed examples of a generic  
 CC formula. The C-terminal amino acid (Met) of the naturally occurring  
 CC peptide has been converted to a methyl ester.  
 CC The peptide is useful for treating benign or malignant tissue  
 CC proliferation, arteriosclerosis, gastrointestinal disorders and  
 CC diabetes. They act as competitive inhibitors of natural peptides,  
 CC since they bind to the cell receptors but have no biological  
 CC activity.  
 CC The analogue may also be of a naturally occurring peptide  
 CC terminating at the C-terminus with a Met residue, such as the  
 CC 10 amino acid C-terminal region of mammalian GRP or amphibian  
 CC bombesin.  
 CC See also AAR11239-242.  
 CC  
 CC Sequence 8 AA;  
 XX  
 SQ  
 Query Match 94.7%; Score 36; DB 12; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 QWAVXHL 8  
 DB 2 gwavahl 8  
 RESULT 8  
 AAR29155  
 ID AAR29155 standard; peptide; 8 AA.  
 XX  
 AC AAR29155;  
 XX  
 DT 16-APR-1993 (first entry)  
 XX  
 DE Bombesin analogue (5).  
 XX  
 KW Hepatoma; liver cancer; antagonist.  
 KW  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT MISC-difference 1  
 FT /note= "D-form residue"  
 FT Modified-site 6  
 FT /note= "NMe-D-Ala"

PI Boddgen AE, Coy DH, Kim SH, Moreau J;  
XX  
DR WPI; 1992-415466/50.  
XX  
PT Treatment of hepatoma - by admin. of admixed bombesin analogue  
PT with carrier  
XX  
PS Claim 15; Page 48; 54pp; English.  
XX  
CC The peptide is an example of a highly generic formula. It is used  
CC in a medicament for treating hepatoma. The cpd. acts as antagonist  
CC to bombesin, which has been detected in a number of human cancer  
CC lines.  
XX  
SQ Sequence 8 AA;  
  
Query Match 94.7%; Score 36; DB 13; Length 8;  
Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; gaps 0;  
  
QY 2 QWAVXHL 8  
||| ||  
||| ||  
Db 2 qwavahl 8  
  
RESULT 10  
AAW64911  
ID AAW64911 standard; peptide: 8 AA.

XX	RESULT 10
XX	AAW64911
ID	AAW64911 standard; peptide; 8 AA.
XX	
AC	AAW64911;
XX	
DT	06-JUL-1999 (first entry)
XX	
DE	Bombesin receptor antagonist.
XX	
KW	Bombesin; antagonist; chlorambucil; peptic ulcer; pancreaticitis;
KW	eating disorder; diabetes; acromegaly; enterocutaneous fistula;
KW	psoriasis; growth retardation; gastrointestinal motility disorder;
KW	antitumour.
XX	
OS	Synthetic.
XX	
Key	
FT	1 Location/Qualifiers
FT	Modified-site
FT	/note="The amino terminal is acylated with acetyl bromoacetyl, chloroacetyl, [bis(2-chloroethyl) L-phenylalanine or a chlorambucil group"
FT	8
FT	/note="The carboxy terminal is in the form of an ethyl ester"
XX	
PN	W09500542-A1.
XX	
PD	05-JAN-1995.
XX	
PF	15-JUN-1994; 94WO-US06757.
XX	
XX	17-DEC-1993; 93US-0168390.
PR	18-JUN-1993; 93US-0078062.
XX	
PA	(PEPT-) PEPTIDE TECHNOLOGIES CORP.
XX	
PI	Chandrasekhar B, Knight M, Takahashi K;
XX	
DR	WPI; 1995-052004/07.
XX	
PT	New bombesin, gastrin releasing peptide or Neuromedin B or C, Lys.
PT	- antagonists for treating conditions such as gastrointestinal disorders, psoriasis and cancers
XX	
PS	Claim 6; Page 34; 45pp; English.
XX	

CC The patent discloses (1) the peptide sequence of bombesin (BBN),  
 CC gastrin releasing peptide (GRP), Neuromedin B or Neuromedin C,  
 CC the peptide sequence having a chlorambucil group attached to the  
 CC amino terminal; (2) a BBN receptor antagonist of formula  
 CC R4-His-Trp-Ala-R1-R2-His-R3-CO-CH2CH3; and (3) a BBN receptor  
 CC antagonist of formula R4-Asn-R5-Trp-Ala-Val-R2-His-Leu-CO-CH2CH3.  
 CC In these formulae, R1 = Val or Thr; R2 = Gly or D-Ala; R3 = Leu or  
 CC Phe; R4 = N-acetyl, bromoacetyl, chloroacetyl, [bis(2-chloroethyl)-  
 CC amino]-L-phenylalanine or a chlorambucil group; and R5 = Gln or His.  
 CC The compounds act as potent BBN/GRP-like peptide antagonists. They  
 CC can be used to inhibit the growth of cells that are sensitive to the  
 CC growth-promoting effects of BBN, GRP or a related peptide such as  
 CC pancreatic cells, gastric cells, neurons, hypothalamic cells and  
 CC cancerous cells or tumours. They can also be used to inhibit the  
 CC binding of BBN, GRP or a related peptide to cells capable of such  
 CC binding. They can be used for treating e.g. peptic ulcer, pancreatitis,  
 CC eating disorders, diabetes, acromegaly, enterocutaneous fistula,  
 CC psoriasis, growth retardation, gastrointestinal motility disorders or  
 CC tumours. The terminal structures of the compounds protect them from  
 CC in vivo proteolysis and provide highly potent antagonist effects that  
 CC persist for extended periods of time upon administration.

SO Sequence 8 AA;

Query Match 94.7%; Score 36; DB 16; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 2 qwawahl 8

RESULT 11

AA09335  
 ID AAR09335 standard; peptide; 9 AA.

AC AAR09335;

DT 30-MAR-1992 (first entry)

DE Sequence of Bombesin receptor peptide ligand with irreversible  
 DE effects.

KW Bombesin receptor; agonist; antagonist.

PA Key Location/Qualifiers

Modified-site 1

/label= H-pMeI

/note= "pMeI= p-bis (2-chloroethyl)

amino-L-phenylalanine"

Modified-site 9

/label= Met-NH2

WO9001037-A.

08-FEB-1990.

19-JUL-1989; 89WO-EP00842.

28-MAR-1989; 89GB-0006900.

21-JUL-1988; 88GB-0017379.

(FARM ) FARMITALIA C ERBA SPA.

de Castiglione R, Galantino M, Corradi F, Gozzini L, Ciomei M;

Molinaro I;

WPI; 1990-067161/09.

Bombesin receptor peptide ligands with irreversible effects - as

agonists and antagonists both weak and strong

XX Claim 2; Page 26; 32pp; English.

PS The inventors claim 36 peptides. Also claimed are:

CC (a) pharmaceutical prepn. of a peptide of the invention; (b) prepn.

CC of the peptides.

SO Sequence 9 AA;

Query Match 94.7%; Score 36; DB 11; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
 |||||  
 Db 2 qwawahl 8

RESULT 12

AA01522  
 ID AAR11522 standard; Protein; 9 AA.

AC AAR11522;

DT 13-JUN-1991 (first entry)

DE Example of peptide agonist of GRP, neuromedin, bombesin and litorin.

KW Non-malignant proliferative disease; cancer.

PA Key Location/Qualifiers

Modified-site 1.1

/label= OTHER

/note= "D-p-chlorophenylalanine"

WO9104040-A.

04-APR-1991.

17-SEP-1990; 90WO-US05271.

05-MAY-1990; 90US-0520225.

15-SEP-1989; 89US-0408125.

21-NOV-1989; 89US-0440039.

(BIOM-) BIOMEASURE INC.

Bogden AE, Moreau J-P;

WPI; 1991-117320/16.

Treatment of non malignant proliferative disease and cancer - by

administration of natural peptide or fragment selected from

gastrin-releasing peptide, neuromedin, amphibian bombesin or

litorin

Claim 22; page 54; 73pp; English.

This is a peptide analogue of mammalian gastrin releasing peptide

(GRP), neuromedin-B or -C, amphibian bombesin and litorin.

It is an agonist of these cpds. and is used to treat smooth muscle

proliferation and cancer of the prostate, breast or lung.

Residue 6 (Ala) is D-alanine.

See also AAR11519-21 and AAR11523-30.

SO Sequence 9 AA;

Query Match 94.7%; Score 36; DB 12; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QMAVXHL 8  
||||| 11  
DB 2 gwavahl 8

## RESULT 13

AAR14865  
ID AAR14865 standard; Protein; 9 AA.

XX  
AC AAR14865;

DT 14-FEB-1992 (first entry)

XX Peptide analogue #6 of litorin, GRP, neuromedin or bombesin.

DE Peptide analogue #6 of litorin, GRP, neuromedin or bombesin.

XX tissue proliferation; gastrin related peptide; peptide hormone.

OS Synthetic.

XX  
Key Modified-site 1

FT Modified-site 6 /label= D-Phe

PN WO9117181-A.

PD 14-NOV-1991.

PF 09-MAY-1991; 91WO-0003265.

PR 09-MAY-1990; 90US-0520226.

XX (TULANE ) TULANE E FUND ADMINISTRATOR.

PA (BIOM-) BIOMEASURE INC.

PI Coy DH, Kim SH, Moreau JP;

XX WPI; 1991-353721/48.

DR peptide agonists of litorin, gastrin releasing peptide -

XX neuromedin B or C or bombesin, for treating cancer, preventing

PT smooth muscle proliferation and suppressing appetite and alcohol

XX craving

PS Claim 8; Page 18; 25pp; English.

XX  
SQ The C-terminal residue is amidated. This peptide is one of 27

XX specific examples of a highly generic formula. The peptides are all

CC analogues of either litorin; the 10 amino acid C-terminal region of

CC mammalian GRP, neuromedin B or neuromedin C; or the 10 amino acid

CC C-terminal region of amphibian bombesin. They act as at least partial

CC agonists of the natural peptides. The peptide analogues are made by

CC standard methods of synthesis and can be cyclised.

CC See AAR14860-R14880 and AAR15035-R15040.

XX  
SQ Sequence 9 AA;

XX  
Query Match 94.7%; Score 36; DB 12; Length 9;

XX Best Local Similarity 85.7%; Pred. No. 3.4e+05;

XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX  
DT 14-FEB-1992 (first entry)

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Key Modified-site 1

FT Modified-site 6 /label= D-Phe

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PD 14-NOV-1991.

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CC agonists of the natural peptides. The peptide analogues are made by

CC standard methods of synthesis and can be cyclised.

CC See AAR14860-R14880 and AAR15035-R15040.

XX  
SQ Sequence 9 AA;

XX  
Query Match 94.7%; Score 36; DB 12; Length 9;

XX Best Local Similarity 85.7%; Pred. No. 3.4e+05;

XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX  
RESULT 15

XX AAR14867

XX ID AAR14867 standard; Protein; 9 AA.

XX  
AC AAR14867;

DT 14-FEB-1992 (first entry)

XX Peptide analogue #8 of litorin, GRP, neuromedin or bombesin.

DE Peptide analogue #8 of litorin, GRP, neuromedin or bombesin.

XX tissue proliferation; gastrin related peptide; peptide hormone.

OS Synthetic.

XX  
Key Location/Qualifiers

